

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVPKVKETWPK 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: PIR.76:*
2: Pirl.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	9	2	PC7073
2	4	22.2	15	2	PA0105
3	3	16.7	6	2	I49808
4	3	16.7	6	2	I65546
5	3	16.7	8	2	G33098
6	3	16.7	8	2	A61597
7	3	16.7	8	2	A35180
8	3	16.7	8	2	S53008
9	3	16.7	9	2	S77984
10	3	16.7	10	1	XASNPC
11	3	16.7	10	1	RHAQ1
12	3	16.7	10	2	PT0322
13	3	16.7	10	2	B61218
14	3	16.7	10	2	S74147
15	3	16.7	11	2	A33917
16	3	16.7	11	2	PC4267
17	3	16.7	11	2	S78765
18	3	16.7	11	2	H84082
19	3	16.7	12	2	S07206
20	3	16.7	12	2	C39109
21	3	16.7	12	2	A60757
22	3	16.7	12	2	S36899
23	3	16.7	12	2	A35585
24	3	16.7	12	2	PA0098
25	3	16.7	12	2	A61503
26	3	16.7	12	2	D20907
27	3	16.7	12	2	P00786
28	3	16.7	13	1	XAVI9B
29	3	16.7	13	2	S39413

30	3	16.7	13	2	H64124
31	3	16.7	13	2	PA0023
32	3	16.7	13	2	H44957
33	3	16.7	14	2	PS2373
34	3	16.7	14	2	PS0371
35	3	16.7	14	2	B56863
36	3	16.7	14	2	PA0015
37	3	16.7	14	2	A61002
38	3	16.7	14	2	A61308
39	3	16.7	14	2	B61308
40	3	16.7	14	2	B39111
41	3	16.7	14	2	S00150
42	3	16.7	14	2	PH1625
43	3	16.7	14	2	PH1627
44	3	16.7	14	2	PH1594
45	3	16.7	14	2	S21747
46	3	16.7	14	2	PA0044
47	3	16.7	15	2	S26791
48	3	16.7	15	2	PA0034
49	3	16.7	15	2	PA0014
50	3	16.7	15	2	FN0173
51	3	16.7	15	2	PA0059
52	3	16.7	15	2	PA0106
53	3	16.7	15	2	PA0080
54	3	16.7	15	2	S10388
55	3	16.7	15	2	S10386
56	3	16.7	15	2	B41436
57	3	16.7	15	2	A32971
58	3	16.7	15	2	PN0662
59	3	16.7	15	4	PH1613
60	3	16.7	15	4	I38032
61	3	16.7	16	2	S03532
62	3	16.7	16	2	D49021
63	3	16.7	16	2	S42237
64	3	16.7	16	2	B44896
65	3	16.7	16	2	S65709
66	3	16.7	16	2	C61414
67	3	16.7	17	2	PN0587
68	3	16.7	17	2	S03531
69	3	16.7	17	2	S50901
70	3	16.7	17	2	A48179
71	3	16.7	17	2	B61414
72	3	16.7	17	2	S89512
73	3	16.7	17	2	S69164
74	3	16.7	17	2	PD0005
75	3	16.7	18	1	PRUFDP
76	3	16.7	18	2	I52651
77	3	16.7	18	2	A25941
78	3	16.7	18	2	A56871
79	3	16.7	18	2	PN0149
80	3	16.7	18	2	I40062
81	3	16.7	18	2	A45590
82	3	16.7	18	2	A32917
83	3	16.7	18	2	G84114
84	3	16.7	18	4	S40664
85	3	16.7	19	2	C21182
86	3	16.7	19	2	S19532
87	3	16.7	19	2	S19613
88	3	16.7	19	2	B46592
89	3	16.7	19	2	S69166
90	3	16.7	20	2	A60728
91	3	16.7	20	2	S13274
92	3	16.7	20	2	S46488
93	3	16.7	20	2	C20554
94	3	16.7	20	2	H49034
95	3	16.7	20	2	S33001
96	3	16.7	20	2	S59494
97	3	16.7	20	2	S18582
98	3	16.7	20	2	T50757
99	3	16.7	20	2	A85645
100	3	16.7	20	2	A05310

hypothetical prote
protein QA300052 -
protein P18 - comm
probable IMP dehyd
hypothetical prote
photosystem I reac
seed storage prote
photosystem II oxy
hemocyanin chain 2
hemocyanin chain 4
Ig heavy chain V r
ovostatin - duck (
Ig H chain V-D-J r
Ig H chain V-D-J r
Ig H chain V-D-J r
Glutamate dehydrog
NADH2 dehydrogenas
Ig heavy chain V r
protein QA300024 -
seed storage prote
seed storage prote
protein QF200021 -
protein QF200076 -
translation elonga
Ig heavy chain J r
Ig heavy chain J r
Ig heavy chain J7
hypothetical prote
heat shock protein
major allergen Myr
chymotrypsin (EC 3
tyrosine 3-monooxy
Ig heavy chain J5
chlorophyll a/b-bi
methane monooxygen
chymotrypsin (EC 3
probable integrin
ferredoxin al - Ja
very-high-density
pigment-dispersing
brain-derived neur
Ig heavy chain J-H
retinol-binding pr
beta-Gliadine I3 -
shikimate 5-dehydr
beta-pigment-dispe
protein phosphatas
hypothetical prote
INS150A/INS150B mu
4K prothoracic tro
globin - polychaet
globin - polychaet
lactase-phlorizin
ferradoxin b - Jap
cytochrome P450 3A
ferradoxin [2Fe-2S
peptidylprolyl iso
hemocyanin subunit
nuclear antigen EB
hypothetical prote
formate dehydrogen
hypothetical prote
puik protein [impo
Amino terminal of
apolipoprotein E -

ALIGNMENTS

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RESULT 1
PC7073
ubiquinol-cytochrome-c reductase (BC 1.10.2.2) core protein II - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Jun-2002
C:Accession: PC7073
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b
A:Reference number: PC7072
A:Accession: PC7073
A:Molecule type: protein
A:Residues: 1-9 <TSU>
C:Keywords: brain; core protein; oxidoreductase

Query Match      22.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
DB      6 PKVK 9

RESULT 2
PA0105
heat shock protein dnaJ type - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0105
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0105
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: heat shock; stress-induced protein

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKET 14
DB      1 VKET 4

RESULT 3
I49808
D-SP2.5 region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I49808
R:Kurosawa, Y.; Toneyawa, S.
J. Exp. Med. 155, 201-218, 1982
A:Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity D
A:Reference number: I49808; MUID:82099938; PMID:5798155
A:Accession: I49808
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:J00432; NID:gl94370; PIDN:AAA37904.1; PID:g450452
C:Genetics:
A:Gene: Igh

Query Match      16.7%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3
DB      1

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QY      14 TMV 16
DB      2 TMV 4

RESULT 4
I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and t
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:gl99565; PIDN:AAA39663.1; PID:g554234

Query Match      16.7%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 MVP 17
DB      1 MVP 3

RESULT 5
G33098
20SK exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: G33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: G33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <NIC>

Query Match      16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GVP 9
DB      1 GVP 3

RESULT 6
A61597
cytochrome P450 AL-1 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: A61597
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto
A:Reference number: A61597; MUID:91292910; PMID:1676625
A:Accession: A61597
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <SHI>

Query Match      16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKE 13

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Db          5 VKE 7
||||
Query Match      16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C:Accession: A35180
R:Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J. Biol. Chem. 265, 5809-5815, 1990
A:Title: Purification of a novel type of calcium-activated neutral protease from rat brain
A:Reference number: A35180; MUID:90202830; PMID:2318836
A:Accession: A35180
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Keywords: hydrolase

Query Match      16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
S53008
citrate synthase - cucurbit
C:Species: Cucurbita sp. (cucurbit)
C:Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S53008
R:Kato, A.; Hayashi, M.; Mori, H.; Nishimura, M.
Plant Mol. Biol. 27, 377-390, 1995
A:Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesized
A:Reference number: S53007; MUID:95195164; PMID:788626
A:Accession: S53008
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <KAT>

Query Match      16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
S77984
cytochrome-c oxidase (EC 1.9.3.1) chain via - bigeye tuna (fragment)
C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C:Accession: S77984
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77984
A:Molecule type: protein
A:Residues: 1-9 <ARN>
A:Experimental source: heart
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: oxidative phosphorylation; respiratory chain
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match      16.7%; Score 3; DB 2; Length 9;

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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 QPE 4
          |||
Db          3 QPE 5

RESULT 10
XASNPC
angiotensin-converting enzyme inhibitor - aspic viper
C:Species: Vipera aspis (aspic viper)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
C:Accession: A60377
R:Komori, Y.; Sugihara, H.
Int. J. Biochem. 22, 767-771, 1990
A:Title: Characterization of a new inhibitor for angiotensin converting enzyme from t
A:Reference number: A60377; MUID:90382616; PMID:2169439
A:Accession: A60377
A:Molecule type: protein
A:Residues: 1-10 <KOM>
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 PKV 11
          |||
Db          6 PKV 8

RESULT 11
RHAQ1
gonadoliberin I - American alligator
N:Alternate names: gonadotropin-releasing hormone I
C:Species: Alligator mississippiensis (American alligator)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C:Accession: A60066
R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swan:
Regul. Pept. 33, 105-116, 1991
A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains
A:Reference number: A60066; MUID:91352338; PMID:1882082
A:Accession: A60066
A:Molecule type: protein
A:Residues: 1-10 <LOV>
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LQP 3
          |||
Db          7 LQP 9

RESULT 12
PT0322
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0322
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0322

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A;Molecule type: DNA
 A;Residues: 1-10 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MG V 8

DB 8 MG V 10

RESULT 13

B61218
 alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
 C;Species: Haynaldia villosa, Dasypyrum villosum
 C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
 C;Accession: B61218
 R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
 Biochem. Genet. 29, 207-211, 1991
 A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa
 A;Reference number: A61218; MUID:91315394; PMID:1859356
 A;Accession: B61218
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <SHE>
 C;Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3

DB 8 LQP 10

RESULT 14

S74147
 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 03-Jun-2002
 C;Accession: S74147
 R;Fukuda, A.; Osawa, T.; Hitomi, K.; Uchida, K.
 Arch. Biochem. Biophys. 333, 419-426, 1996
 A;Title: 4-Hydroxy-2-nonenal cytotoxicity in renal proximal tubular cells: protein modification and its inhibition by NADPH-dependent glutathione S-transferase
 A;Reference number: S74147; MUID:96404942; PMID:8809082
 A;Accession: S74147
 A;Molecule type: protein
 A;Residues: 1-10 <FUK>
 A;Experimental source: LLC-PK1 cells (renal tubular epithelial cells)
 C;Keywords: NAD; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12

DB 2 KVK 4

RESULT 15

A33917
 dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)
 C;Species: Cricetulus griseus (Chinese hamster)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997
 C;Accession: A33917
 R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989
 A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-11 <SIM>
 A;Cross-references: GB:M23652
 C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; arbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-p C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12

DB 5 KVK 7

RESULT 16

PC4267
 ribosomal protein L12.1 - rice (fragment)
 C;Species: Oryza sativa (rice)
 C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
 C;Accession: PC4267
 R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
 submitted to JIPID, April 1997
 A;Reference number: PC4267
 A;Accession: PC4267
 A;Molecule type: protein
 A;Residues: 1-11 <KAW>
 A;Experimental source: strain Japonica Nihonbare

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11

DB 7 PKV 9

RESULT 17

S78765
 ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C;Accession: S78765
 R;Graack, H.R.

submitted to the Protein Sequence Database, July 1999
 A;Reference number: S78765
 A;Accession: S78765

A;Molecule type: protein

A;Residues: 1-11 <GRA>

C;Keywords: mitochondrion

F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10

DB 5 VPK 7

RESULT 18

H84082
 hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: H84082
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;

Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: H84082
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-11 <STO>
 A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07183.1; GSPDB:GN00
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH3464

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
 |||
 Db 3 VKE 5

RESULT 19
 S07206
 kassinin - Senegal running frog
 C;Species: *Kassina senegalensis* (Senegal running frog)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Sep-2000
 C;Accession: S07206
 R;Anastasi, A.; Montecucchi, P.; Ersamer, V.; Visser, J.
 Experientia 33, 857-858, 1977
 A;Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide fro
 A;Reference number: S07206; MUID:77246385; PMID:891753
 A;Accession: S07206
 A;Molecule type: protein
 A;Residues: 1-12 <ANA>
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end
 F;12/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
 |||
 Db 2 VPK 4

RESULT 20
 C39109
 hypothetical 1.2K protein - hepatitis C virus
 N;Alternate names: hypothetical protein 3
 C;Species: hepatitis C virus
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
 C;Accession: C39109; JQ1586
 R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
 A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identificati
 A;Reference number: A39109; MUID:91156678; PMID:1705704
 A;Accession: C39109
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-12 <HAN>

A;Cross-references: GB:M58406
 R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A;Title: Cloning and sequencing of the structural region and expression of putative core
 A;Reference number: JQ1584; MUID:92300349; PMID:1318944
 A;Accession: JQ1586
 A;Molecule type: genomic RNA
 A;Residues: 1-12 <KUM>
 A;Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GVP 9
 |||
 Db 6 GVP 8

RESULT 21
 A60757
 enterotoxin C-1 - *Staphylococcus aureus* (fragments)
 C;Species: *Staphylococcus aureus*
 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 30-Sep-1993
 C;Accession: A60757
 R;Bohach, G.A.; Handley, J.P.; Schlievert, P.M.
 Infect. Immun. 57, 23-28, 1989
 A;Title: Biological and immunological properties of the carboxyl terminus of staphylo
 A;Reference number: A60757; MUID:89079292; PMID:2909489
 A;Accession: A60757
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <BOH>

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 |||
 Db 4 KVK 6

RESULT 22
 S36899
 ribosomal protein S6 - *Mycobacterium bovis* (fragment)
 C;Species: *Mycobacterium bovis*
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C;Accession: S36899
 R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from *Mycc*
 A;Reference number: S36887; MUID:94009653; PMID:8405418
 A;Accession: S36899
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <OHA>
 C;Keywords: protein biosynthesis; ribosome

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIM 6
 |||
 Db 5 EIM 7

RESULT 23
 A35585
 cytokinin-binding factor 1 - durum wheat
 C;Species: *Triticum durum* (durum wheat)
 C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
 C;Accession: A35585
 R;Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.;
 Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988
 A;Title: Characterization of a benzyladenine binding-site peptide isolated from a whe
 by mass spectrometry.
 A;Reference number: A35585; MUID:88320357; PMID:3413067
 A;Accession: A35585
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <BRI>

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3
 |||
 Db 3 LQP 5

RESULT 24

PA0098
 ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0098
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
 A;Reference number: PA0051
 A;Accession: PA0098
 A;Molecule type: protein
 A;Residues: 1-12 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPK 10
 |||
 Db 6 VPK 8

RESULT 25

A61503
 sterol carrier protein-2-like protein - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
 C;Accession: A61503
 R;Reinhart, M.P.; Avarit, S.J.; Foglia, T.
 Comp. Biochem. Physiol. B 100, 243-248, 1991
 A;Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken
 A;Reference number: A61503; PMID:92191564; PMID:1799965
 A;Accession: A61503
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <REI>

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKV 11
 |||
 Db 6 PKV 8

RESULT 26

D20907
 Ig kappa-1 chain J4 segment (b95 allotype) - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 05-Nov-1999
 C;Accession: D20907; D53275
 R;Emorine, L.; Max, E.E.
 Nucleic Acids Res. 11, 8877-8890, 1983
 A;Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
 A;Reference number: A20907; PMID:84169523; PMID:6324107
 A;Accession: D20907
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-12 <EMO>
 A;Cross-references: GB:X00231; NID:g1577; PIDN:CAA25049.1; PID:e8275; PID:g1364234
 R;Ayadi, H.; Marche, P.N.; Cazenave, P.A.
 Immunogenetics 34, 201-207, 1991

A;Title: Evolution of the rabbit immunoglobulin kappa chain genes.
 A;Reference number: A53275; PMID:91372868; PMID:1909995

A;Accession: D53275

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <AYA>

A;Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:P:56166)
 C;Comment: This J4 segment may not be functional because of a short space between the
 C;Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
 |||
 Db 7 TMV 9

RESULT 27

PQ0786
 NADH2 dehydrogenase (EC 1.6.99.3) 26K chain - fava bean mitochondrion (fragment)
 N;Alternate names: complex I 26K chain; NADH-ubiquinone reductase 26K chain
 C;Species: mitochondrion Vicia faba (fava bean)
 C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
 C;Accession: PQ0786
 R;Letierme, S.; Boutry, M.
 Plant Physiol. 102, 435-443, 1993
 A;Title: Purification and preliminary characterization of mitochondrial complex I (N/
 A;Reference number: PQ0775; PMID:94151437; PMID:8108509
 A;Accession: PQ0786
 A;Molecule type: protein
 A;Residues: 1-12 <LET>

C;Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of th

C;Genetics: ranging from 5K to 75K.

C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinon

A;Genome: mitochondrion

C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
 |||
 Db 3 GVP 5

RESULT 28

XAV19B
 angiotensin-converting enzyme inhibitor V-9 - jararaca
 C;Species: Bothrops jararaca (jararaca)
 C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
 C;Accession: A01253
 R;Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocoy, O.
 Biochemistry 10, 4033-4039, 1971
 A;Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararac
 A;Reference number: A90356; PMID:72118526; PMID:4334402
 A;Accession: A01253
 A;Molecule type: protein
 A;Residues: 1-13 <OND>

A;Note: the structure of the peptide was confirmed by synthesis

C;Comment: This peptide also potentiates bradykinin by inhibiting the kinases that i

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid

F/I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEI 5

```

Db          9 PEI 11

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 29
S39413
tubulin beta chain - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S39413
R:Ruediger, M.; Weber, K.
Eur. J. Biochem. 218, 107-116, 1993
A:Title: Characterization of the post-translational modifications in tubulin from the
A:Reference number: S39412; MUID:94062821; PMID:8243458
A:Accession: S39413
A:Molecule type: protein
A:Residues: 1-13 <RUE>
C:Superfamily: tubulin
C:Keywords: heterodimer; microtubule

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 KET 14
          |||
          11 KET 13
          |||

RESULT 30
H64124
hypothetical protein H11460 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 31-Oct-1997
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: H64124
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-13 <TIGR>
A:Cross-references: GB:U32824; GB:L42023; NID:g1574298; PID:g1574306; TIGR:H11460

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          10 KVK 12
          |||
          2 KVK 4

RESULT 31
PA0023
protein QA300052 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997
C:Accession: PA0023
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A:Reference number: PA0001
A:Accession: PA0023
A:Molecule type: protein
A:Residues: 1-13 <KAM>
A:Experimental source: seed
C:Keywords: pyrrolidone carboxylic acid; seed
F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

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Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 KET 14
          |||
          5 KET 7
          |||

RESULT 32
H44957
protein p18 - common tobacco (cv. Samsun NN) (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 30-Sep-1993
C:Accession: H44957
R:Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
Plant Cell Physiol. 31, 215-221, 1990
A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabac
A:Reference number: A44957
A:Accession: H44957
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <TAK>

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 GVP 9
          |||
          2 GVP 4

RESULT 33
PC2373
probable IMP dehydrogenase (EC 1.1.1.205) [similarity] - Bacillus cereus (strain ts-4
C:Species: Bacillus cereus
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: PC2373
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanaka, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulatio
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2373
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MAS>
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          11 VXE 13
          |||
          7 VXE 9

RESULT 34
PS0371
hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C:Species: Synechococcus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R:Phiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHI>

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A;Cross-references: GB:M86238; NID:g154574; PIDN:AAA27351.1; PID:g552030

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3
|||
Db 12 LQP 14

RESULT 35

B56863 photosystem I reaction center complex small chain psaE - Synechococcus sp. (fragment)

C;Species: Synechococcus sp.
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 23-Feb-1996

C;Accession: B56863

R;Hatanaka, H.; Sonoike, K.; Hirano, M.; Kato, S.

Biochim. Biophys. Acta 1141, 45-51, 1993

A;Title: Small subunits of Photosystem I reaction center complexes from Synechococcus el

A;Reference number: A56863; MUID:93168774; PMID:8382079

A;Accession: B56863

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <HAT>

A;Experimental source: thylakoid membranes

A;Note: sequence extracted from NCBI backbone (NCBIP:125606)

A;Note: the species was designated as Synechococcus elongatus

C;Keywords: photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12
|||
Db 6 KVK 8

RESULT 36

PA0015

seed storage protein 12S 2 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997

C;Accession: PA0015

R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JPIPD, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A;Reference number: PA0001

A;Accession: PA0015

A;Molecule type: protein

A;Residues: 1-14 <KAM>

A;Experimental source: seed

C;Keywords: pyroglutamic acid; seed; storage protein

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
|||
Db 5 GVP 7

RESULT 37

A61002

photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)

N;Alternate names: thylakoid membrane protein

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: A61002

R;Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; d

Electrophoresis 11, 528-536, 1990
A;Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequen
A;Reference number: A61002; MUID:91031404; PMID:1699755

A;Accession: A61002

A;Molecule type: protein

A;Residues: 1-14 <BAU>

C;Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
|||
Db 2 GVP 4

RESULT 38

A61308

hemocyanin chain 2 - Sahara scorpion (fragment)

C;Species: Androctonus australis (Sahara scorpion)

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C;Accession: A61308

R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in Androctonus aust:

A;Reference number: A61308; MUID:80047238; PMID:499512

A;Accession: A61308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKE 13
|||
Db 2 VKE 4

RESULT 39

B61308

hemocyanin chain 4 - Sahara scorpion (fragment)

C;Species: Androctonus australis (Sahara scorpion)

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C;Accession: B61308

R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in Androctonus aust:

A;Reference number: A61308; MUID:80047238; PMID:499512

A;Accession: B61308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKE 13
|||
Db 2 VKE 4

RESULT 40

B39111

Ig heavy chain V region - Pacific hagfish (fragment)

C;Species: Eptatretus stouti (Pacific hagfish)

C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996

C;Accession: B39111

R;Varner, J.; Neame, P.; Litman, G.W.

Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991

A;Title: A serum heterodimer from bagfish (Eptatretus stoutii) exhibits structural similarity
 A;Reference number: A39111; MUID:91156684; PMID:2000382

A;Accession: B39111
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <VAR>
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4
 Db 11 QPE 13

RESULT 41

S00150

ovostatin - duck (fragment)

C;Alternate names: ovomacroglobulin

C;Species: Anas platyrhynchos (domestic duck)

C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997

C;Accession: S00150

R;Nagase, H.; Harris Jr., E.D.; Brew, K.

J. Biol. Chem. 261, 1421-1426, 1986

A;Title: Evidence for a thiol ester in duck ovostatin (ovomacroglobulin).

A;Reference number: S00150; MUID:96111792; PMID:3511043

A;Accession: S00150

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <NAG>

A;Note: part of this sequence, including the amino end of the mature chicken and duck ph

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
 Db 10 MVP 12

RESULT 42

PH1625

Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1625

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1625

A;Molecule type: DNA

A;Residues: 1-14 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15
 Db 9 ETM 11

RESULT 43

PH1627

Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1627
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1627

A;Molecule type: DNA

A;Residues: 1-14 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15
 Db 9 ETM 11

RESULT 44

PH1594

Ig H chain V-D-J region (wild-type clone 149) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1594

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1594

A;Molecule type: DNA

A;Residues: 1-14 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 Db 6 TMV 8

RESULT 45

S21747

glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) - Pyrococcus furiosus

C;Species: Pyrococcus furiosus

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002

C;Accession: S21747

R;Robb, F.T.; Park, J.B.; Adams, M.W.W.

Biochim. Biophys. Acta 1120, 267-272, 1992

A;Title: Characterization of an extremely thermostable glutamate dehydrogenase: a key
 A;Reference number: S21747; MUID:92247806; PMID:1576153

A;Accession: S21747

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <ROB>

C;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VXE 13
 Db 1 VXE 3

RESULT 46

PA0044

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 22.5K chain - Arabidopsis thaliana (fra

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 03-Jun-2002
 C:Accession: PA0044
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of Arabidopsis thaliana (mouse-ear cress)
 A:Reference number: PA0001
 A:Accession: PA0044
 A:Molecule type: protein
 A:Residues: 1-14 <KAM>
 A:Experimental source: root
 C:Keywords: NAD; oxidative phosphorylation; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
 ||||
 Db 2 KVK 4

RESULT 47

S26791

Ig heavy chain V region (M63P2) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 02-Aug-1996 #text_change 20-Jun-2000
 C:Accession: S26791; S19879
 R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
 Eur. J. Immunol. 22, 241-245, 1992

A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family
 A:Reference number: S26786; MUID:92111632; PMID:1730251
 A:Accession: S26791
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15 <MOR>
 A:Cross-references: EMBL:X61022; NID:g32791; PIDN:CAA43356.1; PID:g1335124; EMBL:X61234;
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
 ||||
 Db 9 TMV 11

RESULT 48

PA0034

protein QA300024 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0034
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of Arabidopsis thaliana (mouse-ear cress)
 A:Reference number: PA0001
 A:Accession: PA0034
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: leaf

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 ||||
 Db 3 GVP 5

RESULT 49

PA0014

seed storage protein 12S 3 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C:Accession: PA0014
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of Arabidopsis thaliana (mouse-ear cress)
 A:Reference number: PA0001
 A:Accession: PA0014
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: seed

C:Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 ||||
 Db 5 GVP 7

RESULT 50

PN0173

seed storage protein 12S4 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001
 C:Accession: PN0173
 R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
 submitted to JIPID, December 1995

A:Description: Two dimensional electrophoresis of plant proteins and standardization of Arabidopsis thaliana (mouse-ear cress)
 A:Reference number: PN0173
 A:Accession: PN0173
 A:Molecule type: protein
 A:Residues: 1-15 <TSU>
 A:Experimental source: seeds

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 ||||
 Db 5 GVP 7

RESULT 51

PA0059

protein QP200021 - fungus (Fusarium sporotrichioides) (fragment)
 C:Species: Fusarium sporotrichioides
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C:Accession: PA0059
 R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides (fragment)
 A:Reference number: PA0051
 A:Accession: PA0059
 A:Molecule type: protein
 A:Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 ||||
 Db 10 GVP 12

RESULT 52

PA0106
protein QF200076 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0106
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0106
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12
|||
Db 11 KVK 13
|||

RESULT 53
PA0080
translation elongation factor eEF-2 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0080
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0080
A;Molecule type: protein
A;Residues: 1-15 <CHO>
C;Keywords: protein biosynthesis

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
|||
Db 8 GVP 10
|||

RESULT 54
S10388
Ig heavy chain J region (clone Rel02) - little skate (fragment)
C;Species: Raja erinacea (little skate)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Accession: S10388
R;Harding, F.A.; Cohen, N.; Litman, G.W.
Nucleic Acids Res. 18, 1015-1020, 1990
A;Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja
A;Reference number: S08462; MUID:90192082; PMID:2107524
A;Accession: S10388
A;Molecule type: DNA
A;Residues: 1-15 <HAR>
A;Cross-references: EMBL:X16146; NID:G64284; PIDN:CAA34271.1; PID:gl334773
C;Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
|||
Db 9 TMV 11
|||

RESULT 55
S10386

Ig heavy chain J region (clone Rel07) - little skate (fragment)
C;Species: Raja erinacea (little skate)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C;Accession: S10386
R;Harding, F.A.; Cohen, N.; Litman, G.W.
Nucleic Acids Res. 18, 1015-1020, 1990
A;Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja
A;Reference number: S08462; MUID:90192082; PMID:2107524
A;Accession: S10386
A;Molecule type: DNA
A;Residues: 1-15 <HAR>
A;Cross-references: EMBL:X15124
C;Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
|||
Db 9 TMV 11
|||

RESULT 56
B41436
ovoastatin - green sea turtle (fragment)
C;Species: Chelonia mydas (green sea turtle)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
C;Accession: B41436
R;Osada, T.; Sasaki, T.; Ikai, A.
J. Biochem. 103, 212-217, 1988
A;Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin
A;Reference number: A41436; MUID:88227890; PMID:2453503
A;Accession: B41436
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <OSA>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17
|||
Db 10 MVP 12
|||

RESULT 57
A32971
heparin-binding lectin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Feb-1997
C;Accession: A32971
R;Kohnke-Godt, B.; Gabius, H.J.
Biochemistry 28, 6531-6538, 1989
A;Title: Heparin-binding lectin from human placenta: purification and partial molecular
A;Reference number: A32971; MUID:90001207; PMID:2790011
A;Accession: A32971
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <KOH>
C;Keywords: heparin binding

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12
|||
Db 8 KVK 10
|||

RESULT 58

PN0662

dystrophin-associated glycoprotein A3a-I - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-Mar-1999
 C;Accession: PN0662
 R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
 A;Reference number: PN0662; MUID:94156881; PMID:8113213
 A;Accession: PN0662
 A;Molecule type: protein
 A;Residues: 1-15 <VOS>
 C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C;Keywords: glycoprotein; skeletal muscle

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
 |||
 Db 9 GVP 11

RESULT 59

PH1613
 Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1613
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1613
 A;Molecule type: DNA
 A;Residues: 1-15 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
 |||
 Db 5 TMV 7

RESULT 60

I38032
 hypothetical MNI/TEL mutant fusion protein type I - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
 C;Accession: I38032
 R;Buyls, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
 Oncogene 10, 1511-1519, 1995
 A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion
 A;Reference number: I38031; MUID:95249265; PMID:7731705
 A;Accession: I38032
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-15 <BUI>
 A;Cross-references: EMBL:X85025; NID:g971467; PIDN:CAA59398.1; PID:g971468
 C;Comment: This sequence is the chimeric product of a translocation mutation.
 C;Genetics:
 A;Gene: MNI/BTV6; MNI/TEL
 A;Map position: 22q11/12p13
 C;Keywords: fusion protein

Query Match 16.7%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3
 |||
 Db 9 LQP 11

RESULT 61

S03532
 Ig heavy chain J region (JH-7) - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
 C;Accession: S03532
 R;Schwager, J.; Grossberger, D.; du Pasquier, L.
 EMBO J. 7, 2409-2415, 1988
 A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian X.
 A;Reference number: S01158; MUID:89052653; PMID:2903824
 A;Accession: S03532
 A;Molecule type: DNA
 A;Residues: 1-16 <SCH>
 A;Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33046.1; PID:gl334660
 A;Note: the authors translated the codon AAC for residue 1 as Asp
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
 |||
 Db 10 TMV 12

RESULT 62

D49021
 Ig heavy chain J7 region - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C;Accession: D49021
 R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
 J. Exp. Med. 171, 1721-1737, 1990
 A;Title: Eleven distinct V-H gene families and additional patterns of sequence varia
 A;Reference number: A47624; MUID:90237760; PMID:2110243
 A;Accession: D49021
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-16 <HAI>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
 |||
 Db 10 TMV 12

RESULT 63

S42237
 hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
 C;Species: Staphylococcus aureus
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Oct-1999
 C;Accession: S42237
 R;Noguchi, N.; Aoki, T.; Sasatsu, M.; Kono, M.; Shishido, K.; Ando, T.
 FEMS Microbiol. Lett. 37, 283-288, 1986
 A;Title: Determination of the complete nucleotide sequence of pNS1, a staphylococcal
 A;Reference number: S42236
 A;Accession: S42237
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-16 <NOG>
 A;Cross-references: EMBL:M16217; NID:gl50832; PIDN:AAA19178.1; PID:g501833

C;Genetics:
A;Genome: plasmid pMS1

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
|||
DB 14 VKE 16

RESULT 64

B44896
heat shock protein 18 - Streptomyces albus (fragment)
C;Species: Streptomyces albus
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C;Accession: B44896
R;Giuglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.
J. Bacteriol. 173, 7374-7381, 1991
A;Title: A survey of the heat shock response in four Streptomyces species reveals two groups of heat shock proteins
A;Reference number: A44896; MUID:92041638; PMID:1682303
A;Accession: B44896
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <GUG>
A;Note: sequence extracted from NCBI backbone (NCBIP:65107)

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
|||
DB 14 VKE 16

RESULT 65

S65709
major allergen Myr p I - bulldog ant (Myrmecia pilosula) (fragment)
C;Species: Myrmecia pilosula
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S65709
R;Street, M.D.; Donovan, G.R.; Baldo, B.A.
Biochim. Biophys. Acta 1305, 87-97, 1996
A;Title: Molecular cloning and characterization of the major allergen Myr p II from the bulldog ant (Myrmecia pilosula)
A;Reference number: S65709; MUID:96180991; PMID:8605256
A;Accession: S65709
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <STR>

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
|||
DB 7 PKV 9

RESULT 66

C61414
chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)
C;Species: Pseudemys scripta (slider)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C;Accession: C61414
R;Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determination of slider turtle chymotrypsin
A;Reference number: A61414; MUID:76146602; PMID:4807189
A;Accession: C61414
A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-16 <BHA>
C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
|||
DB 2 GVP 4

RESULT 67

PN0587
tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - Japanese macaque (fragment)
N;Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
C;Species: Macaca fuscata (Japanese macaque)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
C;Accession: PN0587
R;Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A;Reference number: PN0575; MUID:93371398; PMID:7689834
A;Accession: PN0587
A;Molecule type: genomic RNA
A;Residues: 1-17 <ICH>
A;Cross-references: GB:L14801
A;Experimental source: kidney
C;Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biogenesis.
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
|||
DB 15 LQP 17

RESULT 68

S03531
Ig heavy chain J5 region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
C;Accession: S03531; C49021
R;Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis
A;Reference number: S01158; MUID:89052653; PMID:2903824
A;Accession: S03531
A;Molecule type: DNA
A;Residues: 1-17 <SCH>
A;Cross-references: EMBL:X14918; NID:964805; PIDN:CAA33044.1; PID:g1334658
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation in the immunoglobulin V region; immunoglobulin homology
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: C49021
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 3-17 <HAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
|||

```

Db      11 TMV 13

RESULT 69
S50901
Chlorophyll a/b-binding protein Lhcb4 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIa protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50901
R;Walters, R.G.; Ruban, A.V.; Horton, P.
R;J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclohexylphosphoribosylated LHCIIa and LHCIIc
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50901
A;Molecule type: protein
A;Residues: 1-17 <WAL>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosynthesis; photosynthesis

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOP 3
      |||
Db      4 LOP 6

RESULT 70
A48179
methane monooxygenase (EC 1.14.13.25) regulatory protein B - Methylococcus capsulatus (Bath)
C;Species: Methylococcus capsulatus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Accession: A48179
R;Pilkington, S.J.; Salmond, G.P.C.; Murrell, J.C.; Dalton, H.
R;FEMS Microbiol. Lett. 72, 345-348, 1990
A;Title: Identification of the gene encoding the regulatory protein B of soluble methane monooxygenase
A;Reference number: A48179
A;Accession: A48179
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <PIL>
C;Keywords: oxidoreductase

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 IMG 7
      |||
Db      10 IMG 12

RESULT 71
B61414
Chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)
C;Species: Chrysemys picta (painted turtle)
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Accession: B61414
R;Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determined from chymotrypsinogen cDNA
A;Reference number: A61414; MUID:76146602; PMID:4807189
A;Accession: B61414
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BHA>
C;Keywords: hydrolase; serine proteinase

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 IMG 7
      |||
Db      10 IMG 12

RESULT 72
S59512
probable integrin alpha3 betal - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-May-1999
C;Accession: S59512
R;McComick, J.I.; Johnstone, R.M.
Biochem. J. 311, 743-751, 1995
A;Title: Identification of the integrin alpha(3)beta(1) as a component of a partially purified integrin alpha3 betal - mouse (fragment)
A;Reference number: S59512; MUID:96067588; PMID:7487928
A;Accession: S59512
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <MCC>

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VKE 13
      |||
Db      10 VKE 12

RESULT 73
S69164
ferredoxin al - Japanese radish (fragments)
C;Species: Kaiware daikon (Japanese radish)
C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C;Accession: S69164
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Accession: S69164
A;Molecule type: protein
A;Residues: 1-17 <OBA>
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 KVK 12
      |||
Db      4 KVK 6

RESULT 74
PD0005
very-high-density lipoprotein - sand crayfish (fragment)
N;Alternate names: VHDL
C;Species: Ibacus ciliatus (sand crayfish)
C;Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: PD0005
R;Komatsu, M.; Ando, S.
Biosci. Biotechnol. Biochem. 62, 459-463, 1998
A;Title: A very-high-density lipoprotein with clotting ability from hemolymph of sand crayfish
A;Reference number: PD0005; MUID:98233268; PMID:9571775
A;Accession: PD0005
A;Molecule type: protein
A;Residues: 1-17 <KOM>
C;Comment: This protein plays an important role in the defense process of crustacea,

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 LQP 3
|||
Db 1 LQP 3

RESULT 75
DRUPPD
pigment-dispersing hormone - Atlantic sand fiddler crab
N:Alternate names: PDH
C:Species: Uca pugilator (Atlantic sand fiddler crab)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
C:Accession: A25144
R:Rao, K.R.; Riehm, J.P.; Zahnow, C.A.; Kleinholz, L.H.; Tarr, G.E.; Johnson, L.; Norton
Proc. Natl. Acad. Sci. U.S.A. 82, 5319-5322, 1985
A:Title: Characterization of a pigment-dispersing hormone in eyestalks of the fiddler cr
A:Reference number: A25144
A:Accession: A25144
A:Molecule type: protein
A:Residues: 1-18 <RAO>
C:Superfamily: pigment-dispersing hormone
C:Keywords: amidated carboxyl end; neuropeptide
F:18/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match: 16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
|||
Db 12 PKV 14

Search completed: November 25, 2003, 19:36:08
Job time : 13.3488 secs

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OM protein - protein search, using sw model
Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-21
Perfect score: 18
Sequence: 1 LQPEIMGVVKVETWPK 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	19	1	LPGE_ECOLI
2	3	16.7	7	1	E105_LITRU
3	3	16.7	8	1	VGLG_HSV2B
4	3	16.7	9	1	COXE_THUOB
5	3	16.7	10	1	BPP_VIPAS
6	3	16.7	10	1	GONI_ALIMI
7	3	16.7	10	1	UPA5_HUMAN
8	3	16.7	11	1	CS15_BACSU
9	3	16.7	12	1	PORD_METTM
10	3	16.7	12	1	TKN_KASSE
11	3	16.7	13	1	BPPI_BORJA
12	3	16.7	13	1	E121_LITRU
13	3	16.7	13	1	E122_LITRU
14	3	16.7	15	1	RS6_BACST
15	3	16.7	16	1	FIBA_MELME
16	3	16.7	16	1	FIBA_MUSVI
17	3	16.7	16	1	MMPX_SOLTU
18	3	16.7	16	1	ODPB_SOLTU
19	3	16.7	18	1	AL13_CARMA
20	3	16.7	18	1	DRPH_UCAPU
21	3	16.7	18	1	FL24_PROVU
22	3	16.7	19	1	FIBB_PIG
23	3	16.7	20	1	CS21_STRIR
24	3	16.7	20	1	LECB_IRIHO
25	3	16.7	20	1	PUFK_RHOSH
26	2	11.1	4	1	DML_PSECH
27	2	11.1	6	1	ASP2_LACSN
28	2	11.1	6	1	E101_LITRU
29	2	11.1	6	1	OVN_LEPDE
30	2	11.1	6	1	UN06_CLOPA
31	2	11.1	7	1	LANC_CARUI
32	2	11.1	7	1	TPFY_PACDA
33	2	11.1	7	1	UF04_MOUSE

34	2	11.1	7	1	WWA3_ACHFU	P35921	achatina fu
35	2	11.1	8	1	CKKN_MACEU	P30369	macropus eu
36	2	11.1	8	1	FUSS_FUSSO	P81010	fusarium so
37	2	11.1	8	1	NPB_BOVIN	P15507	bos taurus
38	2	11.1	8	1	PPK3_PERAM	P82618	periplaneta
39	2	11.1	8	1	RS7_MYCIT	P33564	mycobacteri
40	2	11.1	8	1	UH05_RAT	P35675	rattus norv
41	2	11.1	8	1	UPA3_HUMAN	P30087	homo sapien
42	2	11.1	9	1	AL10_CARMA	P81813	carcinus ma
43	2	11.1	9	1	BS43_SERPL	P83375	serattia pl
44	2	11.1	9	1	CONO_CONGE	P05486	conus geogr
45	2	11.1	9	1	FAR3_PENMO	P83318	penaeus mon
46	2	11.1	9	1	FAR4_PENMO	P83319	penaeus mon
47	2	11.1	9	1	FLA3_TREHY	P80159	treponema h
48	2	11.1	9	1	FRF1_SARBU	P83350	sarcophaga
49	2	11.1	9	1	LMT3_LOCOM	P41489	locusta mig
50	2	11.1	9	1	NEF_HV128	P12481	human immu
51	2	11.1	9	1	RT33_BOVIN	P82926	bos taurus
52	2	11.1	9	1	SAP_STOVA	P24047	stomophaute
53	2	11.1	9	1	TKCI_CALVO	P41517	calliphora
54	2	11.1	9	1	TKL1_LOCOM	P16223	locusta mig
55	2	11.1	9	1	TRP4_LEUMA	P81736	leucophaea
56	2	11.1	9	1	UF02_MOUSE	P38640	mus musculu
57	2	11.1	9	1	ULAD_HUMAN	P31929	homo sapien
58	2	11.1	9	1	ULAK_MOUSE	P99031	mus musculu
59	2	11.1	9	1	UPA7_HUMAN	P30093	homo sapien
60	2	11.1	10	1	COXA_ONCMY	P80328	oncorhynchu
61	2	11.1	10	1	COXH_ONCMY	P80331	oncorhynchu
62	2	11.1	10	1	COXK_ONCMY	P80332	oncorhynchu
63	2	11.1	10	1	FAR6_PANRE	P82660	panagrellus
64	2	11.1	10	1	GAJU_HUMAN	P01358	homo sapien
65	2	11.1	10	1	LABA_JATMU	P13270	jatropha mu
66	2	11.1	10	1	LPK2_LOCOM	P41488	locusta mig
67	2	11.1	10	1	ODP2_BOVIN	P11180	bos taurus
68	2	11.1	10	1	PNEU_HUMAN	P22103	homo sapien
69	2	11.1	10	1	PNEU_RAT	P21996	rattus norv
70	2	11.1	10	1	PORB_METTM	P80901	methanobact
71	2	11.1	10	1	RL16_ACHLA	P29221	acholeplasm
72	2	11.1	10	1	SP34_DICMG	P81545	dictyosteli
73	2	11.1	10	1	SPI_HALRO	Q10997	halocynthia
74	2	11.1	10	1	SYK_CAMPUP	Q46464	campylobact
75	2	11.1	10	1	TKL2_LOCOM	P16224	locusta mig
76	2	11.1	10	1	TKL3_LOCOM	P30249	locusta mig
77	2	11.1	10	1	TKL4_LOCOM	P30250	locusta mig
78	2	11.1	10	1	TKU2_UREUN	P40752	urechis uni
79	2	11.1	10	1	TRP5_LEUMA	P81737	leucophaea
80	2	11.1	10	1	TRP7_LEUMA	P81739	leucophaea
81	2	11.1	10	1	TRP8_LEUMA	P81740	leucophaea
82	2	11.1	10	1	TRP9_LEUMA	P81741	leucophaea
83	2	11.1	10	1	UPA4_HUMAN	P30090	homo sapien
84	2	11.1	10	1	UPA8_HUMAN	P30094	homo sapien
85	2	11.1	10	1	UPA9_HUMAN	P30095	homo sapien
86	2	11.1	10	1	URE3_MORMO	P17339	morganella
87	2	11.1	10	1	VEG6_BACSU	P80699	bacillus su
88	2	11.1	11	1	BPPB_AKHA	P01021	agkistrodon
89	2	11.1	11	1	COXA_CANFA	P99501	canis fami
90	2	11.1	11	1	HS70_PINPS	P81672	pinus pinas
91	2	11.1	11	1	MLG_THETS	P41989	theromyzon
92	2	11.1	11	1	MORN_HUMAN	P01163	homo sapien
93	2	11.1	11	1	RS30_ONCMY	P83328	oncorhynchu
94	2	11.1	11	1	TINI_HOFTI	P82651	hoplobatrach
95	2	11.1	11	1	TKC2_CALVO	P41518	calliphora
96	2	11.1	11	1	TKN1_PSEGU	P42986	pseudophryn
97	2	11.1	11	1	TKN1_UPERU	P08612	uperoleia r
98	2	11.1	11	1	TKN2_PSEGU	P42987	pseudophryn
99	2	11.1	11	1	TKN2_UPERU	P08616	uperoleia r
100	2	11.1	11	1	TKN3_PSEGU	P42988	pseudophryn

ALIGNMENTS

```
LPGE_ECOLI
ID _LPGE_ECOLI STANDARD; PRT; 19 AA.
AC P33236;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gef leader peptide.
GN GEFL OR B0018.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92048481; PubMed=1943701;
RA Poulsen L.K., Refn A., Molin S., Andersson P.;
RT "The gef gene from Escherichia coli is regulated at the level of
RT translation";
RL Mol. Microbiol. 5:1639-1648(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
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DR EMBL; AE000112; AAC73129.1; ALT_TERM.
DR EcoGene; EG12074; GefL.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0BEB CRC64;

Query Match 22.2%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVKE 13
Db 13 KVKE 16

RESULT 2
E105_LITRU
ID E105_LITRU STANDARD; PRT; 7 AA.
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Watnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
```

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 7 AMIDATION.
SQ SEQUENCE 7 AA; 834 MW; 6DD059076B0B5030 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEI 5
Db 4 PEI 6

RESULT 3
VGLG_HSV2B
ID _VGLG_HSV2B STANDARD; PRT; 8 AA.
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON_TER 8
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
Db 3 GVP 5

RESULT 4
COXE_THUOB
ID COXE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
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CC      MITOCHONDRIAL ELECTRON TRANSPORT.
CC      -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC      c + 2 H(2)O.
CC      -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC      -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
CC      PIR: S77984; S77984.
DR      InterPro: IPR001349; COX6A.
DR      PROSITE: PS01329; COX6A; PARTIAL.
KW      Oxidoreductase; Inner membrane; Mitochondrion.
FT      NON_TER 1
FT      NON_TER 9
FT      NON_TER 9
SQ      SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 1; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QPE 4
Db       |||
         3 QPE 5

RESULT 5
BPP VIPAS
ID      BPP VIPAS STANDARD; PRT; 10 AA.
AC      P31351;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Bradykinin-potentiating peptide (Angiotensin-converting
DE      enzyme inhibitor).
OS      Vipera aspis (Aspic viper).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC      Viperidae; Viperinae; Vipera.
OX      NCBI_TaxID=8706;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RX      MEDLINE=90382616; PubMed=2169439;
RA      Komori Y., Sugihara H.;
RT      "Characterization of a new inhibitor for angiotensin converting
RT      enzyme from the venom of Vipera aspis aspis.";
RL      Int. J. Biochem. 22:767-771(1990).
CC      -!- FUNCTION: This peptide both inhibits the activity of the
CC      angiotensin-converting enzyme and enhances the action of
CC      bradykinin by inhibiting the kinases that inactivate it.
CC      It acts as an indirect hypotensive agent.
CC      PIR: A60377; XASNPC.
DR      Hypotensive agent; Pyrrolidone carboxylic acid.
KW      MOD_RES 1
FT      MOD_RES 1
FT      MOD_RES 1
SQ      SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
Db       |||
         6 PKV 8

RESULT 6
GONI_ALLMI
ID      GONI_ALLMI STANDARD; PRT; 10 AA.
AC      P37041; P20407;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Gonadoliberin I (Gonadotropin-releasing hormone I) (LH-RH I)
DE      (Luliberin I).
OS      Alligator mississippiensis (American alligator).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC      Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX      NCBI_TaxID=8496;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Brain;
RX      MEDLINE=91352338; PubMed=1882082;
RA      Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA      Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT      "Primary structure of two forms of gonadotropin-releasing hormone
RT      from brains of the American alligator (Alligator mississippiensis).";
RL      Regul. Pept. 33:105-116(1991).
CC      -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Belongs to the GnRH family.
CC      PIR: A60066; RHAQ1.
DR      InterPro: IPR002012; GnRH.
DR      Pfam: PF00446; GnRH; 1.
DR      PROSITE: PS00473; GnRH; 1.
KW      Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT      MOD_RES 1
FT      MOD_RES 10
FT      MOD_RES 10
SQ      SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQP 3
Db       |||
         7 LQP 9

RESULT 7
UPA5_HUMAN
ID      UPA5_HUMAN STANDARD; PRT; 10 AA.
AC      P30091;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Plasma;
RX      MEDLINE=93092937; PubMed=1459097;
RA      Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA      Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA      Hochstrasser D.F.;
RT      "Plasma protein map: an update by microsequencing.";
RL      Electrophoresis 13:707-714(1992).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC      -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC      ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC      PROTEIN.
DR      SWISS-2DPAGE; P30091; HUMAN.
FT      NON_TER 1
FT      NON_TER 9
FT      VARIANT 9
FT      VARIANT 9
SQ      SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
Db       |||
         4 PKV 6

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RESULT 8
CS15_BACSU
ID _TKN KASSE STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to the SWISS-PROT data bank.
RN [2]
RP CHARACTERIZATION
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: In response to low temperature.
CC -1- CAUTION: Could not be found in the genome of B. subtilis 168.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6E6CEB6322C330 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12
Db 5 KVK 7

RESULT 9
PORD_METTMM
ID _PORD_METTMM STANDARD; PRT; 12 AA.
AC P80903;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase
delta chain) (PORD) (Pyruvic-ferredoxin oxidoreductase delta subunit)
(Fragment).
GN PORD.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases
in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CoA + CO(2) + reduced ferredoxin.
CC -1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
GAMMA CHAIN.
CC -1- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
of 80 degrees Celsius.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1241 MW; 2D54065D1BD1ADD8 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12
Db 5 KVK 7

RESULT 10
TKN_KASSE STANDARD; PRT; 12 AA.
AC P08611;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin.
OS Kassina senegalensis (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=77246385; PubMed=891753;
RA Anastasi A., Montecucchi P.C., Erspamer V., Visser J.;
RT "Amino acid composition and sequence of kassinin, a tachykinin
dodecapeptide from the skin of the African frog Kassina
senegalensis.";
RL Experientia 33:857-858(1977).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SWEETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07206; S07206.
DR PDB; 1MYU; 16-OCT-02.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW 3D-structure.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1336 MW; 91757AB89DD6DAB5 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPK 10
Db 2 VPK 4

RESULT 11
BPPI_BOTJA
ID _BPPI_BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3.1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca) and
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]

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RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RA "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.7e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 PEI 5
Db |||
9 PEI 11

RESULT 12
EI21_LITRU STANDARD; PRT; 13 AA.
AC P82097;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.7e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 10 KVK 12
Db |||
5 KVK 7

RESULT 13
EI22_LITRU STANDARD; PRT; 13 AA.
ID EI22_LITRU

AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B357322 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.7e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 10 KVK 12
Db |||
5 KVK 7

RESULT 14
RS6_BACST STANDARD; PRT; 15 AA.
ID RS6_BACST
AC P59682;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S6 (BS9) (Fragment).
GN RPSF.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RC STRAIN=10;
RX PubMed=4607606;
RA Yaguchi M., Matheson A.T., Visentin L.P.;
RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and
RT structural correspondence of 30 S ribosomal proteins from Escherichia
RT coli and Bacillus stearothermophilus.";
RL FEBS Lett. 46:296-300(1974).
CC -!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
DR HAMAP; MF00360; -; 1.
DR PROSITE; PS01048; RIBOSOMAL_S6; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1974 MW; 18C5E2E951E09572 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 EIM 6
Db |||
5 EIM 7

RESULT 15

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FIBA_MELME
ID FIBA_MELME STANDARD; PRT; 16 AA.
AC P14456;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain (Contains: Fibrinopeptide A) (Fragment).
GN FGA.
OS Meles meles (Eurasian badger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OC Meles.
OX NCBI_TaxID=9662;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19,1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
DB 3 VKE 5

RESULT 16
FIBA_MUSVI
ID FIBA_MUSVI STANDARD; PRT; 16 AA.
AC P14458;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain (Contains: Fibrinopeptide A) (Fragment).
GN FGA.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19,1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
SQ SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;

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Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
DB 3 VKE 5

RESULT 17
MMXP_SOLITU
ID MMXP_SOLITU STANDARD; PRT; 16 AA.
AC P80501;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unidentified mitochondrial matrix protein (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RC TISSUE=Tuber;
RX MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Kruft V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
RT of the protein complexes of plant mitochondria.";
RL Plant J. 9:357-368(1996).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Mitochondrion.
FT NON TER 16
SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
DB 4 VPK 6

RESULT 18
ODPB_SOLITU
ID ODPB_SOLITU STANDARD; PRT; 16 AA.
AC P81419;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
DE (EC 1.2.4.1) (PDBE1-B) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Romano; TISSUE=Tuber;
RX MEDLINE=98399821; PubMed=9729464;
RA Millar A.H., Knorrpp C., Leaver C.J., Hill S.A.;
RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and
RT identification of catalytic components in potato.";
RL Biochem. J. 334:571-576(1998).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-

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CC      acetyldihydrolipoamide + CO(2).
CC      -!- COFACTOR: THIAMINE PYROPHOSPHATE.
CC      -!- SUBUNIT: TRIMER OF TWO ALPHA AND TWO BETA SUBUNITS (BY
CC      SIMILARITY).
CC      -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW      Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW      Phosphorylation; Mitochondrion.
FT      NON_TER 16 16
SQ      SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKE 13
DB      4 VKE 6

RESULT 19
AL13 CARMA
ID      AL13 CARMA STANDARD; PRT; 18 AA.
AC      P01816;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Carcinustatin 13.
OS      Carcinus maenas (Common shore crab) (Green crab).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Portunoidae; Portunidae; Carcinus.
NCBI_TaxID=6759;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX      MEDLINE=98121193; PubMed=9461295;
RA      Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA      Thorpe A.;
RT      "Isolation and identification of multiple neuropeptides of the
RT      allatostatin superfamily in the shore crab Carcinus maenas.";
RL      Eur. J. Biochem. 250:727-734 (1997).
CC      -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC      -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW      Neuropeptide; Amidation; Multigene family.
FT      MOD_RES 18 18
FT      MOD_RES 18 18
FT      MOD_RES 18 18
SQ      SEQUENCE 18 AA; 2225 MW; 353112C8160AE27 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      11 PKV 13

RESULT 20
DRPH UCAPU
ID      DRPH UCAPU STANDARD; PRT; 18 AA.
AC      P08871;
DT      01-NOV-1988 (Rel. 09, Created)
DT      01-NOV-1988 (Rel. 09, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Pigment-dispersing hormone (PDH) (light adapting distal retinal
DE      pigment hormone) (DRPH).
OS      Uca pugilator (Atlantic sand fiddler crab) (Celuca pugilator).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae; Uca complex;
OC      Celuca.
NCBI_TaxID=6772;
RN      [1]
RP      SEQUENCE.

Rao K.R., Riehm J.P., Zahnow C.A., Kleinholz L.H., Tarr G.E.,
Johnson L., Norton S., Landau M., Semmes O.J., Sattalberg R.M.,
Jorenbj W.H., Hintz M.F.;
"Characterization of a pigment-dispersing hormone in eyestalks of the
fiddler crab Uca pugilator.";
Proc. Natl. Acad. Sci. U.S.A. 82:5319-5322(1985).
[2]
RP      SEQUENCE.
RX      MEDLINE=9330895; PubMed=8472537;
RA      Loehr J., Klein J., Webster S.G., Dirksen H.;
"Quantification, immunoaffinity purification and sequence analysis of
a pigment-dispersing hormone of the shore crab, Carcinus maenas
(L.).";
Comp. Biochem. Physiol. 104B:699-706(1993).
CC      -!- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT
CC      INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND
CC      THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.
CC      -!- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
DR      PIR; A25144; DRUFPD.
KW      Hormone; Amidation.
FT      DOMAIN 6 9
FT      MOD_RES 18 18
FT      MOD_RES 18 18
SQ      SEQUENCE 18 AA; 1928 MW; 25D5CE8D016F544E CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      12 PKV 14

RESULT 21
RL24 PROVU
ID      RL24 PROVU STANDARD; PRT; 18 AA.
AC      P20032;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      50S ribosomal protein L24 (Fragment).
OS      Proteus vulgaris.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Proteus.
NCBI_TaxID=585;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89125589; PubMed=2464692;
RA      Cerretti D.P., Matheakis L.C., Kearney K.R., Vu L., Nomura M.;
RT      "Translational regulation of the spc operon in Escherichia coli.
RT      Identification and structural analysis of the target site for S8
RT      repressor protein.";
RL      J. Mol. Biol. 204:309-329(1988).
CC      -!- FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND
CC      IS INVOLVED IN THE EARLY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT
CC      INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT.
CC      -!- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
EMBL; M36264; AAA25661.1; -.
DR      InterPro; IPR005825; Ribosomal_L24_26.
DR      ProSITE; PS01108; RIBOSOMAL_L24; PARTIAL.
KW      Ribosomal protein.
FT      NON_TER 1 1
SQ      SEQUENCE 18 AA; 2202 MW; 43606F53C5CBA57C CRC64;

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Query Match 16.7%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KET 14
 Db 14 KET 16

RESULT 22
 FIBB_PIG STANDARD; PRT; 19 AA.
 ID_FIBB_PIG
 AC P14477;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR InterPro; IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma; Sulfation.
 FT PEPTIDE 1 19 FIBRINOPEPTIDE B.
 FT MOD RES 4 4 SULFATION.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2200 MW; 09F87E44F4F3863D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKV 11
 Db 12 PKV 14

RESULT 23
 CS21_STRTR STANDARD; PRT; 20 AA.
 ID_CS21_STRTR
 AC P81621;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 21 kDa cold-shock induced protein (Fragment).
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=PB18;
 RX MEDLINE=99456673; PubMed=10525839;
 RA Perrin C., Guimont C., Braquart P., Gaillard J.L.;
 RT "Expression of a new cold shock protein of 21.5 kDa and of the major
 RT cold shock protein by Streptococcus thermophilus after cold shock.";

RL Curr. Microbiol. 39:342-347(1999).
 CC -!- INDUCTION: By cold shock.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2390 MW; 9C2CA57F266B80AD CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KET 14
 Db 5 KET 7

RESULT 24
 LECB_IRIHO STANDARD; PRT; 20 AA.
 ID_LECB_IRIHO
 AC P36231;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE N-acetyl-D-galactosamine-binding lectin subunit B (A-disaccharide-
 DE binding lectin subunit B) (Fragment).
 OS Iris hollandica (Dutch iris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
 OC Iris.
 OX NCBI_TaxID=35876;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Golden Harvest, and cv. Prof. Blaauw; TISSUE=Bulb;
 RX MEDLINE=94117801; PubMed=8125993;
 RT "Isolation and characterization of an
 RT N-acetyl-D-galactosamine-binding lectin from Dutch Iris bulbs which
 RT recognizes the blood group A disaccharide (GalNAc alpha 1-3Gal).";
 RL J. Biol. Chem. 269:7686-7673(1994).
 CC -!- FUNCTION: GAL / GALNAC-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE
 CC AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES
 CC IRRESPECTIVE OF BLOOD GROUP TYPE.
 CC -!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A AND B CHAINS.
 KW Lectin.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2246 MW; DE08DA025FD17D56 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ETM 15
 Db 10 ETM 12

RESULT 25
 PUFK_RHOSH STANDARD; PRT; 20 AA.
 ID_PUFK_RHOSH
 AC Q53121; O08033;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transcriptional regulatory protein pufK.
 GN PUFK.
 OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RX MEDLINE=96349111; PubMed=8760918;
 RA Gong L., Kaplan S.;
 RT "Translational control of puf operon expression in Rhodobacter

RT spherooides 2.4.1.1";
RL Microbiology 142:2057-2069(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RA MCGllynn P.;
RT "R.sphaeroides genes bchC, bchX, bchY, bchZ and pufo.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=20115911; PubMed=10648776;
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
RL nucleoides 2.4.1.1";
RN [3]
CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF PUBF.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S82643; AAB46798.1; --
DR EMBL: AJ010302; CAA38751.1; --
DR EMBL: AF195122; AAF24301.1; --
DR PIR: T50757; T50757.
KW Transcription regulation.
SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
DB 1 MVP 3

RESULT 26
DCML_PSECH STANDARD; PRT; 4 AA.
ID DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTL.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: PLO140; PLO140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4 4

SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MG 7
DB 1 MG 2

RESULT 27
ASP2_LACSN STANDARD; PRT; 6 AA.
ID ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82855;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5E132A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KE 13
DB 2 KE 3

RESULT 28
EI01_LITRU STANDARD; PRT; 6 AA.
ID EI01_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
||
Db 2 VP 3

RESULT 29

OVM LEPDE
ID OVM LEPDE STANDARD; PRT; 6 AA.
AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (Ldb-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=91271080; PubMed=2052497;
RA Spittels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
R Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
stimulating head peptide in the Colorado potato beetle, Leptinotarsa
decemlineata.";
RL Peptides 12:31-36(1991).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD RES 6 6
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4
||
Db 5 PE 6

RESULT 30

UN06 CLOPA
ID UN06 CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 6 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
NON_TER 6 6
FT SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI 5
||
Db 5 EI 6

RESULT 31

LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
R Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
NON_TER 7 7
FT SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
||
Db 5 QP 6

RESULT 32

TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (pdt-1).
OS Pachymedusa dactinolor (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactinolor tryptophyllin-1 (pdt-1): structural
characterization, pharmacological activity and cloning of precursor
cDNA";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:negative regulation of smooth muscle contra. .; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
MOD_RES 3 3
FT MOD_RES 7 7
AMIDATION.

```
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
DB 6 VP 7

RESULT 33
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=9500907;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
DB 1 PK 2

RESULT 34
WWA3_ACHFU
ID WWA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WWamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion; PubMed=8495720;
RX MEDLINE=93265912;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 12 KE 13
DB 2 KE 3

RESULT 35
CCKN_MACEU
ID CCKN_MACEU STANDARD; PRT; 8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC SPECIES=M.eugenii, and D.viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A43001; A43001.
DR PIR; P00012; P00012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MG 7
DB 3 MG 4

RESULT 36
FUSS_FUSSO
ID FUSS_FUSSO STANDARD; PRT; 8 AA.
AC P810T0;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocremoneycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RA Submitted (JUL-1997) to the SWISS-PROT data bank.
KW Allergen.
FT NON TER 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IM 6
DB 2 IM 3

RESULT 37
NPB_BOVIN
ID_NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Mejane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 4 QP 5

RESULT 38
PPK3_PERAM
ID_PPK3_PERAM STANDARD; PRT; 8 AA.
AC P826T8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex; PubMed=10196736;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).

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CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
DB 2 VP 3

RESULT 39
RS7_MYCIT
ID_RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN RPSG.
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1167;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC tRNA (by similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (by similarity).
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L08171; AAA25376.1; -.
DR PIR; S35538; S35538.
DR HAMAP; MF_00480; -.
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding; rRNA-binding; tRNA-binding.
FT INIT_MET 0
FT NON_TER 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
DB 7 PK 8

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RESULT 40
UHO9_RAT
ID UHO9_RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PE 4
Db 7 PE 8

RESULT 41
UPA1_HUMAN
ID UPA1_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1 1
FT UNSURE 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VP 9
Db 6 VP 7

RESULT 42
AL10_CARMA

AL10_CARMA STANDARD; PRT; 9 AA.
P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QP 3
Db 3 QP 4
RESULT 43
BS43_SERPL
ID BS43_SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against Erwinia amylovora, the fire blight pathogen."
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC E. amylovora.
DR InterPro; IPR006498; Tail tube.
DR Pfam; PF04985; Phage tube; 1.
KW Antibiotic; Bacteriocin.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GV 8
Db 5 GV 6

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RESULT 44
CONO CONGE
ID _CONO CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=8058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
DB 7 PK 8

RESULT 45
FAR3 PENMO
ID _FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP3 (SQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaisithangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 2 QP 3

RESULT 46
FAR4 PENMO
ID _FAR4 PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaisithangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 2 QP 3

RESULT 47
FLA2 TREHY
ID _FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
```

RT composed of two sheath proteins and three core proteins.";
 RL J. Gen. Microbiol. 138:2697-2706(1992).
 CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
 CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
 CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
 CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND
 CC FLAB3 (32 kDa).
 CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
 KW Flagella; Periplasmic.
 FT UNSURE 2 2
 FT UNSURE 8 9
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ET 14
 ||
 1 ET 2

RESULT 48
 FRP1_SARBU STANDARD; PRT; 9 AA.
 AC P83350;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FMRamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AMIDATION, AND FUNCTION.
 RC TISSUE=CNS;
 RX MEDLINE=22342733; PubMed=12438695;
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.
 RT "Identification in Drosophila melanogaster of the invertebrate G
 RT protein-coupled FMRamide receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
 CC junctions.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 1 QP 2

RESULT 49
 LMT3_LOCMI STANDARD; PRT; 9 AA.
 AC P41489;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 OS Locustamyotropin 3 (LOW-MT-3).
 OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.,
 RT "Isolation, identification and synthesis of locustamyotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamyotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR PIR; A61620; A61620.
 DR INTERPRO; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 3 QP 4

RESULT 50
 NEF_HVIZ8 STANDARD; PRT; 9 AA.
 AC P12481;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Negative factor (F-protein) (27 kDa protein) (3'ORF) (Fragment).
 GN NEF.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11881;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88281278; PubMed=3395517;
 RA Younko J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.;
 RT "Nucleotide sequence analysis of the env gene of a new Zairian
 RT isolate of HIV-1.";
 RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
 CC -!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating
 CC activities. It seems to down-regulate the CD4(T4) antigen.
 CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
 CC ZAIREAN MALE.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL; J03653; AAA44687.1; --
 DR HIV; J03653; NEFSJY1.
 KW AIDS; Myristate; GTP-binding.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 967 MW; 319CB325A3733878 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;

Qy 6 MG 7
Db 1 MG 2

RESULT 51
RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C.; Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 5 QP 6

RESULT 52
SAP_STOVA
ID SAP_STOVA STANDARD; PRT; 9 AA.
AC P24047;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Sperm-activating peptide (SAP).
OS Stomopneustes variolaris (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
OC Stomopneustes.
OX NCBI_TaxID=7663;
RN [1]
RP SEQUENCE, AND DISULFIDE BOND.
RC TISSUE=Egg jelly;
RX MEDLINE=92097763; PubMed=1756858;
RA Yoshino K.-I., Takao T., Shimomishi Y., Suzuki N.;
RT "Determination of the amino acid sequence of an intramolecular
RT disulfide linkage-containing sperm-activating peptide by tandem mass
RT spectrometry.";
RL FEBS Lett. 294:179-182(1991).
CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
CC THROUGH INTRACELLULAR ALKALINIZATION. TRANSIENT ELEVATIONS OF
CC CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT
CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF

CC GUANYLATE CYCLASE.
FT DISULFID 3
SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PE 4
Db 4 PE 5

RESULT 53
TKC1_CALVO
ID TKC1_CALVO STANDARD; PRT; 9 AA.
AC P41517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin I.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessal D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9
FT MOD_RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GV 8
Db 7 GV 8

RESULT 54
TKL1_LOCMI
ID TKL1_LOCMI STANDARD; PRT; 9 AA.
AC P16223;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE

CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
 ||
 Db 7 GV 8

RESULT 55
 TRP4_LEUMA
 ID TRP4 LEUMA STANDARD; PRT; 9 AA.
 AC P81736;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tachykinin-related peptide 4 (LemRP 4).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 CC Blaberidae; Leucophaea.
 CC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Midgut;
 RX MEDLINE=97053012; PubMed=8897641;
 RA Muren J.E., Naessel D.R.;
 RT "Isolation of five tachykinin-related peptides from the midgut of
 the cockroach Leucophaea maderae: existence of N-terminally extended
 RT isoforms.";
 RL Regul. Pept. 65:185-196(1996).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
 CC -!- OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: MIDGUT.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 953 MW; 2403987699C865A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MG 7
 ||
 Db 6 MG 7

RESULT 56
 UF02_MOUSE
 ID UF02 MOUSE STANDARD; PRT; 9 AA.
 AC P38640;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P3) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

RT "Separation and sequencing of familiar and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI 5
 ||
 Db 4 EI 5

RESULT 57
 ULAD_HUMAN
 ID ULAD HUMAN STANDARD; PRT; 9 AA.
 AC P31929;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
 DT SWISS-2DPAGE; P31929; HUMAN.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VK 12
 ||
 Db 2 VK 3

RESULT 58
 ULAK_MOUSE
 ID ULAK MOUSE STANDARD; PRT; 9 AA.
 AC P99031;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
 DE (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

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CC      PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.
DR      SWISS-2DPAGE; P99031; MOUSE.
FT      NON TER          9
SQ      SEQUENCE 9 AA; 1106 MW; E1E842C3240B145A CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 KV 11
DB      6 KV 7

RESULT 59
UPA7 HUMAN
ID      UPA7 HUMAN      STANDARD;      PRT;      9 AA.
AC      P30093;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Plasma;
RX      MEDLINE=93092937; PubMed=1459097;
RA      Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA      Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA      Hochstrasser D.F.;
RT      "Plasma protein map: an update by microsequencing.";
RL      Electrophoresis 13:707-714(1992).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
DR      SWISS-2DPAGE; P30093; HUMAN.
FT      NON TER          1
FT      NON TER          5
FT      NON TER          9
SQ      SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PE 4
DB      4 PE 5

RESULT 60
COXA_ONCMY
ID      COXA_ONCMY      STANDARD;      PRT;      10 AA.
AC      P80328;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX      NCBI_TaxID=8022;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Liver;
RX      MEDLINE=94237150; PubMed=8181469;
RA      Freund R., Kadenbach B.;
RT      "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT      of cytochrome c oxidase isolated from rainbow trout.";
RL      Eur. J. Biochem. 221:1111-1116(1994).
CC      -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC      OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC      -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome
CC      c + 2 H(2)O.
CC      -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR      PIR; S43630; S43630.
KW      Oxidoreductase; Inner membrane; Mitochondrion.
FT      NON TER          10
FT      NON TER          10
SQ      SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VP 9
DB      4 VP 5

RESULT 62
COXA_ONCMY
ID      COXA_ONCMY      STANDARD;      PRT;      10 AA.
AC      P80332;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Cytochrome c oxidase polypeptide Vifa-heart (EC 1.9.3.1) (Fragment).
OS      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX      NCBI_TaxID=8022;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Liver;
RX      MEDLINE=94237150; PubMed=8181469;
RA      Freund R., Kadenbach B.;
RT      "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT      of cytochrome c oxidase isolated from rainbow trout.";
RL      Eur. J. Biochem. 221:1111-1116(1994).

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OX NCB1_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RT "Identification of tissue-specific isoforms for subunits Vb and Villa
of cytochrome c oxidase isolated from rainbow trout.";
RL Bur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR; S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11
DB 3 KV 4

RESULT 63
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF6 (NGAPQPFVFP-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCB1_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRamide-related
peptides (Farpe) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 5 QP 6

RESULT 64
GAJU_HUMAN
ID GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 18-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75150968; PubMed=5538385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHU1.
DR MIM; 137220; -.
DR GO; GO:0007586; P.digestion; NAS.
FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.
FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.
SQ SEQUENCE 10 AA; 1004 MW; CFEEC6AB02C3387D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11
DB 5 KV 6

RESULT 65
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Labaditin.
OS Jatropa multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Jatropa.
OX NCB1_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=latex;
RA Kosari S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropa
multifida L. (Euphorbiaceae). Isolation and sequence determination
by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE
CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY
SEEMS TO BE BASED ON AN INTERACTION WITH C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR
TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
SQ SEQUENCE 10 AA; 1089 MW; D98AD6362D1B362 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
DB 2 GV 3

RESULT 66
LPK2_LOCMI
ID LPK2_LOCMI STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOM-PK-2) [FXPRL-amide].
OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Brain;
 RX MEDLINE=94094539; PubMed=7903606;
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustapyrokinin II from
 RT Locusta migratoria, another member of the FXPRL-amide peptide
 RT family.";
 RL Comp. Biochem. Physiol. 106C:103-109(1993).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC
 CC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 DE 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1145 MW; CFPAP4271A9D1B772 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 VP 9
 DB 3 VP 4
 RESULT 67
 ID _ODP2 BOVIN STANDARD; PRT; 10 AA.
 AC P11180;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
 DE complex (EC 2.3.1.12) (E2) (Fragment).
 GN DLAT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=88024154; PubMed=3117054;
 RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
 RT "Primary structure around the lipate-attachment site on the E2
 RT component of bovine heart pyruvate dehydrogenase complex.";
 RL Biochem. J. 245:919-922(1987).
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
 CC multiple copies of three enzymatic components: pyruvate
 CC dehydrogenase (E1), dihydrolipoamide components: pyruvate
 CC lipoyltransferase (E2), dihydrolipoamide acetyltransferase (E3) and
 CC lipoyltransferase (E3).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
 CC acetyldihydrolipoamide.
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
 CC COFACTOR.
 CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
 CC SYMMETRY.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
 CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
 DR InterPro; IPR003016; Lipoyl.
 DR PROSITE; PS00189; LIPOYL; PARTIAL.
 KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
 KW Lipoyl.

ET NON TER 1 1
 FT BINDING 5 5 LIPOYL.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1066 MW; 889BECDD1ADD33AB1 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 ET 14
 DB 2 ET 3
 RESULT 68
 ID _PNEU HUMAN STANDARD; PRT; 10 AA.
 AC P22103;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pneumadin (PNM).
 DE Pneumadin (PNM).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Lung;
 RX MEDLINE=91110910; PubMed=2274681;
 RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
 RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
 RL Regul. Pept. 30:77-87(1990).
 CC -!- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
 DR PIR; B33143; B33143.
 DR GO; GO:0030103; P:vasopressin secretion; NAS.
 KW Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GV 8
 DB 9 GV 10
 RESULT 69
 ID _PNEU RAT STANDARD; PRT; 10 AA.
 AC P21996;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pneumadin (PNM).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE, AND SYNTHESIS.
 RP TISSUE=Lung;
 RX MEDLINE=91110910; PubMed=2274681;
 RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
 RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
 RL Regul. Pept. 30:77-87(1990).
 CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
 DR PIR; A33143; A33143.
 KW Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1048 MW; 641D0DDAA723276B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
||
DB 9 GV 10

RESULT 70
PORB METTM STANDARD; PRT; 10 AA.
AC P80901;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)
DE (Fragment).
GN PORB.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
in Methanobacterium thermoautotrophicum";
RL Eur. J. Biochem. 244:862-868(1997).
CC -|- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CoA + CO(2) + reduced ferredoxin.
CC -|- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
GAMMA CHAIN.
CC -|- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
of 80 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4
||
DB 4 PE 5

RESULT 71
RL16 ACHLA STANDARD; PRT; 10 AA.
AC P292Z1;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).
GN RPLP.
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210505; PubMed=1556079;
RA Lim F.O., Sears B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
organism and Acholeplasma laidlawii deduced from two ribosomal protein
gene sequences";
RT J. Bacteriol. 174:2606-2611(1992).
RL J. Bacteriol. 174:2606-2611(1992).
CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS

CC LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
(BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL; M74771; AAA21914.1; --
DR PIR; F41839; F41839.
DR InterPro; IPR000114; Ribosomal L16.
DR PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
||
DB 4 PK 5

RESULT 72
SP34 DICMU STANDARD; PRT; 10 AA.
AC P81545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Surface protein P34 (fragment).
GN P34.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE.
RX Schreiner S.J.;
RC STRAIN=DM-7;
RT "Characterization of a surface protein in macrocysts of Dictyostelium
mucoroides";
RL Submitted (NOV-1998) to the SWISS-PROT data bank.
CC -|- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
CC REPRODUCTION.
CC -|- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
KW Cell wall.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1190 MW; 1B6A707AA3345B50 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI 5
||
DB 2 EI 3

RESULT 73
SPI HALRO STANDARD; PRT; 10 AA.
ID SPI HALRO
AC Q10597;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Serine proteinase inhibitor (Fragment).
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyridae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=96321313; PubMed=8759295;
 RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
 RT "Purification and characterization of a 58,000-Da proteinase
 inhibitor from the hemolymph of a solitary ascidian, Halocynthia
 roretzi";
 RT roretzi";
 RT Comp. Biochem. Physiol. 114B:1-9(1996).
 CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;
 [1]
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 KV 11
 ||
 Db 8 KV 9
 ||
 RESULT 74
 SYK CAMUP
 ID SYK CAMUP STANDARD; PRT; 10 AA.
 AC Q45464;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
 DE (Fragment).
 GN LYSS.
 OS Campylobacter upsaliensis.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=28080;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43954;
 RX MEDLINE=97149302; PubMed=8996110;
 RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
 RT "Characterization of Campylobacter upsaliensis fur and its
 localization in a highly conserved region of the Campylobacter
 genome";
 RT Gene 183:219-224(1996).
 RL Gene 183:219-224(1996).
 CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
 + L-lysyl-tRNA(Lys).
 CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

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 DR EMBL; L77076; AAB41342.1; -;
 DR HAMAP; MF_00252; -; 1.
 DR InterPro; IPR006195; tRNA_ligase_II.

DR PROSITE; PS50862; AA_TRNA_LIGASE_II; PARTIAL.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Magnesium.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;
 [1]
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 KE 13
 ||
 Db 6 KE 7
 ||
 RESULT 75
 TKL2 LOEMI
 ID TKL2 LOEMI STANDARD; PRT; 10 AA.
 AC P16224;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Locustatachykinin II (TK-II).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Locustatachykinin I and II, two novel insect neuropeptides with
 homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10
 10
 AMIDATION.
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;
 [1]
 Query Match 11.1%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GV 8
 ||
 Db 8 GV 9
 ||

Search completed: November 25, 2003, 19:28:21
 Job time : 6.45515 secs

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OM protein - protein search, using sw model
Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-21
Perfect score: 18
Sequence: 1 LQPEINGVPKVKTWPK 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0
Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

- Database : SPTREMBL 23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	12	Q50019	Q50019 mycobacteri
2	4	22.2	12	Q31851	Q31851 arabidopsis
3	4	22.2	16	O54357	O54357 bacillus am
4	4	22.2	18	Q919D5	Q919D5 human papil
5	4	22.2	18	Q919B3	Q919B3 human papil
6	4	22.2	18	Q919B5	Q919B5 human papil
7	4	22.2	18	Q919B7	Q919B7 human papil
8	4	22.2	18	Q919C5	Q919C5 human papil
9	4	22.2	18	Q919D1	Q919D1 human papil
10	4	22.2	18	Q919D3	Q919D3 human papil
11	4	22.2	18	Q919B9	Q919B9 human papil
12	4	22.2	18	Q919A8	Q919A8 human papil
13	4	22.2	18	Q919C7	Q919C7 human papil
14	4	22.2	18	Q919C9	Q919C9 human papil
15	4	22.2	19	Q9R4Q2	Q9R4Q2 pseudomonas
16	4	22.2	19	Q9N195	Q9N195 bos taurus

Q95M23	sus scrofa	8	6	Q95M23	17	3	16.7
Q8JJ35	ficedula hy	8	13	Q8JJ35	18	3	16.7
Q93E0	streptococc	9	2	Q93E0	19	3	16.7
Q96P97	homo sapien	9	4	Q96P97	20	3	16.7
P82440	nicotiana t	9	10	P82440	21	3	16.7
Q8AYL5	carassius a	9	13	Q8AYL5	22	3	16.7
Q8AUM7	carassius a	9	13	Q8AUM7	23	3	16.7
Q50843	methanococc	10	1	Q50843	24	3	16.7
Q86324	rous sarcom	10	15	Q86324	25	3	16.7
Q86325	rous sarcom	10	15	Q86325	26	3	16.7
Q86326	rous sarcom	10	15	Q86326	27	3	16.7
O60614	homo sapien	11	4	O60614	28	3	16.7
Q9NV38	homo sapien	11	4	Q9NV38	29	3	16.7
O19718	homo sapien	11	7	O19718	30	3	16.7
Q8UUP1	xenopus lae	11	13	Q8UUP1	31	3	16.7
Q9K7A4	bacillus ha	11	16	Q9K7A4	32	3	16.7
Q9ICE5	human immun	12	15	Q9ICE5	33	3	16.7
O31295	buchnera ap	13	2	O31295	34	3	16.7
Q9UE87	homo sapien	13	4	Q9UE87	35	3	16.7
Q8WEJ9	ginkgo bilo	13	8	Q8WEJ9	36	3	16.7
Q9380	brassica ol	13	10	Q9380	37	3	16.7
O88176	mus musculu	13	11	O88176	38	3	16.7
Q9UWM2	pyrococcus	14	1	Q9UWM2	39	3	16.7
O55326	synchococc	14	2	O55326	40	3	16.7
O8J1G2	ashbya goss	14	3	O8J1G2	41	3	16.7
Q9P2A2	homo sapien	14	4	Q9P2A2	42	3	16.7
Q16045	homo sapien	14	4	Q16045	43	3	16.7
O8HYM2	felis silve	14	6	O8HYM2	44	3	16.7
P82341	pisum sativ	14	10	P82341	45	3	16.7
Q89818	murine minu	14	12	Q89818	46	3	16.7
O8AXQ7	xenopus lae	14	13	O8AXQ7	47	3	16.7
Q9UR63	emeritella	15	3	Q9UR63	48	3	16.7
Q9UE41	homo sapien	15	4	Q9UE41	49	3	16.7
Q9UCU7	homo sapien	15	4	Q9UCU7	50	3	16.7
Q9UCY1	homo sapien	15	4	Q9UCY1	51	3	16.7
O46661	macropus ro	15	6	O46661	52	3	16.7
Q9TR64	oryctolagus	15	6	Q9TR64	53	3	16.7
Q9MZ5	oryctolagus	15	6	Q9MZ5	54	3	16.7
Q9TH04	grus americ	15	8	Q9TH04	55	3	16.7
Q9AT15	lycopersico	15	10	Q9AT15	56	3	16.7
P93515	arabidopsis	15	10	P93515	57	3	16.7
Q9S8N8	hordeum vul	15	10	Q9S8N8	58	3	16.7
Q9PRZ0	bothrops ja	15	13	Q9PRZ0	59	3	16.7
Q51950	staphylococ	16	2	Q51950	60	3	16.7
Q9FI87	streptococc	16	2	Q9FI87	61	3	16.7
Q9FIS4	streptococc	16	2	Q9FIS4	62	3	16.7
Q9TQ27	bos taurus	16	6	Q9TQ27	63	3	16.7
Q9QV11	rattus sp.	16	11	Q9QV11	64	3	16.7
Q9QUW8	cavia (guin	16	11	Q9QUW8	65	3	16.7
Q88250	sendai viru	16	11	Q88250	66	3	16.7
Q04246	sendai viru	16	12	Q04246	67	3	16.7
Q88249	sendai viru	16	12	Q88249	68	3	16.7
Q91154	sendai viru	16	12	Q91154	69	3	16.7
Q50842	methanococc	17	1	Q50842	70	3	16.7
Q8VME2	pseudomonas	17	1	Q8VME2	71	3	16.7
Q9EUB3	corynebacte	17	2	Q9EUB3	72	3	16.7
Q14001	homo sapien	17	4	Q14001	73	3	16.7
Q9UCC6	homo sapien	17	4	Q9UCC6	74	3	16.7
Q9XSG1	bos taurus	17	6	Q9XSG1	75	3	16.7
Q9TQ25	macaca fasc	17	6	Q9TQ25	76	3	16.7
Q9TR21	sus scrofa	17	6	Q9TR21	77	3	16.7
Q9THQ0	mus sp. bet	17	7	Q9THQ0	78	3	16.7
Q9T2S2	solanum tub	17	8	Q9T2S2	79	3	16.7
Q9T2H4	spinacia ol	17	8	Q9T2H4	80	3	16.7
Q9JK08	mus musculu	17	11	Q9JK08	81	3	16.7
Q919B0	human papil	17	12	Q919B0	82	3	16.7
Q52411	thermophili	18	2	Q52411	83	3	16.7
Q9P897	emeritella	18	3	Q9P897	84	3	16.7
Q9UCF4	homo sapien	18	4	Q9UCF4	85	3	16.7
Q9TWW7	procambarus	18	5	Q9TWW7	86	3	16.7
Q95MB1	equus cabal	18	6	Q95MB1	87	3	16.7
Q9TOR0	sus scrofa	18	6	Q9TOR0	88	3	16.7
Q9TS26	sus scrofa	18	6	Q9TS26	89	3	16.7

90 Q9888 psophocarpus
 91 P70649 mus sp. syn
 92 P70650 mus sp. syn
 93 Q9109 mus musculus
 94 Q90791 gallus gall
 95 Q86733 gallus gall
 96 Q57600 gallus gall
 97 O12692 simian-huma
 98 Q9K610 bacillus ha
 99 Q9K37 salmonella
 100 Q9K4X0 planktothri

ALIGNMENTS

RESULT 1

Q50019 PRELIMINARY; PRT; 12 AA.
 ID Q50019
 AC Q50019
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
 DE U2266a.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Robison K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U15182; AAAG2981.1; -.
 SQ SEQUENCE 12 AA; 1402 MW; DF569D9F7FD1F5A2 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGVP 9
 Db 1 MGVP 4

RESULT 2

Q31851 PRELIMINARY; PRT; 12 AA.
 ID Q31851
 AC Q31851
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glyceralddehyde-3-phosphate dehydrogenase (Fragment).
 OS Arabidopsis thaliana (Mouse-ear cross).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia; TISSUE=leaf;
 RX MEDLINE=94187724; PubMed=8139555;
 RA Conley T.R., Park S.-C., Kwon H.-B., Peng H.-S., Shih M.-C.;
 RT "Characterization of cis-acting elements in light regulation of the
 RT nuclear gene encoding the A subunit of chloroplast isozymes
 RT Glyceralddehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";
 RL Mol. Cell. Biol. 14:2525-2533 (1994).
 DR EMBL; L14743; AAA31640.1; -.
 KW Chloroplast.

FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPKV 11
 Db 8 VPKV 11

RESULT 3

O54357 PRELIMINARY; PRT; 16 AA.
 ID O54357
 AC O54357
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PTSI system enzyme I (Fragment).
 OS PTSI.
 GN Bacillus amyloliquefaciens.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H;
 RA Nicholson W.L., Pajardo-Cavazos P.;
 RT "DNA repair and the ultraviolet radiation resistance of bacterial
 RT spores: from the laboratory to the environment.";
 RL (In) Pandalai S. (eds.);
 RL RECENT RESEARCH ADVANCES IN MICROBIOLOGY, pp.1-1, Research Signpost,
 RL Tivandrum, India (1998).
 DR EMBL; U60821; AAB97621.1; -.
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1873 MW; D38C93850AEF4266 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
 Db 9 VKET 12

RESULT 4

Q919D5 PRELIMINARY; PRT; 18 AA.
 ID Q919D5
 AC Q919D5
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein (Fragment).
 GN E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CC1;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF404692; AAL01341.1; -.
 FT NON TER 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 LOPE 4
      ||||
Db      15 LOPE 18

RESULT 5
Q919B3
ID Q919B3      PRELIMINARY;      PRT;      18 AA.
AC Q919B3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC12;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404703; AAL01364.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOPE 4
      ||||
Db      15 LOPE 18

RESULT 6
Q919B5
ID Q919B5      PRELIMINARY;      PRT;      18 AA.
AC Q919B5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404702; AAL01362.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOPE 4
      ||||
Db      15 LOPE 18

RESULT 7
Q919D1
ID Q919D1      PRELIMINARY;      PRT;      18 AA.
AC Q919D1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).

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Q919B7
ID Q919B7      PRELIMINARY;      PRT;      18 AA.
AC Q919B7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC10;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404701; AAL01360.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOPE 4
      ||||
Db      15 LOPE 18

RESULT 8
Q919C5
ID Q919C5      PRELIMINARY;      PRT;      18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404697; AAL01352.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOPE 4
      ||||
Db      15 LOPE 18

RESULT 9
Q919D1
ID Q919D1      PRELIMINARY;      PRT;      18 AA.
AC Q919D1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).

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GN E7
OS Human papillomavirus type 16..
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC3;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404694; AAL01346.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 10
Q919D3 ID Q919D3 PRELIMINARY; PRT; 18 AA.
AC Q919D3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC2;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404693; AAL01344.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 11
Q919B9 ID Q919B9 PRELIMINARY; PRT; 18 AA.
AC Q919B9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=HPV16E6CC9;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404700; AAL01358.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 12
Q919A8 ID Q919A8 PRELIMINARY; PRT; 18 AA.
AC Q919A8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC15;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404706; AAL01369.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 13
Q919C7 ID Q919C7 PRELIMINARY; PRT; 18 AA.
AC Q919C7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC5;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404696; AAL01350.1; -.
FT NON_TER 18
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SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 14
Q919C9 PRELIMINARY; PRT; 18 AA.
AC Q919C9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C4;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404695; AAL01348.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 15 LOPE 18

RESULT 15
Q9R4Q2 PRELIMINARY; PRT; 19 AA.
AC Q9R4Q2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ribosomal protein S21 (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]_TaxID=287;
RP SEQUENCE.
RX MEDLINE=95244309; PubMed=7727274;
RA Ochi K.;
RT "Comparative ribosomal protein sequence analyses of a phylogenetically
RT defined genus, Pseudomonas, and its relatives.";
RL Int. J. Syst. Bacteriol. 45:268-273 (1995).
DR InterPro; IPR001911; Ribosomal S21.
DR Pfam; PF01165; Ribosomal S21; I.
DR PRINTS; PR00976; RIBOSOMALS21.
DR SEQUENCE 19 AA; 2244 MW; 0475DD42A464271C CRC64;

Query Match 22.2%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVKE 13
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Db 4 KVKE 7

RESULT 16
Q9N195 PRELIMINARY; PRT; 19 AA.
AC Q9N195;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Parvalbumin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RA Ariza F., Harrison B., Drinkwater R.;
RT "The Assignment by Linkage Mapping of Five Genes from Human Chromosome
RT 22 to Bovine Chromosome 5, 14 and 17.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217654; AAF26420.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2151 MW; D5EA9D89EC3EE951 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
Db 16 VKET 19

RESULT 17
Q95M23 PRELIMINARY; PRT; 8 AA.
AC Q95M23;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).
GN ATP1A1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_TaxID=9823;
RP SEQUENCE FROM N.A.
RC STRAIN=Pietrain;
RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
RA Geldermann H., Kopecky M.;
RT "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and
RT linkage assignments of ATP1A1 and IVL to chromosome 4.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344138; CAC51422.1; -.
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
Db 4 KET 6

RESULT 18
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Q8JJ35 Q8JJ35 PRELIMINARY; PRT; 8 AA.
 AC Q8JJ35
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Arp-citrate lyase (Fragment).
 GN ACP.
 OS Ficedula hypoleuca.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
 OX NCBI_TaxID=46689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O84;
 RA MEDLINE=21918460; PubMed=11918793;
 RX Primer C.R., Borge T., Lindell J., Saetre G.-P.;
 RT "single-nucleotide polymorphism characterization in species with
 RT limited available sequence information: high nucleotide diversity
 RT revealed in the avian genome.";
 RL Mol. Ecol. 11:603-612(2002).
 DR EMBL; AF454211; AAM22897.1; -.
 KW Lyase.
 FT NON_TER 1 1
 FT NON_TER 8 8
 FT SEQUENCE 8 AA; 981 MW; 98C77B544681AB02 CRC64;
 SQ
 Query Match 16.7%; Score 3; DB 13; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 ETM 15
 Db 2 ETM 4
 RESULT 19
 Q93E20 Q93E20 PRELIMINARY; PRT; 9 AA.
 ID Q93E20
 AC Q93E20
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE ScpB (Fragment).
 GN ScpB.
 OS Streptococcus agalactiae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O90R;
 RX MEDLINE=21424698; PubMed=11532154;
 RA Franken C., Haase G., Brandt C., Weber-Heynemann J., Martin S.,
 RA Lamler C., Podbielski A., Lutticken R., Spellerberg B.;
 RT "Horizontal gene transfer and host specificity of beta-haemolytic
 RT streptococci: the role of a putative composite transposon containing
 RT scpB and lmb.";
 RL Mol. Microbiol. 41:925-935(2001).
 DR EMBL; AF327852; AAL10713.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 9 AA; 1146 MW; 543721AB1326C403 CRC64;
 SQ
 Query Match 16.7%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 KET 14
 Db 5 KET 7
 RESULT 20

Q96P97 Q96P97 PRELIMINARY; PRT; 9 AA.
 AC Q96P97
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Reptin52 protein (Fragment).
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
 RT "Characterization of TPA-responsive genes in U937 cells using ordered
 RT differential display PCR.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401216; AAL02172.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 9 AA; 981 MW; 5CDDAA681AB1873 CRC64;
 SQ
 Query Match 16.7%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 ETM 15
 Db 4 ETM 6
 RESULT 21
 P82440 P82440 PRELIMINARY; PRT; 9 AA.
 ID P82440
 AC P82440
 DT 01-JUN-2000 (TReMBLrel. 14, Created)
 DT 01-JUN-2000 (TReMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE 42 kDa cell wall protein (Fragment).
 DE Nicotiana tabacum (Common tobacco).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture.";
 RL Planta 200:0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON_TER 9 9
 FT SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;
 SQ
 Query Match 16.7%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QPE 4
 Db 1 QPE 3
 RESULT 22
 Q8AYL5 Q8AYL5 PRELIMINARY; PRT; 9 AA.
 ID Q8AYL5
 AC Q8AYL5;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

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DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OC NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT "Promoter characteristics of two CYP19 genes differentially expressed
RT in the brain and ovary of teleost fish.";
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR ENBL; AF324897; AAN32618.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;

Query Match 16.7%; Score 3; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOP 3
Db 6 LOP 8

RESULT 23
Q8AUM7
ID Q8AUM7 PRELIMINARY; PRT; 9 AA.
AC Q8AUM7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OC NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT "Promoter characteristics of two CYP19 genes differentially expressed
RT in the brain and ovary of teleost fish.";
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR ENBL; AF324895; AAN32616.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match 16.7%; Score 3; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOP 3
Db 6 LOP 8

RESULT 24
Q50843
ID Q50843 PRELIMINARY; PRT; 10 AA.
AC Q50843;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE RNA polymerase gene 3' flanking region with AT-rich DNA sequence
DE (fragment).
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OC NCBI_TaxID=2188;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85230552; PubMed=4006907;
RA Bollscheueller C., Kuehn R., Klein A.;
RT "Non-repetitive AT-rich sequences are found in intergenic regions of
RT Methanococcus voltae DNA.";
RL EMBO J. 4:805-809(1985);
DR ENBL; X02517; CAA26353.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1149 MW; 27F22A2772CAA9C8 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPK 10
Db 6 VPK 8

RESULT 25
Q86324
ID Q86324 PRELIMINARY; PRT; 10 AA.
AC Q86324;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.
OC NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=98083689; PubMed=9421881;
RA Hara H., Kaji A.;
RT "The U3 region of the long terminal repeat of a subgroup A
RT transformation-defective rous sarcoma virus (tdPH2010) converts a
RT noncytopathic virus to a cytopathic virus.";
RL Virus Genes 15:171-180(1997).
DR ENBL; U41726; AAB60580.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPE 4
Db 4 QPE 6

RESULT 26
Q86325
ID Q86325 PRELIMINARY; PRT; 10 AA.
AC Q86325;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.
OC NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=98083689; PubMed=9421881;
RA Hara H., Kaji A.;
RT "The U3 region of the long terminal repeat of a subgroup A
RT transformation-defective rous sarcoma virus (tdPH2010) converts a

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RT noncytopathic virus to a cytopathic virus.";
RL Virus Genes 15:171-180(1997).
DR EMBL; U41727; AAB60581.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4
Db |||
4 QPE 6

RESULT 27
Q86326
ID Q86326 PRELIMINARY; PRT; 10 AA.
AC Q86326;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=82271824; PubMed=6287213;
RA Takeya T., Hanafusa H., Jungmans R.P., Ju G., Skalka A.M.;
RT "Comparison between the viral transforming gene (src) of recovered
RL avian sarcoma virus and its cellular homolog.";
RL Mol. Cell. Biol. 1:1024-1037(1981).
DR EMBL; U41729; AAA84421.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4
Db |||
4 QPE 6

RESULT 28
O60614
ID O60614 PRELIMINARY; PRT; 11 AA.
AC O60614;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MTG8 related protein (Fragment).
GN MTGRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

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RX MEDLINE=99009318; PubMed=9790752;
RA Calabi F., Cilli V.;
RT "CBFA2T1, a gene rearranged in human leukemia, is a member of a
RT multigene family.";
RL Genomics 52:332-341(1998).
DR EMBL; AF052211; AAC64700.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1047 MW; CF001CE4DDDB6772 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
Db |||
3 GVP 5

RESULT 29
Q9NY38
ID Q9NY38 PRELIMINARY; PRT; 11 AA.
AC Q9NY38;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Heavy metal-responsive transcription factor (Fragment).
GN MTF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
RA Georgiev O., Schaffner W.;
RT "Characterization of the mouse gene for the heavy metal-responsive
RT transcription factor MTF-1.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251881; CAB71327.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
Db |||
4 MVP 6

RESULT 30
O19718
ID O19718 PRELIMINARY; PRT; 11 AA.
AC O19718;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DRI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86206008; PubMed=3458223;
RA Gregersen P.K., Shen M., Song Q.-L., Merryman P., Degar S., Seki T.,
RA Maccari J., Goldberg D., Murphy H., Schwenzer J., Wang C.Y.,
RA Winchester R.J., Nepom G.T., Silver J.;
RT "Molecular diversity of HLA-DR4 haplotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2642-2646(1986).

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DR EMBL; M15074; AAA59810.1; -;
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1143 MW; 4E6AADA061B776D7 CRC64;
 Query Match 16.7%; Score 3; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQP 3
 Db 4 LQP 6
 RESULT 31
 Q8UUPI PRELIMINARY; PRT; 11 AA.
 AC Q8UUPI;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Beta-TrCP protein (Fragment).
 GN BETA-TRCP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carnevali F.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ballarino M.;
 RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis";
 RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.
 DR EMBL; AJ428930; CAD21927.1; -;
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;
 Query Match 16.7%; Score 3; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQP 3
 Db 8 LQP 10
 RESULT 32
 Q9K7A4 PRELIMINARY; PRT; 11 AA.
 AC Q9K7A4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein BH3464.
 GN BH3464.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001518; BAB07183.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 11 AA; 1219 MW; 5F7D235CB7272B13 CRC64;
 Query Match 16.7%; Score 3; DB 16; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 VKE 13
 Db 3 VKE 5
 RESULT 33
 Q9ICE5 PRELIMINARY; PRT; 12 AA.
 AC Q9ICE5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=546CP-H7, 546CP-E4, and 546CP-F5;
 RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
 RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from a patient with HIV dementia: evidence for monocyte trafficking into brain.";
 RL J. Neurovirol. 0:0-0(2000).
 DR EMBL; AF217155; AAF75497.1; -;
 DR EMBL; AF217153; AAF75495.1; -;
 DR EMBL; AP217154; AAF75496.1; -;
 SQ SEQUENCE 12 AA; 1636 MW; 7ED6A2917A24005B CRC64;
 Query Match 16.7%; Score 3; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 VKE 13
 Db 3 VKE 5
 RESULT 34
 O31295 PRELIMINARY; PRT; 13 AA.
 AC O31295;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
 GN LEUA.
 OS Buchnera aphidicola.
 OG Plasmid pBts1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97386415; PubMed=9244264;
 RA Van Ham R.C.H.J., Moya A., Latorre A.;
 RT "Putative origin of plasmids carrying the genes involved in leucine biosynthesis in Buchnera aphidicola (endosymbiont of aphids).";
 RL J. Bacteriol. 179:4768-4777(1997).
 DR EMBL; Y11966; CAA72696.1; -;
 KW Lyase; Plasmid.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1487 MW; 1BD1D3E72A9E2050 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKV 11
 ||||
 Db 3 PKV 5

RESULT 35

Q9UE87 PRELIMINARY; PRT; 13 AA.
 AC Q9UE87;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Transforming growth factor alpha (Fragment).
 GN TGFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=9219018; PubMed=2907605;
 RA Jakobovits E.B., Schlokat U., Vannice J.L., Derynck R., Levinson A.D.;
 RA "The human transforming growth factor alpha promoter directs
 transcription initiation from a single site in the absence of a TATA
 sequence.";
 RL Mol. Cell. Biol. 8:5549-5554(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92168034; PubMed=1791840;
 RA Saeki T., Cristiano A., Lynch M.J., Brattain M., Kim N., Normanno N.,
 RA Kenney N., Ciardiello F., Salomon D.S.;
 RA "Regulation by estrogen through the 5'-flanking region of the
 transforming growth factor alpha gene.";
 RL Mol. Endocrinol. 5:1955-1963(1991).
 RN [3]
 RP SEQUENCE FROM N.A.

RX MEDLINE=93364904; PubMed=8358733;
 RA Lynch M.J., Pelosi L., Carboni J.M., Merwin J., Wang R.C.,
 RA Lin P.F., Henry D.L., Brattain M.G.;
 RA "Transforming growth factor-beta 1 induces transforming growth factor-
 alpha promoter activity and transforming growth factor-alpha secretion
 in the human colon adenocarcinoma cell line FET.";
 RL Cancer Res. 53:4041-4047(1993).
 DR EMBL; M96868; AAA79958.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1318 MW; 2C6E4395FCBE36D8 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17
 ||||
 Db 1 MVP 3

RESULT 36

Q8WEJ9 PRELIMINARY; PRT; 13 AA.
 AC Q8WEJ9;
 DT 01-NAR-2002 (TrEMBLrel. 20, Created)
 DT 01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE NADH dehydrogenase (Fragment).
 GN NAD1.
 OS Ginkgo biloba (Ginkgo).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

OX NCBI_TaxID=3311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21555473; PubMed=11697913;
 RA Gugerli F., Sperisen C., Buchler U., Brunner I., Brodbeck S.,
 RA Palmer J.D., Qiu Y.L.;
 RA "The evolutionary split of pinaceae from other conifers: evidence from
 an intron loss and a multigene phylogeny.";
 RL Mol. Phylogenet. Evol. 21:167-175(2001).
 DR EMBL; AF227466; AAL38910.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1419 MW; C00F6805F94945BD CRC64;

Query Match 16.7%; Score 3; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17
 ||||
 Db 1 MVP 3

RESULT 37

ID Q39380 PRELIMINARY; PRT; 13 AA.
 AC Q39380;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE IFA binding protein (Spi0) (Fragment).
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Dok; TISSUE=Curd surface;
 RA Willis G.;
 RA "An investigation of nuclear lamin homologues in plants: an apparently
 non-intermediate filament sequence that bind a polyclonal anti-lamin
 antiserum.";
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X97678; CAA66268.1; -.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1413 MW; D1D4EA3926B42772 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPK 10
 ||||
 Db 6 VPK 8

RESULT 38

ID O88176 PRELIMINARY; PRT; 13 AA.
 AC O88176;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Neural cell adhesion molecule (Fragment).
 GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db |||
7 LQP 9

RESULT 39
Q9UWM2 PRELIMINARY; PRT; 14 AA.
AC Q9UWM2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE L-glutamate:NAD(P)+ oxidoreductase (EC 1.4.1.3) (Fragment).
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RN SEQUENCE.
RX MEDLINE=92247806; PubMed=1576153;
RA Robb F.T., Park J.B., Adams M.W.;
RT "Characterization of an extremely thermostable glutamate
dehydrogenase: a key enzyme in the primary metabolism of the
RT hyperthermophilic archaeobacterium, Pyrococcus furiosus.";
RL Biochim. Biophys. Acta 1120:267-272(1992).
SQ SEQUENCE 14 AA; 1684 MW; 1E8EF0500B25D50B CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
Db |||
1 VKE 3

RESULT 40
Q55326 PRELIMINARY; PRT; 14 AA.
AC Q55326;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative ORF1 (Fragment).
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32049;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=PR6;
RX MEDLINE=92201692; PubMed=1551590;
RA Rhel E., Stirewalt V.L., Gasparich G.E., Bryant D.A.;
RT "The psac genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa:
cloning and sequence analysis.";
RL Gene 112:123-128(1992).
DR EMBL; M86238; AAA27351.1; -.
FT NON_TER 14 14

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SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB998BCA CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db |||
12 LQP 14.

RESULT 41
Q8JIG2 PRELIMINARY; PRT; 14 AA.
AC Q8JIG2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE YPL156 (Fragment).
GN YPL156.
OS Ashbya gossypii (Brenothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Ashbya.
OX NCBI_TaxID=33169;
RN [1]
RN SEQUENCE FROM N.A.
RA Alberti-Segui C., Dietrich F., Philippsen P.;
RT "Identification of kinesin-related proteins in the filamentous fungus
RT Ashbya gossypii.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378570; AA87139.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1646 MW; 8C3A12EB808B1D15 CRC64;

Query Match 16.7%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
Db |||
3 PKV 5

RESULT 42
Q9P2A2 PRELIMINARY; PRT; 14 AA.
AC Q9P2A2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Truncated aldo-keto reductase (Fragment).
GN TRUNCATED AKR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20138537; PubMed=10672042;
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
RA Watanabe K., Ito S.;
RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
RT three aldo-keto reductase genes.";
RL Genes Cells 5:111-125(2000).
DR EMBL; AB037903; BAA92888.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LQP 3
Db 7 LQP 9

RESULT 43

ID Q16045 PRELIMINARY; PRT; 14 AA.
AC Q16045;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE D3 dopamine receptor (Fragment).
GN D3R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93326145; PubMed=7916609;
RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;
RT Expression of the D3 dopamine receptor gene and a novel variant
RT transcript generated by alternative splicing in human peripheral blood
RL Lymphocytes.";
RL Biochem. Biophys. Res. Commun. 194:368-374(1993).
KW EMBL; S63845; AAB27543.2; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1586 MW; EA310BEFE94CF1B1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3
Db 12 LQP 14

RESULT 44

ID Q8HYM2 PRELIMINARY; PRT; 14 AA.
AC Q8HYM2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Interferon regulatory factor 6 (Fragment).
GN IRF6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Susott B.E., Rollo W.A., Venta P.J., Ewart S.L.;
RT "Characterization of 8 Feline Type I Markers.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF459807; RAO15587.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1684 MW; CS93CC0754F47BB9 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12
Db 3 KVK 5

RESULT 45

F82341
ID P82341 PRELIMINARY; PRT; 14 AA.
AC P82341;
DT 01-JUN-2000 (TREMBlrel. 14, Created)
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT251) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5, ITS MW IS: 16.9 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1590 MW; 6D968D2994D0185B CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEI 5
Db 6 PEI 8

RESULT 46

ID Q89818 PRELIMINARY; PRT; 14 AA.
AC Q89818;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Hypothetical 1.9 kDa protein.
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LYMPHOTROPIC VARIANT;
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice,
RT MVM(1), and comparison with the DNA sequence of the fibrotropic
RT prototype strain.";
RL J. Virol. 570:656-669(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MVM(P);
RX MEDLINE=83143341; PubMed=6298737;
RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
RT "The complete DNA sequence of minute virus of mice, an autonomous
RT parvovirus";
RL Nucleic Acids Res. 11:999-1018(1983).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=MVM(P);
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;

RT "DNA sequence of the lymphotropic variant of minute virus of mice,
 RT WMV(1), and comparison with the DNA sequence of the fibrotropic
 RT prototype strain.";
 RL J. Virol. 57:656-669(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WMV(P);
 RX MEDLINE=87061199; PubMed=373817;
 RA Morgan W.R., Ward D.C.;
 RT "Three splicing patterns are used to excise the small intron common to
 RT all minute virus of mice RNAs.";
 RL J. Virol. 60:1170-1174(1986).
 DR EMBL; M12032; AAA69571.1; -;
 DR EMBL; J02275; AAA67113.1; -;
 DR EMBL; V01115; CAA24312.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 14 AA; 1927 MW; 12535381FB864D1B CRC64;

Query Match 16.7%; Score 3; DB 12; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
 ||||
 Db 9 PEI 11

RESULT 47
 Q8AXQ7 PRELIMINARY; PRT; 14 AA.
 AC Q8AXQ7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mannose-binding lectin-associated serine protease (Fragment).
 GN MASP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]_TaxID=8355;
 RP SEQUENCE FROM N.A.
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Takahashi M.,
 RA Matsushita M., Fujita T.;
 RT "Ancient origin and extensive distribution of mannose-binding lectin-
 RT associated serine protease-3 in vertebrate lineage.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078909; BAC41345.1; -;
 KW Lectin; Protease.
 FT NON_TER 1
 FT NON_TER 14
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1533 MW; 99DD285F40C2B15 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 ||||
 Db 2 GVP 4

RESULT 48
 Q9UR63 PRELIMINARY; PRT; 15 AA.
 ID Q9UR63;
 AC Q9UR63;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
 DE isoform (EC 3.2.1.26) (Fragment).
 OS Emericella nidulans (Aspergillus nidulans).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichosporaceae; Emericella.
 OC NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96409246; PubMed=8814228;
 RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;
 RT "Purification and partial characterization of the high and low
 RT molecular weight form (S- and F-form) of invertase secreted by
 RT *Aspergillus nidulans*.";
 RL Biochim. Biophys. Acta 1296:207-218(1996).
 SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match 16.7%; Score 3; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOP 3
 ||||
 Db 1 LOP 3

RESULT 49
 Q9UE41 PRELIMINARY; PRT; 15 AA.
 ID Q9UE41;
 AC Q9UE41;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Collagen.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89325561; PubMed=2753125;
 RA Viikula M., Peltonen L.;
 RT "Structural analyses of the polymorphic area in type II collagen
 RT gene.";
 RL FEBS Lett. 250:171-174(1989).
 DR EMBL; X16158; CAA34281.1; -;
 SQ SEQUENCE 15 AA; 1334 MW; D6DC3824197ABEF6 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
 ||||
 Db 1 GVP 3

RESULT 50
 Q9UCC7 PRELIMINARY; PRT; 15 AA.
 ID Q9UCC7;
 AC Q9UCC7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Midkine (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94059921; PubMed=8241100;
 RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
 RT "Identification of novel heparin-releasable proteins, as well as the
 RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
 RL Arterioscler. Thromb. 13:1798-1805(1993).
 SQ SEQUENCE 15 AA; 1527 MW; C34B6B97878474AC CRC64;


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Query Match      16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 KVK 12
Db      |||
       7 KVK 9

RESULT 51
Q9UCV1 PRELIMINARY; PRT; 15 AA.
ID Q9UCY1;
AC Q9UCY1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Thromboxane A2 receptor isoform alpha (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96193877; PubMed=8613548;
RA Hirata T., Ushikubi F., Kakizuka A., Okuma M., Narumiya S.;
RT "Two thromboxane A2 receptor isoforms in human platelets. Opposite
RT coupling to adenylyl cyclase with different sensitivity to Arg60 to Leu
RT mutation."
RL J. Clin. Invest. 97:949-956(1996).
SQ SEQUENCE 15 AA; 1656 MW; 5BC77C6B9EB97FB78 CRC64;

Query Match      16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQP 3
Db      |||
       4 LQP 6

RESULT 52
O46661 PRELIMINARY; PRT; 15 AA.
ID O46661;
AC O46661;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (Fragment).
GN G6PD.
OS Macropus robustus robustus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224585; PubMed=9060417;
RA Loebl D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the G6PD gene of the
RT wallaroo (Macropus robustus) by polymerase chain reaction."
RL Mamm. Genome 8:146-147(1997).
DR EMBL; U53768; AAC48786.1; -.
DR InterPro; IPR001282; G6PD.
DR Pfam; PF00479; G6PD; 1.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1704 MW; 039588640B5E5671E CRC64;

Query Match      16.7%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 IMG 7

Query Match      16.7%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VPK 10
Db      |||
       12 VPK 14

RESULT 53
Q9TR64 PRELIMINARY; PRT; 15 AA.
ID Q9TR64;
AC Q9TR64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nucleoside diphosphate kinase, NDK, P19-17.143 kDa A subunit
DE (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=95285334; PubMed=7767789;
RA Weber B., Weber W., Buck F., Hilz H.;
RT "Isolation of the myc transcription factor nucleoside diphosphate
RT kinase and the multifunctional enzyme glyceraldehyde-3-phosphate
RT dehydrogenase by cAMP affinity chromatography."
RL Int. J. Biochem. Cell Biol. 27:215-224(1995).
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1820 MW; 2728CBD4FDAE6316 CRC64;

Query Match      16.7%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QPE 4
Db      |||
       7 QPE 9

RESULT 54
Q9MZRS PRELIMINARY; PRT; 15 AA.
ID Q9MZRS;
AC Q9MZRS;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin 4 variant IL-4int2A (Fragment).
GN IL-4.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen, and Lymph node;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus)."
RL Cytokine 12:555-565(2000).
DR EMBL; AF169172; AAF86656.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1586 MW; 876C550E85307B55 CRC64;

Query Match      16.7%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VPK 10
Db      |||
       12 VPK 14

RESULT 55

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Q9TH04
ID Q9TH04 PRELIMINARY; PRT; 15 AA.
AC Q9TH04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
GN ND6.
OS Grus americana (whooping crane).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=9117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMS B3394;
RA Glenn T.C., Stephan W., Braun M.J.;
RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial
RT DNA Variation."
RL Conserv. Biol. 0:0-0(1999).
DR EMBL; AF112373; AAD23994.1; --
KW Mitochondrion.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1759 MW; A7F711A65B9F934F CRC64;

Query Match 16.7%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGW 8
Db |||
8 MGW 10

RESULT 56
Q9AT15
ID Q9AT15 PRELIMINARY; PRT; 15 AA.
AC Q9AT15;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Plasma membrane H⁺-ATPase (Fragment).
GN LHA1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Ewing N.N., Wimmers L.E., Meyer D.J., Chetelat R.T., Bennett A.B.;
RT "Molecular cloning of tomato plasma membrane H⁺-ATPase."
RL Life Sci. Adv. Plant Physiol. 94:1874-1881(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Ewing N.N., Bennett A.B.;
RT "Assessment of the number and expression of P-type H(+) -ATPase genes
RT in tomato."
RL Life Sci. Adv. Plant Physiol. 106:547-557(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Dahmani Z., Ewing N.N.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF353103; AAK31206.1; --
FT NON_TER 15
SQ SEQUENCE 15 AA; 1673 MW; 5F70477FC08C809E CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
Db |||
13 KET 15

RESULT 57
P93515
ID P93515 PRELIMINARY; PRT; 15 AA.
AC P93515;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Copper amine oxidase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96227319; PubMed=8654815;
RA Moller S.G., McPherson M.J.;
RT "Molecular and functional studies of copper amine oxidase from
RT Arabidopsis thaliana".
RL Biochem. Soc. Trans. 23:630S-630S(1995).
DR EMBL; S82296; AAB37690.1; --
DR InterPro; IPR000269; CuNH oxidase.
DR Pfam; PF01179; Cu_amine_oxid; 1.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1842 MW; 12BF8E81198BC5CE CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
Db |||
2 MVP 4

RESULT 58
Q9S8N8
ID Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RX MEDLINE=94170739; PubMed=8125056;
RA Flengsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis."
RL Electrophoresis 14:1060-1066(1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db |||
3 LQP 5

RESULT 59

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Q9PRZ0
ID Q9PRZ0 PRELIMINARY; PRT; 15 AA.
AC Q9PRZ0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RX MEDLINE=94080171; PubMed=8257916;
RA Machado O.L., Oliveira-Carvalho A.L., Zingali R.B., Carlini C.R.;
RT "Purification, physicochemical characterization and N-terminal-amino
acid sequence of a phospholipase A2 from Bothrops jararaca venom.";
RL Braz. J. Med. Biol. Res. 26:163-166(1993).
SQ SEQUENCE 15 AA; 1734 MW; AF893A50F081B0A0 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ETM 15
Db 6 ETM 8

RESULT 60
Q51950
ID Q51950 PRELIMINARY; PRT; 16 AA.
AC Q51950;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF E.
OS Staphylococcus aureus.
OG Plasmid pNS1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Noguchi N., Aoki T., Sasatsu M., Kono M., Shishido K., Ando T.;
RT "Determination of the complete nucleotide sequence of pNS1, a
staphylococcal tetracycline-resistance plasmid propagated in Bacillus
subtilis";
RL FEMS Microbiol. Lett. 37:283-288(1986).
DR EMBL; M16217; AAA19178.1; -.
KW Plasmid.
SQ SEQUENCE 16 AA; 1929 MW; 0F038C3A8B79F3B0 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKE 13
Db 14 VKE 16

RESULT 61
Q9F1S7
ID Q9F1S7 PRELIMINARY; PRT; 16 AA.
AC Q9F1S7;
DT 01-NAR-2001 (TREMBlrel. 16, Created)
DT 01-NAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamide aminoimidazole transformylase (EC 6.3.2.6)
(Fragment).
GN PURH.
OS Streptococcus suis.

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=205; PubMed=11133943;
RX MEDLINE=20576151; Otsaki Y., Otsaki M., Takamatsu D., Shimoji Y.;
RA "Evidence for horizontal transfer of the SsdATII restriction-
modification genes to the Streptococcus suis genome.";
RT "Evidence for horizontal transfer of the SsdATII restriction-
modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045610; BAB20834.1; -.
KW Ligase.
FT NON TER 1
SQ SEQUENCE 16 AA; 1935 MW; 1FC8D8B8AE391D40 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
Db 5 TMV 7

RESULT 62
Q9F1S4
ID Q9F1S4 PRELIMINARY; PRT; 16 AA.
AC Q9F1S4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamide aminoimidazole transformylase (EC 6.3.2.6)
(Fragment).
GN PURH.
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=220; PubMed=11133943;
RX MEDLINE=20576151; Otsaki Y., Otsaki M., Takamatsu D., Shimoji Y.;
RA "Evidence for horizontal transfer of the SsdATII restriction-
modification genes to the Streptococcus suis genome.";
RT "Evidence for horizontal transfer of the SsdATII restriction-
modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045612; BAB20838.1; -.
KW Ligase.
FT NON TER 1
SQ SEQUENCE 16 AA; 1949 MW; 6978D8B8AE391D44 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16
Db 5 TMV 7

RESULT 63
Q9TQZ7
ID Q9TQZ7 PRELIMINARY; PRT; 16 AA.
AC Q9TQZ7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Factor H (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=96202005; PubMed=8615824;
RA Soames C.J., Day A.J., Sim R.B.;
RT "Prediction from sequence comparisons of residues of factor H involved
RL in the interaction with complement component C3b.";
RL Biochem. J. 315:523-531(1996).
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
DB 10 KET 12

RESULT 64
Q9QV11 PRELIMINARY; PRT; 16 AA.
ID Q9QV11
AC Q9QV11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Hepatic glycoen associated protein phosphatase 1 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=95237359; PubMed=7720853;
RA Moorhead G., Mackintosh C., Morrice N., Cohen P.;
RT "Purification of the hepatic glycoen-associated form of protein
RT phosphatase-1 by microcystin-Sepharose affinity chromatography.";
RL FEBS Lett. 362:101-105(1995).
SQ SEQUENCE 16 AA; 1750 MW; F1CB6485F4B54AE1 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
DB 13 TMV 15

RESULT 65
Q9QUW8 PRELIMINARY; PRT; 16 AA.
ID Q9QUW8
AC Q9QUW8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein isomerase-related protein precursor 71.5 kDa isoform
DE (Fragment).
OS Cavia (guinea pigs).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae.
OX NCBI_TaxID=10140;
RN [1]
RP SEQUENCE
RX MEDLINE=96070119; PubMed=8535285;
RA Bonifacio M.D., Steeves T., Saunders D.M., Sinosich M.J.;
RT "Isolation of ERp72 from guinea pig term placenta using heparin
RT Sepharose affinity chromatography.";
RL Biochem. Mol. Biol. Int. 36:1143-1152(1995).
SQ SEQUENCE 16 AA; 1880 MW; 21B44A5F5767CB17 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
DB 11 VKE 13

RESULT 66
Q88250 PRELIMINARY; PRT; 16 AA.
ID Q88250
AC Q88250;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60152; AAA47808.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1648 MW; 049B529F01B29066 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 4 GVP 6

RESULT 67
Q04246 PRELIMINARY; PRT; 16 AA.
ID Q04246
AC Q04246;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60155; AAA47805.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1634 MW; 73989D9F01B298D0 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 4 GVP 6
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RESULT 68
Q88249          PRELIMINARY;          PRT;          16 AA.
AC Q88249;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCS, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60154; AAA47807.1; -.
FT NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1649 MW; 049B529F01B298C4 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 4 GVP 6

RESULT 69
Q99154          PRELIMINARY;          PRT;          16 AA.
AC Q99154;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCS, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60153; AAA47806.1; -.
FT NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1606 MW; 739B529F01B298D0 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 4 GVP 6

RESULT 70
Q50842          PRELIMINARY;          PRT;          17 AA.
AC Q50842;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-NOV-1996 (TReMBLrel. 01, Last annotation update)
DE 01-NOV-1996 (TReMBLrel. 01, Last annotation update)

DE RNA polymerase (Fragment).
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85230552; PubMed=4006907;
RA Bollschweiler C., Kuehn R., Klein A.;
RT "Non-repetitive AT-rich sequences are found in intergenic regions of
RT Methanococcus voltae DNA.";
RL EMBO J. 4:805-809(1985).
DR EMBL; X02517; CAA26352.1; -.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 17 AA; 1954 MW; 65BC6ED9F34B80DA CRC64;

Query Match 16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
DB 8 VPK 10

RESULT 71
Q8VME2          PRELIMINARY;          PRT;          17 AA.
AC Q8VME2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE PaC protein (Fragment).
GN PaC.
OS Pseudomonas putida.
OG Plasmid pMW0.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RA Grreated A., Lambertson L., Williams P.A., Thomas C.M.;
RT "Complete nucleotide sequence of IncP-9 plasmid pMW0.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344068; CAC86875.1; -.
KW Plasmid.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1903 MW; A58E0B85C355A999 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 13 LQP 15

RESULT 72
Q9EUB3          PRELIMINARY;          PRT;          17 AA.
AC Q9EUB3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CmlB (CmlA).
GN CMLB OR CMLA.
OS Corynebacterium striatum.
OG Plasmid pTP10.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=43770;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=M82B; PLASMDID=PTP10;
RX MEDLINE=20194806; PubMed=10732668;
RA Tauch A., Krief S., Kalinowski J., Puhler A.;
RT "The 51,409-bp R-plasmid pTP10 from the multiresistant clinical
RT isolate Corynebacterium striatum M82B is composed of DNA segments
RT initially identified in soil bacteria and in plant, animal, and human
RT pathogens.";
RL Mol. Gen. Genet. 263:1-11(2000).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=M82B; PLASMDID=PTP10;
RX MEDLINE=98414982; PubMed=9735314;
RA Tauch A., Zheng Z., Puhler A., Kalinowski J.;
RT "Corynebacterium striatum chloramphenicol resistance transposon
RT Tn5564: genetic organization and transposition in Corynebacterium
RT glutamicum.";
RL Plasmid 40:126-139(1998).
DR EMBL; AF024666; AAG03379.1; -.
DR EMBL; AF024666; AAG03369.1; -.
KW Plasmid.
SQ SEQUENCE 17 AA; 1715 MW; 13CA5DE6CA436B0F CRC64;

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
Db 3 GVP 5

RESULT 73
Q14001 PRELIMINARY; PRT; 17 AA.
AC Q14001;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclic nucleotide phosphodiesterase (Fragment).
GN CGIPDEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079687; PubMed=8921398;
RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
RT "Molecular cloning and chromosomal assignment of the human homologue
RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
RT in fat metabolism located at 11p15.1.";
RL Genomics 37:211-218(1996).
DR EMBL; X95522; CAA64776.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
Db 14 LQP 16

RESULT 74
Q9UCC6 PRELIMINARY; PRT; 17 AA.
AC Q9UCC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

```

```

DE Pleiotrophin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 17 AA; 1925 MW; 442BC8BEFD417ADD CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
Db 9 KVK 11

RESULT 75
Q9XSG1 PRELIMINARY; PRT; 17 AA.
AC Q9XSG1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SMCX (Fragment).
GN SMCX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Poloumienko A., Blecher S.;
RT "Exon-intron structure of SMCX and SMCY genes in bovine and swine.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135448; AAD34440.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
Db 2 PEI 4

Search completed: November 25, 2003, 19:33:59
Job time : 36.8023 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVFKVETWVPK 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03.*

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Ewe colostrinin pe
5	18	100.0	18	23	Colostrinin consti
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Neural cell regula
8	18	100.0	18	23	Retinoblastoma bin
9	5	27.8	11	21	AA165837

10	5	27.8	12	22	AA887422	Human gene 3 encod
11	5	27.8	14	14	AA438371	OmpA2-R-7 signal p
12	5	27.8	16	24	ABP82578	G protein-coupled
13	5	27.8	16	24	ABP82609	G protein-coupled
14	4	22.2	4	20	AAW93084	Human erythropoiet
15	4	22.2	4	23	ABG32218	Sheep colostrinin
16	4	22.2	6	14	AA32746	PK40 TAU/neurofila
17	4	22.2	6	20	AA27421	PK40 protein kinas
18	4	22.2	6	23	AAW51129	Bovine TAU/neurofi
19	4	22.2	7	14	AA33159	HPV E7 protein - R
20	4	22.2	7	20	AAV49017	Membrane dipeptida
21	4	22.2	7	21	AA38822	T7 phage coat prot
22	4	22.2	7	22	AA38822	Colostrinin derive
23	4	22.2	7	22	AA38822	Colostrinin peptid
24	4	22.2	7	22	AA38822	Colostrinin peptid
25	4	22.2	7	22	AA38822	Colostrinin consti
26	4	22.2	7	22	AA38822	Colostrinin consti
27	4	22.2	7	22	AA38822	Colostrinin consti
28	4	22.2	7	22	AA38822	Colostrinin consti
29	4	22.2	7	22	AA38822	Colostrinin consti
30	4	22.2	7	22	AA38822	Colostrinin consti
31	4	22.2	7	22	AA38822	Colostrinin consti
32	4	22.2	7	22	AA38822	Colostrinin consti
33	4	22.2	7	22	AA38822	Colostrinin consti
34	4	22.2	7	22	AA38822	Colostrinin consti
35	4	22.2	7	22	AA38822	Colostrinin consti
36	4	22.2	7	22	AA38822	Colostrinin consti
37	4	22.2	7	22	AA38822	Colostrinin consti
38	4	22.2	7	22	AA38822	Colostrinin consti
39	4	22.2	7	22	AA38822	Colostrinin consti
40	4	22.2	7	22	AA38822	Colostrinin consti
41	4	22.2	7	22	AA38822	Colostrinin consti
42	4	22.2	7	22	AA38822	Colostrinin consti
43	4	22.2	7	22	AA38822	Colostrinin consti
44	4	22.2	7	22	AA38822	Colostrinin consti
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48	4	22.2	7	22	AA38822	Colostrinin consti
49	4	22.2	7	22	AA38822	Colostrinin consti
50	4	22.2	7	22	AA38822	Colostrinin consti
51	4	22.2	7	22	AA38822	Colostrinin consti
52	4	22.2	7	22	AA38822	Colostrinin consti
53	4	22.2	7	22	AA38822	Colostrinin consti
54	4	22.2	7	22	AA38822	Colostrinin consti
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61	4	22.2	7	22	AA38822	Colostrinin consti
62	4	22.2	7	22	AA38822	Colostrinin consti
63	4	22.2	7	22	AA38822	Colostrinin consti
64	4	22.2	7	22	AA38822	Colostrinin consti
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80	4	22.2	7	22	AA38822	Colostrinin consti
81	4	22.2	7	22	AA38822	Colostrinin consti
82	4	22.2	7	22	AA38822	Colostrinin consti

HER2/NEU DR 3a mot

83 MHC class-I associ
84 HPV 16 E7 A2 MHC-b
85 HPV 16 E7 A2 MHC-b
86 HPV 16 E7 A2 MHC-b
87 HPV strain 16 E7 p
88 HPV E7 peptide whi
89 Polyepitopic pep
90 A polyepitopic pep
91 HPV type 16 L1 pro
92 Immunogenic HIV pe
93 MHC class I molecu
94 MHC class I molecu
95 Human leukocyte an
96 Human leukocyte an
97 Human leukocyte an
98 Human leukocyte an
99 Human leukocyte an
100 Human leukocyte an

ALIGNMENTS

RESULT 1
AAB72266
ID AAB72266 standard; peptide; 18 AA.
XX
AC AAB72266;
XX
DT 14-MAY-2001 (first entry)
XX
XX Colostrinin derived cytokine inducing peptide SEQ ID 21.
DE
XX Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
XX WO200111937-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 17-AUG-2000; 2000WO-US22818.
XX
XX PR 17-AUG-1999; 99US-0149311.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX (REG-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX
XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX
XX Claim 1; Page 34; 50pp; English.

CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPEIMGVPKVKETWVPK 18
Db 1 LQPEIMGVPKVKETWVPK 18
RESULT 2
AAB72519
ID AAB72519 standard; Peptide; 18 AA.
XX
AC AAB72519;
XX
DT 09-MAY-2001 (first entry)
XX
XX Colostrinin peptide #20.
XX
XX Dermatological; oxidative stress regulator; colostrinin.
XX Unidentified.
XX
XX WO200112650-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 17-AUG-2000; 2000WO-US22665.
XX
XX PR 17-AUG-1999; 99US-0149310.
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX
XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
XX Claim 6; Page 25; 48pp; English.
XX
XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPEIMGVPKVKETWVPK 18
Db 1 LQPEIMGVPKVKETWVPK 18
RESULT 3
AAB72551
ID AAB72551 standard; Peptide; 18 AA.
XX
AC AAB72551;
XX
DT 09-MAY-2001 (first entry)
XX


```

DE Colostrinin peptide #20.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX Unidentified.
XX OS
XX WO200112651-A2.
XX PN
XX 22-FEB-2001.
XX PD
XX PF 17-AUG-2000; 2000WO-US22774.
XX PR
XX PR 17-AUG-1999; 99US-0149633.
XX PA
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI
XX PI Boldogh I;
XX DR
XX DR WPI; 2001-226545/23.
XX XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX PT regulator, for promoting neural cell differentiation and treating
XX PT damaged neural cells in a patient -
XX PT
XX PS
XX PS Claim 6; Page 21; 35pp; English.
XX CC
XX The present invention relates to a method for promoting neural cell
XX CC differentiation and treating damaged neural cells, using colostrinin and
XX CC colostrinin constituent peptides (e.g. the present peptide) as a neural
XX CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX CC
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVFKVKTWVPK 18
DB |||||||||||||||
1 LQPEIMGVFKVKTWVPK 18

RESULT 4
AAB59329
ID AAB59329 standard; Peptide; 18 AA.
XX AC
XX AAB59329;
XX DT
XX DT 21-MAR-2001 (first entry)
XX DE
XX DE Ewe colostrinin peptide fragment C-4.
XX KW
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX OS
XX OS Ovis sp.
XX PN
XX PN WO2000075173-A2.
XX PD
XX PD 14-DEC-2000.
XX PF
XX PF 02-JUN-2000; 2000WO-GB02128.
XX PR
XX PR 02-JUN-1999; 99GB-0012852.
XX XX
XX (REGE-) REGEN THERAPEUTICS PLC.
XX PA
XX PA Georgiades JA;
XX PI
XX PI WPI; 2001-071058/08.
XX DR
XX DR Peptides having an N-terminal amino acid sequence isolated from
XX PT

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
XX PT characterized by amyloid plaques -
XX PS
XX PS Claim 7; Page 27; 63pp; English.
XX CC
XX The present invention provides the sequences of a number of peptides
XX CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX CC fragment of colostrum. These peptides can be used in the treatment of
XX CC central nervous system disorders such as senile dementia, Parkinson's
XX CC disease, Alzheimer's disease, psychosis and neurosis, immune system
XX CC disorders such as bacterial and viral infections, to improve the
XX CC development of a child's immune system, as a dietary supplement, and to
XX CC promote the dissolution of beta-amyloid plaques.
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVFKVKTWVPK 18
DB |||||||||||||||
1 LQPEIMGVFKVKTWVPK 18

RESULT 5
AAE20248
ID AAE20248 standard; peptide; 18 AA.
XX AC
XX AAE20248;
XX DT
XX DT 18-JUN-2002 (first entry)
XX DE
XX DE Colostrinin constituent peptide #20.
XX KW
XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX KW transplantation; implantation; dermatological; vulnery.
XX OS
XX OS Unidentified.
XX FH
XX FH Key Location/Qualifiers
XX FT
XX FT Modified-site 18 /note= "Optionally C-terminal amide"
XX XX
XX PN
XX PN WO200213850-A1.
XX PD
XX PD 21-FEB-2002.
XX PF
XX PF 17-AUG-2000; 2000WO-US22776.
XX PR
XX PR 17-AUG-2000; 2000WO-US22776.
XX XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX PA
XX PI
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX DR
XX DR WPI; 2002-269151/31.
XX XX
XX Composition useful for the modulation of blood cell proliferation in a
XX PT patient comprises a blood cell regulator selected from colostrinin, its
XX PT constituent peptide and/or analog -
XX PS
XX PS Claim 6; Page 25; 51pp; English.
XX CC
XX The invention relates to a composition which comprises a blood cell
XX CC regulator selected from colostrinin, its constituent peptide and/or
XX CC analogue. The invention is used for modulating the oxidative stress
XX CC level in a cell e.g. mammalian or human cell present in a cell culture,
XX CC tissue, organ, or organism; or for treating oxidative damage to the skin
XX CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETMVPK 18
 |||||
 Db 1 LQPEIMGVPKVKETMVPK 18

RESULT 6

AAM51055
 ID AAM51055 standard; Peptide; 18 AA.

XX AAM51055;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 103-120).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 103-120. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunologic regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETMVPK 18
 |||||
 Db 1 LQPEIMGVPKVKETMVPK 18

RESULT 7

AAO14597

XX AAO14597 standard; peptide; 18 AA.

XX AAO14597;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 20.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.3e-12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVGVKVKETWPK 18
| | | | | | | | | | | | | | | | | |

Db 1 LQPEIMGVGVKVKETWPK 18

RESULT 8

AAV65836

ID AAV65836 standard; Peptide; 10 AA.

XX

AC AAV65836;

XX

DT 10-FEB-2000 (first entry)

XX

DE Retinoblastoma binding protein 1 isoform I mutant peptide 6.

XX

KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;

KW mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO9958552-A2.

XX

PD 18-NOV-1999.

XX

PF 03-MAY-1999; 99WO-NO00143.

XX

PR 08-MAY-1998; 98NO-0002097.

XX

PA (NHYP) NORSK HYDRO AS.

XX

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

XX

DR WPI; 2000-039064/03.

XX

PT New peptides derived from genes with frameshift mutations, used to

PT develop products for the treatment and prophylaxis of cancers -

XX

PS Claim 13; Page 28; 166pp; English.

XX

CC Peptides AAV6584-Y66142 are fragments of mutant proteins arising from a

CC frameshift mutation in a gene from a cancer cell. The peptides are

CC characterised in that they:

CC (i) are at least 8 amino acids long and a fragment of a mutant protein

CC arising from a frameshift mutation in a gene of a cancer cell;

CC (ii) consist of at least one amino acid of the mutant part of a protein

CC sequence encoded by the gene;

CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal

CC part of the protein sequence preceding the amino terminus of the mutant

CC sequence and may further extend to the carboxyl terminus of the mutant

CC part of the protein as determined by a new stop codon generated by the

CC frameshift mutation; and

CC (iv) induce, either in their full lengths or after processing by an

CC antigen presenting cell (APC), T cell responses.

CC The genes that the peptides are derived from, are characterised as

CC susceptible to frameshift mutation by having a mono nucleoside base

CC repeat sequence of at least 5 residues, or a di-nucleoside base repeat

CC sequence of at least 4 di-nucleoside base units. The peptides are

CC created by the addition or deletion of 1 or 2 nucleoside base residues

CC from the repeat sequence. The novel peptides can elicit T cell responses

CC and toxicity against tumours and cancer cells carrying genes with

CC frameshift mutations. The novel peptides and DNA sequences can be used

CC for the preparation of a composition for the treatment or prophylaxis of

CC cancer.

XX

SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVKE 13
| | | | |

Db 2 PKVKE 6

RESULT 9

AAV65837

ID AAV65837 standard; Peptide; 11 AA.

XX

AC AAV65837;

XX

DT 10-FEB-2000 (first entry)

XX

DE Retinoblastoma binding protein 1 isoform I mutant peptide 7.

XX

KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;

KW mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO9958552-A2.

XX

PD 18-NOV-1999.

XX

PF 03-MAY-1999; 99WO-NO00143.

XX

PR 08-MAY-1998; 98NO-0002097.

XX

PA (NHYP) NORSK HYDRO AS.

XX

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

XX

DR WPI; 2000-039064/03.

XX

PT New peptides derived from genes with frameshift mutations, used to

PT develop products for the treatment and prophylaxis of cancers -

XX

PS Claim 13; Page 28; 166pp; English.

XX

CC Peptides AAV6584-Y66142 are fragments of mutant proteins arising from a

CC frameshift mutation in a gene from a cancer cell. The peptides are

CC characterised in that they:

CC (i) are at least 8 amino acids long and a fragment of a mutant protein

CC arising from a frameshift mutation in a gene of a cancer cell;

CC (ii) consist of at least one amino acid of the mutant part of a protein

CC sequence encoded by the gene;

CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal

CC part of the protein sequence preceding the amino terminus of the mutant

CC sequence and may further extend to the carboxyl terminus of the mutant

CC part of the protein as determined by a new stop codon generated by the

CC frameshift mutation; and

CC (iv) induce, either in their full lengths or after processing by an

CC antigen presenting cell (APC), T cell responses.

CC The genes that the peptides are derived from, are characterised as

CC susceptible to frameshift mutation by having a mono nucleoside base

CC repeat sequence of at least 5 residues, or a di-nucleoside base repeat

CC sequence of at least 4 di-nucleoside base units. The peptides are

CC created by the addition or deletion of 1 or 2 nucleoside base residues

CC from the repeat sequence. The novel peptides can elicit T cell responses

CC and toxicity against tumours and cancer cells carrying genes with

CC frameshift mutations. The novel peptides and DNA sequences can be used

CC for the preparation of a composition for the treatment or prophylaxis of

CC cancer.

XX

SQ Sequence 11 AA;

Query Match 27.8%; Score 5; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVKE 13
 |||||
 Db 2 PKVKE 6

RESULT 10
 AAB87422
 ID AAB87422 standard; peptide; 12 AA.
 XX
 AC AAB87422;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human gene 3 encoded secreted protein fragment, SEQ ID NO:163.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiotensin disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnery;
 KW cell culture; chemotaxis; food additive;
 KW binding partner identification.
 XX
 OS Homo sapiens.
 XX
 XX WO200118022-A1.
 XX
 PD 15-MAR-2001.
 XX
 XX
 PF 31-AUG-2000; 2000WO-US24008.
 XX
 PR 03-SEP-1999; 99US-0152315.
 PR 03-SEP-1999; 99US-0152317.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 XX Ni J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;
 PI Soppet DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DW;
 PI Moore PA, Shi Y, Wei Y, Florence KA;
 XX
 XX WPI; 2001-203081/20.
 XX
 XX Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -
 PT
 PS Disclosure; Page 18; 607pp; English.
 XX

CC AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted
 CC protein genes, and AAB87342-AAB87413 represent the proteins they encode.
 CC AAB87414-AAB87454 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,

CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.
 XX
 SQ Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPKV 11
 |||||
 Db 1 GVPKV 5

RESULT 11
 AAR43871
 ID AAR43871 standard; Protein; 14 AA.
 XX
 AC AAR43871;
 XX
 DT 25-MAR-2003 (updated)
 DT 23-DEC-1993 (first entry)
 XX
 DE OmpA2-R-7 signal peptide.
 XX
 KW Polypeptide; antibodies; HTLV; AIDS; vaccine.
 XX
 OS Human T-cell lymphotropic virus.
 XX
 PN EP552850-A1.
 XX
 PD 28-JUL-1993.
 XX
 PF 10-OCT-1985; 93EP-0200929.
 XX
 PR 10-OCT-1984; 84US-0659339.
 PR 23-JAN-1985; 85US-0693866.
 PR 10-OCT-1985; 85EP-0307260.
 XX
 XX (CENZ) CENTOCOR INC.
 PA
 XX Chang NT, Gallo RC, Wong-staal F;
 PI
 XX WPI; 1993-236543/30.
 DR N-PSDB; AAQ45924.
 DR
 XX Cloning and expression of new HTLV-III DNA - used to obtain
 PT polypeptide(s) and antibodies for diagnosis, prevention and
 PT treatment of HTLV-III infection, partic. AIDS
 XX
 PS Disclosure; Figure 6a; 31pp; English.
 XX

CC A fragment of DNA approximately 200-500 base pairs in length is
 CC ligated into a recombinant vector (OmpA1-R-6; ompA2-R-7 or ompA3-R-3)
 CC and used to transform E.coli. These cells then express a polypeptide
 CC which is immunoreactive with HTLV-III-specific antibody. The
 CC HTLV-III polypeptides can be used for the production
 CC of antibodies, in immunoassays for the detection of HTLV-
 CC III-specific antibodies and in vaccines for the prevention of AIDS.
 CC The antibodies can also be used to detect HTLV-III polypeptides.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 14 AA;
 Query Match 27.8%; Score 5; DB 14; Length 14;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PKVKE 13
 |||||
 Db 10 PKVKE 14
 |||||
 RESULT 12
 ID ABP82578
 XX ABP82578 standard; Peptide; 16 AA.
 AC ABP82578;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1251.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 XX WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-257144P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burmer GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX
 PS Claim 1; Fig 2; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 16 AA;

Query Match 27.8%; Score 5; DB 24; Length 16;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PKVKE 13
 |||||
 Db 2 PKVKE 6
 |||||

RESULT 13 ABP82609

ID ABP82609 standard; Peptide; 16 AA.

AC ABP82609;

DT 04-MAR-2003 (first entry)

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1282.

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

OS Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX

PS Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:

CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting

CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 16 AA;

Query Match 27.8%; Score 5; DB 24; Length 16;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVKE 13
 DB 8 PKVKE 12

RESULT 14
 AAW93084
 ID AAW93084 standard; Protein; 4 AA.

AC AAW93084;

DT 19-MAY-1999 (first entry)

DE Human erythropoietin modified signal peptide N-terminal #3.

XX Erythropoietin; human; EPO; therapy; erythrocyte production; stimulation.

KW Erythropoietin.

OS Synthetic.

OS Homo sapiens.

PN WO9905268-A1.

XX 04-FEB-1999.

PF 22-JUL-1998; 98WO-EF04590.

XX 10-JUL-1998; 98US-0113692.

PR 23-JUL-1997; 97EP-0112640.

PR 03-DEC-1997; 97DE-1053681.

XX (BOE) BOEHRINGER MANNHEIM GMBH.

XX Auer J, Brandt M, Honold K, Koll H, Stern A;

XX WPI: 1999-142926/12.

DR N-PSDB; AAX22430.

XX New human cells containing erythropoietin gene controlled by

PT heterologous promoter - for large scale production of pure,

PT glycosylated erythropoietin

XX Claim 11; Page 32; 70pp; German.

XX This invention describes human cells containing a copy of an endogenous
 CC gene for erythropoietin (EPO) linked to a heterologous promoter,
 CC functional in human cells, and capable of producing at least 200 ng
 CC EPO/million cells/24 hr. The invention also describes a DNA construct for
 CC activating an endogenous EPO gene in a human cell comprising (i) two

CC flanking sequences, homologous to regions (i.e. the 5'-untranslated
 CC region, exon 1 or intron 1) of the human EPO gene locus and capable of
 CC homologous recombination, including in the exon 1 region a modified
 CC sequence encoding Met-X1-X2-X3 where X1 = Gly or Ser; X2 = Ala, Val, Leu,
 CC Ile, Ser or Pro; X3 = Pro, Arg, Cys or His; but X1-X2-X3 is not
 CC Gly-Val-His (ii) a positive selection marker gene (iii) a heterologous
 CC expression control sequence and (iv) optionally an amplification gene.
 CC The method of the invention can be used to produce EPO for therapeutic
 CC use (stimulation of erythrocyte production). The new cells make possible
 CC economical, large scale production of pure human EPO, and are
 CC significantly more productive than transformed CHO cells. Altering the
 CC signal sequence and/or the distance between promoter and start signal
 CC optimises EPO expression.

XX Sequence 4 AA;

Query Match 22.2%; Score 4; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGVP 9
 DB 1 MGVP 4

RESULT 15
 ABG32218
 ID ABG32218 standard; peptide; 4 AA.

XX AC ABG32218;

XX 05-NOV-2002 (first entry)

XX Sheep colostrinin derived peptide #12.

KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;
 KW central nervous system disorder; neurological disorder; neurosis;
 KW mental disorder; psychosis; neurodegenerative disorder;
 KW Alzheimer's disease; motor neuron disease; immune system disorder;
 KW acquired immunological deficiency; bacterial infection; viral infection;
 KW amyloid plaque; dietary supplement; cachexia; weight loss;
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;
 KW drug addiction; drug withdrawal.

OS Ovis aries.

XX WO200246211-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-GB05376.

XX 06-DEC-2000; 2000GB-0029777.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI: 2002-619016/66.

XX Novel peptides isolated from colostrinin polypeptide, useful for
 PT treating viral and bacterial infections, disorders of immune system and
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food
 PT additive -

XX Claim 1; Page 8; 16pp; English.

XX The invention relates to a peptide derived from colostrinin (a colostrum
 CC protein known to be a cytokine inducer) substantially entirely consists
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included
 CC are a composition comprising two or more of the peptides in combination
 CC with a carrier, a dietary supplement comprising an orally ingestible
 CC combination of the peptide in combination with a carrier and an antibody

CC which binds to the peptide, and which is obtainable by using peptide as
 CC an antigen. The peptide is useful as a medicament for treating chronic
 CC disorders of central nervous system e.g., neurological disorders and/or
 CC mental disorders such as psychosis and/or neurosis, dementia,
 CC neurodegenerative disorders such as Alzheimer's disease, motor
 CC neuron disease, chronic disorders of immune system, diseases
 CC with bacterial and viral etiologies, acquired immunological deficiencies,
 CC chronic bacterial, viral infections. The peptide is also useful for
 CC treating diseases characterised by presence of amyloid plaque. The
 CC peptide is also useful as a dietary supplement for babies, small
 CC children, adults who have been subjected to chemotherapy and/or
 CC adults who have suffered from cachexia or weight loss due to chronic
 CC disease. The peptide is also useful for treating senile dementia,
 CC Parkinson's disease, emotional disturbances and depression. The peptides
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,
 CC after a period of detoxification, and in persons dependent on stimulants.
 CC The present sequence is a colostrinin derived peptide of the invention.

SQ Sequence 4 AA;
 Query Match 22.2%; Score 4; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
 Db 1 PKVK 4

RESULT 16
 AAR32746
 ID AAR32746 standard; peptide; 6 AA.

AC AAR32746;

DT 25-MAR-2003 (updated)
 DT 18-JUN-1993 (first entry)

DE PK40 TAU/neurofilament protein kinase tryptic peptide.

XX Neurodegenerative disease; treatment; diagnosis; Alzheimer's;
 XX kinase inhibitor; paired helical fragments; PHF; tangles; formation.

OS Homo sapiens.

PN WO9303148-A2.

XX 18-FEB-1993.

XX 10-JUL-1992; 92WO-US05825.

XX 09-AUG-1991; 91US-0742880.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Ingram VM, Roder HM;

XX WPI; 1993-076505/09.

XX Prepn. contg. isolated, pure non-skeletal associated kinase -
 XX used in treatment and diagnosis of neurodegenerative conditions
 XX e.g. Alzheimer's disease

XX Example; Page 76; 88pp; English.

XX The sequence is that of a tryptic peptide of TAU/neurofilament
 CC protein kinase PK40. Antibodies (monoclonal or polyclonal) specific
 CC for PK40 which are capable of binding to and inhibiting the kinase
 CC activity of PK 40 may be used to reduce phosphorylation activity in
 CC the cell, and to reduce or prevent formation of paired helical
 CC fragments (PHF) or tangles. This allows investigation e.g. of the
 CC contribution of such phosphorylation activity to cell maintenance
 CC and to neurocellular states characteristic of neurodegenerative

CC diseases, partic. Alzheimer's and ageing. The sequence shows a very
 CC close match to the ERK-kinase family proteins and so PK40 can be
 CC considered to be a member of the cell cycle-associated ERK kinase
 CC family.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEIM 6
 Db 2 PEIM 5

RESULT 17
 AAY27421

ID AAY27421 standard; peptide; 6 AA.

XX AAY27421;

DT 26-NOV-1999 (first entry)

XX PK40 protein kinase tryptic peptide.

XX TAU hyper-phosphorylation; adenosine triphosphate; ATP binding site;
 XX PK40; TAU kinase; neurofilament protein kinase; Alzheimer's disease;
 XX tryptic peptide; ERK-kinase.

OS Homo sapiens.

PN US5955444-A.

XX 21-SEP-1999.

XX 07-JUN-1995; 95US-0480793.

XX 10-JUL-1992; 92US-0912293.

XX 09-AUG-1991; 91US-0742880.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Roder HM, Ingram VM;

XX WPI; 1999-560501/47.

XX Inhibiting abnormal TAU hyper-phosphorylation in cells for the
 XX treatment of Alzheimer's disease

XX Example 11; Columns 33-34; 19pp; English.

XX The invention relates to a new method for inhibiting abnormal TAU hyper-
 CC phosphorylation activity in cells. The method comprises contacting a
 CC cell with an inhibitor which binds to an adenosine triphosphate (ATP)
 CC binding site on PK40 (a TAU/neurofilament protein kinase) and therefore
 CC inhibits the phosphorylating activity of PK40 (which is characteristic of
 CC abnormal TAU hyper-phosphorylation in Alzheimer's disease). The method
 CC may be used for inhibiting TAU hyper-phosphorylation activity in cells.
 CC In particular, it may be used for inhibiting the phosphorylating activity
 CC of PK40 which is characteristic of abnormal TAU hyper-phosphorylation in
 CC Alzheimer's disease. Sequences AAY27408-422 represent peptides obtained
 CC by tryptic digestion of PK40 kinase. Peptides AAY27410-422 has high
 CC homology to the ERK-kinase family proteins.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEIM 6

Db |||||
 2 PEIM 5

RESULT 18

AAM51129

ID AAM51129 standard; Peptide; 6 AA.

XX AC AAM51129;

XX DT 06-JUN-2002 (first entry)

XX DE Bovine TAU/neurofilament protein kinase PK40 tryptic peptide 14.

XX KW PK40; TAU; neurofilament; protein kinase; enzyme; human;

XX KW ERK kinase; phosphorylation; ageing; Alzheimer's disease;

XX KW Parkinson's disease; Huntington's disease; brain infarct;

XX KW neurotropic; neuroprotective; diagnosis; therapy.

XX OS Bos taurus.

XX PN US2002025942-A1.

XX PD 28-FEB-2002.

XX PF 20-MAR-1998; 98US-0045020.

XX PR 10-JUL-1992; 92US-0912293.

XX PR 07-JUN-1995; 95US-0480793.

XX PR 09-AUG-1991; 91US-0742880.

XX PA (INGR/) INGRAM V M.

XX PA (RODE/) RODER H M.

XX PI Ingram VM, Roder HM;

XX DR WPI; 2002-255975/30.

XX PT Preparation for phosphorylating dephosphorylated neurofilament-M,
XX PT comprises isolated, pure, nonskeletal-associated kinase -
XX Example 11; Page 17; 21pp; English.
XX CC The present sequence is that of tryptic peptide 14, which is 1 of
XX CC 15 peptides (see AAM51116-30) obtained by trypsin digestion of a
XX CC novel TAU/neurofilament protein kinase, termed PK40, isolated from
XX CC bovine brain. PK40 is capable of phosphorylating completely
XX CC dephosphorylated (cd) neurofilament-M (NF-M) so as to cause a
XX CC complete shift on SDS-PAGE of the apparent K_r to that of native
XX CC NF-M. It also causes a partial shift of cdNF-H. PK40 is capable
XX CC of causing a complete shift of bovine cdTAU or human TAU isoform
XX CC expressed in *Escherichia coli*. Under saturation phosphorylation
XX CC conditions, PK40 causes a change in the isoform pattern that
XX CC closely resembles the pattern of human TAU proteins extracted from
XX CC paired helical filaments. PK40 also phosphorylates both KSP sites
XX CC of TAU and abolishes the TAU 1 epitope. PK40 was identified using
XX CC a novel kinase immunoassay of the invention. Peptides 3-15 show
XX CC homology to ERK1 and ERK2, suggesting that PK40 is a member of the
XX CC cell cycle-associated ERK kinase family. A novel assay that can be
XX CC used as a diagnostic test for early Alzheimer's disease measures
XX CC the level of neuroprotein phosphorylation activity in a human cell
XX CC by PK40 or PK36. The assay can also be used to diagnose other
XX CC conditions affected by neuronal degeneration such as Parkinson's
XX CC disease, Huntington's disease, normal ageing and brain infarcts.
XX CC An inhibitor of PK40 (e.g. an antibody or ATP) may be useful in the
XX CC treatment of these conditions.

XX SQ Sequence 6 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEIM 6
 |||||
DB 2 PEIM 5

RESULT 19

AAR33159

ID AAR33159 standard; peptide; 7 AA.

XX AC AAR33159;

XX DT 25-MAR-2003 (updated)

XX DT 25-JUN-1993 (first entry)

XX DE HPV E7 protein - RBG protein binding inhibitor peptide.

XX KW Human papilloma virus; retinoblastoma gene; genital warts;

XX KW cervical cancer; treatment.

XX OS Synthetic.

XX PN EP531080-A2.

XX PD 10-MAR-1993.

XX PF 01-SEP-1992; 92EP-0307905.

XX PR 04-SEP-1991; 91US-0754829.

XX PA (MERI) MERCK & CO INC.

XX PI Oliff AI, Riemen MW;

XX DR WPI; 1993-078581/10.

XX PT New polypeptide(s) which inhibit human papilloma virus binding to
XX PT RBG protein - useful for treating genital warts and cervical cancer
XX PS Claim 7; Page 15; 15pp; English.
XX CC The sequence is that of a peptide which inhibits binding of human
XX CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
XX CC protein. It can be used in the treatment of conditions caused by HPV,
XX CC esp. genital warts and cervical cancer.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 7 AA;

Query Match

Best Local Similarity 22.2%; Score 4; DB 14; Length 7;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
 |||||
DB 2 LQPE 5

RESULT 20

AAY49017

ID AAY49017 standard; Peptide; 7 AA.

XX AC AAY49017;

XX DT 20-MAR-2003 (updated)

XX DT 10-DEC-1999 (first entry)

XX DE Membrane dipeptidase-binding adrenal gland homing peptide #16.

XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;

XX KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;

XX KW membrane dipeptidase.

XX OS Synthetic.

OS Homo sapiens.
 XX WO9946284-A2.
 XX PD 16-SEP-1999.
 XX PF 10-MAR-1999; 99WO-US05284.
 XX PR 13-MAR-1998; 98US-0042107.
 XX PR 26-FEB-1999; 99US-0258754.
 XX PA (BURN-) BURNHAM INST.
 XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX WPI; 1999-571717/48.
 XX DR
 XX PT New peptides which selectively home to organs or tissues, used for,
 XX PT e.g. identifying target ligands and for therapy of pathological
 XX PT conditions -
 XX PS Claim 65; Page 155; 193pp; English.
 XX CC The present invention describes peptides that selectively home to a
 XX CC tissue or organ. The peptides can be used for identifying an organ
 XX CC or tissue, for identifying a target molecule expressed by an organ or
 XX CC tissue or for treating an organ or tissue pathology, where the organ or
 XX CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,
 XX CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the
 XX CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences
 XX CC which are used in the exemplification of the present invention.
 XX CC (Updated on 20-MAR-2003 to correct PR field.)
 XX CC
 XX SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PKVK 12
 Db ||||
 1 PKVK 4
 RESULT 21
 AAB35822
 ID AAB35822 standard; peptide; 7 AA.
 XX AC AAB35822;
 XX AC
 XX DT 26-FEB-2001 (first entry)
 XX DE T7 phage coat protein C-terminus modification K+ peptide.
 XX KW Epitope identification; display system; gene delivery; drug delivery;
 XX KW bacteriophage T7.
 XX OS Synthetic.
 XX WO200065350-A1.
 XX PN 02-NOV-2000.
 XX PD 27-APR-2000; 2000WO-US11270.
 XX PF 27-APR-1999; 98US-0131151.
 XX PR 07-JUN-1999; 99US-0139431.
 XX XX (MTRU-) MTRUS CORP.
 XX PA Wolff JA;
 XX PI WPI; 2000-687379/67.
 XX DR

XX Identifying new peptide ligands that protect phage which delivers drugs
 PT and genes in vivo, by binding to blood proteins, comprises exposing an
 PT epitope display system to blood products -
 XX Example 1; Page 55; 87pp; English.
 XX PS
 XX CC This invention relates to a process comprising exposing an epitope
 CC display system to blood products to identify useful epitopes. The process
 CC is useful for identifying new peptide ligands that protect the display
 CC system e.g. phage, which delivers drugs and genes in vivo. The delivery
 CC system may be inhibited through binding to complement, the process
 CC reveals peptides which may be used to protect the system from this
 CC inhibition. the present sequence represents a peptide which can be used
 CC to modify the C-terminal of a T7 phage coat protein. The peptide protects
 CC against inactivation.
 XX SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PKVK 12
 Db ||||
 4 PKVK 7
 RESULT 22
 AAB72261
 ID AAB72261 standard; peptide; 7 AA.
 XX AC AAB72261;
 XX AC
 XX DT 14-MAY-2001 (first entry)
 XX DE Colostrinin derived cytokine inducing peptide SEQ ID 16.
 XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX OS Synthetic.
 XX WO200111937-A2.
 XX PN 22-FEB-2001.
 XX PD 17-AUG-2000; 2000WO-US22818.
 XX PF 17-AUG-1999; 99US-0149311.
 XX PR (TEXA) UNIV TEXAS SYSTEM.
 XX PA (REGG-) REGEN THERAPEUTICS PLC.
 XX XX
 XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2001-202804/20.
 XX DR
 XX PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX PS
 XX CC Claim 1; Page 34; 50pp; English.
 XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.
XX
SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
Db 4 LOPE 7

RESULT 23

AAB72514
ID AAB72514 standard; Peptide; 7 AA.

XX AAB72514;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #15.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22665.

XX 17-AUG-1999; 99US-0149310.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX

PS Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidizing species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX

SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
Db 4 LOPE 7

RESULT 24

AAB72546
ID AAB72546 standard; Peptide; 7 AA.

XX AAB72546;
AC 09-MAY-2001 (first entry)
DT Colostrinin peptide #15.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrinum.
XX Unidentified.
XX WO200112651-A2.
XX 22-FEB-2001.
XX 17-AUG-2000; 2000WO-US22774.
XX 17-AUG-1999; 99US-0149633.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Boldogh I;
XX WPI; 2001-226545/23.
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX Claim 6; Page 21; 35pp; English.
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX

SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
Db 4 LOPE 7

RESULT 25

AAB59317
ID AAB59317 standard; Peptide; 7 AA.

XX AAB59317;

XX 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment B-2.

XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX

XX Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REGF-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOPE 4
 Db ||||
 4 LOPE 7
 RESULT 26
 AAEE20243
 ID AAEE20243 standard; peptide; 7 AA.
 XX
 AC AAEE20243;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #15.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "Optionally C-terminal amide"
 FT
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US22776.
 XX
 PR 17-AUG-2000; 2000WO-US22776.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2002-269151/31.
 XX
 CC Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell

CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOPE 4
 Db ||||
 4 LOPE 7
 RESULT 27
 AAMS1050
 ID AAMS1050 standard; Peptide; 7 AA.
 XX
 AC AAMS1050;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Colostrinin constituent peptide.
 XX
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "optional C-terminal amidation"
 FT
 PN WO200213849-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US22775.
 XX
 PR 17-AUG-2000; 2000WO-US22775.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI (REGG-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2002-269150/31.
 XX
 CC Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. The peptide is
 CC classified as having a beta-casein homologue precursor. Methods

CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide.
 CC
 CC Sequence 7 AA;
 CC
 CC Query Match 22.2%; Score 4; DB 23; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 LQPE 4
 CC |||||
 CC Db 4 LQPE 7
 CC
 CC RESULT 28
 CC AAO14592
 CC ID AAO14592 standard; peptide; 7 AA.
 CC AC AAO14592;
 CC XX
 CC DT 27-MAY-2002 (first entry)
 CC XX
 CC DE Neural cell regulatory colostrinin peptide 15.
 CC XX
 CC KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 CC KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 CC KW neural cell treatment.
 CC XX
 CC OS Unidentified.
 CC XX
 CC FH Key Location/Qualifiers
 CC FT Modified-site 7
 CC FT /note="Optional C-terminal amide"
 CC XX
 CC PN WO200213851-A1.
 CC XX
 CC PD 21-FEB-2002.
 CC XX
 CC PF 17-AUG-2000; 2000WO-US22777.
 CC XX
 CC PR 17-AUG-2000; 2000WO-US22777.
 CC XX
 CC PA (TEXA) UNIV TEXAS SYSTEM.
 CC XX
 CC PI Boldogh I, Stanton JG, Hughes TK;
 CC XX
 CC DR WPI; 2002-269152/31.
 CC XX
 CC PT Promoting cell differentiation in a patient involves use of blood cell
 CC PT regulator selected from colostrinin, its constituent peptide and/or
 CC PT analog
 CC XX
 CC PS Claim 7; Page 21; 37pp; English.
 CC XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the

CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 CC
 CC Sequence 7 AA;
 CC
 CC Query Match 22.2%; Score 4; DB 23; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 LQPE 4
 CC |||||
 CC Db 4 LQPE 7
 CC
 CC RESULT 29
 CC AAR10631
 CC ID AAR10631 standard; Protein; 8 AA.
 CC XX
 CC AC AAR10631;
 CC XX
 CC DT 25-MAR-2003 (updated)
 CC DT 18-APR-1991 (first entry)
 CC XX
 CC DE Human Papilloma Virus-16 "[Gln27]-E7-(20-27)-AMIDE" peptide.
 CC XX
 CC KW papilloma virus; retinoblastoma gene-binding protein; genital warts;
 CC KW cervical cancer.
 CC XX
 CC OS Synthetic.
 CC XX
 CC PN EP412762-A.
 CC XX
 CC PD 13-FEB-1991.
 CC XX
 CC PF 06-AUG-1990; 90EP-0308652.
 CC XX
 CC PR 09-APR-1990; 90US-0506981.
 CC PR 07-AUG-1989; 89US-0390569.
 CC XX
 CC PA (MERI) MERCK & CO INC.
 CC PA (OLIF/) OLIFF A I.
 CC XX
 CC PI Oliff AI, Riemen MW;
 CC XX
 CC DR WPI; 1991-045887/07.
 CC XX
 CC PT Papilloma virus and retinoblastoma gene-binding protein
 CC PT inhibitors - involves a specified aminoacid sequence contg. 13
 CC PT residues for treatment of genital warts and cervical cancer
 CC XX
 CC PS Claim 12; Page 11; 11pp; English.
 CC XX
 CC The peptide carries an amide group at the C-terminus. The sequence
 CC comprises residues 20 to 27 of the deduced HPV-16 E7 protein
 CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2, p.379,
 CC Plenum Press, N.Y. 1987) but with Gln replacing Asp at position 27.
 CC The peptides are used as screening tools and in the prevention,
 CC therapy, prophylaxis and treatment of HPV-induced diseases. They
 CC can also be used to raise antibodies either as vaccines or to
 CC heighten the immune response to an HPV infection all ready present.
 CC See also AAR10628-R10630, AAR10632-7.
 CC CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 CC Sequence 8 AA;
 CC
 CC Query Match 22.2%; Score 4; DB 12; Length 8;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LQPE 4
DB      2 LQPE 5

RESULT 30
AAR33158
ID AAR33158 standard; peptide; 8 AA.
XX
XX
AC AAR33158;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
DE HPV E7 protein - RBG protein binding inhibitor peptide.
XX
KW Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX
OS Synthetic.
XX
PN EP531080-A2.
XX
PD 10-MAR-1993.
XX
PF 01-SEP-1992; 92EP-0307905.
XX
PR 04-SEP-1991; 91US-0754829.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Oliff AI, Riemen MW;
XX
DR WPI; 1993-078581/10.
XX
PT New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
PS Claim 7; Page 15; 15pp; English.
XX
CC The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 8 AA;

Query Match      22.2%; Score 4; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
DB      2 LQPE 5

RESULT 31
AAW77186
ID AAW77186 standard; peptide; 8 AA.
XX
XX
AC AAW77186;
XX
DT 23-NOV-1998 (first entry)
XX
DE Pharmaceutically active peptide 27.
XX
KW Pharmaceutically active peptide; target; organ; lymphocyte; treatment;
KW pharmaceutical agent; disease; radioactive isotope; imaging agent.
XX
OS Synthetic.
OS Homo sapiens.
XX

PN WO9839469-A1.
XX
PD 11-SEP-1998.
XX
PF 04-MAR-1998; 98WO-US04188.
XX
PR 04-MAR-1997; 97US-0810074.
PR 04-MAR-1997; 97US-0039509.
XX
PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX
PI Belkind A, Golan I, Hagai Y, Lazarovits J, Levanon A;
PI Nimrod A, Panet A, Vogel T, Zeelson E;
XX
DR WPI; 1998-495863/42.
XX
PT New peptide(s) binding targets in organs and lymphocytes - for the
PT targetted delivery of toxins, anti-cancer drugs and cardiovascular
PT agents to arteries, veins, placenta, liver
XX
PS Claim 54; Page 97; 114pp; English.
XX
CC Sequences shown in AAW77160 to AAW77214 and AAW79167 represent
CC non-naturally- occurring pharmacuetically active peptides. These novel
CC peptides specifically bind to undetermined and determined targets in
CC various organs and in lymphocytes. The peptides can be used in
CC compositions, where they can be linked to pharmaceutical agents, to treat
CC various diseases and conditions. The peptides or chimeric polypeptides
CC comprising these pharmacuetically active peptides and a second peptide
CC may be labelled with a marker (radioactive isotope, etc) to form an
CC imaging agent. This agent is used to bind an organ so that the organ can
CC be imaged.
XX
XX
SQ Sequence 8 AA;

Query Match      22.2%; Score 4; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
DB      3 PKVK 6

RESULT 32
AAB35995
ID AAB35995 standard; Protein; 8 AA.
XX
XX
AC AAB35995;
XX
DT 01-MAR-2001 (first entry)
XX
DE Sorbitol dehydrogenase subunit 3 internal peptide.
XX
KW Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol;
KW L-sorbose production; 2-keto-L-gulonic acid.
XX
OS Gluconobacter oxydans.
XX
PN WO200065066-A1.
XX
PD 02-NOV-2000.
XX
PF 23-APR-1999; 99WO-IB00736.
XX
PR 23-APR-1999; 99WO-IB00736.
XX
PA (CHOI/) CHOI E.
PA (RHEE/) RHEE S.
PA (LEEE/) LEE E.
XX
PI Choi E, Rhee S, Lee E;
XX

```

DR WPI; 2000-687351/67.
 XX Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule
 PT isolated from Gluconobacter suboxydans useful for the fermentative
 PT production of 2-keto-L-gulonic acid and L-sorbose from D-sorbitol -
 XX Example 2; Page 37; 96pp; English.
 XX This invention relates to an isolated membrane-bound sorbitol
 CC dehydrogenase (SDH) from Gluconobacter oxydans. The invention includes
 CC polynucleotides (AAC83153 - AAC83154) encoding the 3 subunits of SDH
 CC (AAB35987 - AAB35989). Also included in the invention are two
 CC polynucleotide sequences AAC83156 and AAC83157 which contain the subunit
 CC coding regions. The sorbitol dehydrogenase polynucleotide sequences are
 CC useful for producing L-sorbose from D-sorbitol and for increasing the
 CC production of 2-keto-L-gulonic acid by transforming a host cell,
 CC especially Gluconobacter with the DNA and selecting the transformed host
 CC cell. The present sequence represents the SDH subunit 3 internal
 CC peptide.
 XX Sequence 8 AA;
 SQ Query Match 22.2%; Score 4; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GVPK 10
 Db |||||
 5 GVPK 8
 RESULT 33
 ABP14637
 ID ABP14637 standard; Peptide; 8 AA.
 XX AC ABP14637;
 XX DT 15-JUL-2002 (first entry)
 DE HIV A03 super motif pol peptide #11.
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 OS WO200124810-A1.
 PN 12-APR-2001.
 XX PD 05-OCT-2000; 2000WO-US27766.
 XX PF 05-OCT-1999; 99US-0412863.
 XX PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HW;
 XX WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PS Claim 32; Page 168; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,

CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX Sequence 8 AA;
 SQ Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PKVK 12
 Db |||||
 5 PKVK 8
 RESULT 34
 ABP17276
 ID ABP17276 standard; Peptide; 8 AA.
 XX AC ABP17276;
 XX DT 15-JUL-2002 (first entry)
 DE HIV B27 super motif pol peptide #10.
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 OS WO200124810-A1.
 PN 12-APR-2001.
 XX PD 05-OCT-2000; 2000WO-US27766.
 XX PF 05-OCT-1999; 99US-0412863.
 XX PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HW;
 XX WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PS Claim 32; Page 223; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
 ||||
 Db 1 PKVK 4

RESULT 35
 ABP21662
 ID ABP21662 standard; Peptide; 8 AA.

XX AC ABP21662;
 XX DT 15-JUL-2002 (first entry)
 XX DE HIV A03 motif pol peptide #657.
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 XX KW vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 XX KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 XX PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 313; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
 ||||
 Db 5 PKVK 8

RESULT 36
 ABP23544
 ID ABP23544 standard; Peptide; 8 AA.

XX AC ABP23544;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A11 motif pol peptide #486.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 XX KW vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 XX KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 XX PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 351; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db ||||
5 PKVK 8

RESULT 37
AAG62330
ID AAG62330 standard; peptide; 8 AA.
XX
AC AAG62330;
XX
DT 24-AUG-2001 (first entry)
XX
DE Casein-related peptide SEQ ID 29.
XX
KW Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.
XX
OS Synthetic.
XX
PN WO200134828-A1.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-JP07930.
XX
PR 11-NOV-1999; 99JP-0321084.
XX
PA (CALV) CALPIS CO LTD.
XX
PI Yamamoto N, Ueno K, Ejiri M;
XX
DR WPI; 2001-343606/36.
XX
PT Production of tripeptides for treating hypertension and stress by
PT processing casein with proteinase and peptidase -
XX
PS Example 4; Page 13; 32pp; Japanese.
XX
CC This invention relates to a method for the production of tripeptides. The
CC method comprises treating material containing milk casein with a
CC proteinase to produce intermediate peptide containing ValProPro or
CC IleProPro with no proline residue any where else in the peptide. Use of
CC the peptides may result in hypotensive and tranquiliser activity. The
CC peptide can be used in treatments to lower blood pressure and in the
CC treatment of stress. The present sequence represents a peptide used in an
CC example illustrating the method of the invention.

XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db ||||
5 LOPE 8

RESULT 38

AAR10635
ID AAR10635 standard; Protein; 9 AA.
XX
AC AAR10635;
XX
DT 25-MAR-2003 (updated)
DT 18-APR-1991 (first entry)
XX
DE Human Papilloma Virus-16 "[Gln26]-E7-(20-28)-AMIDE" peptide.
XX
KW Papilloma virus; retinoblastoma gene-binding protein; genital warts;
KW cervical cancer.
XX
OS Synthetic.
XX
PN EP412762-A.
XX
PD 13-FEB-1991.
XX
PF 06-AUG-1990; 90EP-0308652.
XX
PR 09-APR-1990; 90US-0506981.
PR 07-AUG-1989; 89US-0390569.
XX
PA (MERI) MERCK & CO INC.
PA (OLIF) OLIFF A I.
XX
PI Oliff AI, Riemen MW;
XX
WPI; 1991-045887/07.
XX
DR Papilloma virus and retinoblastoma gene-binding protein
PT inhibitors - involves a specified aminoacid sequence contg. 13
PT residues for treatment of genital warts and cervical cancer
XX
PS Claim 12; Page 11; 11pp; English.
XX
CC The peptide carries an amide group at the C-terminus. The sequence
CC comprises residues 20 to 28 of the deduced HPV-16 E7 protein
CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2,p.379,
CC Plenum Press, N.Y. 1987) but with Gln replacing Thr at position 26.
CC The peptides are used as screening tools and in the prevention,
CC therapy, prophylaxis and treatment of HPV-induced diseases. They
CC can also be used to raise antibodies either as vaccines or to
CC heighten the immune response to an HPV infection all ready present.
CC See also AAR10628-R10634, AAR10636-7.
XX
XX (Updated on 25-MAR-2003 to correct PA field.)
SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db ||||
2 LOPE 5

RESULT 39
AAR33157
ID AAR33157 standard; peptide; 9 AA.
XX
AC AAR33157;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
DE HPV E7 protein - RBG protein binding inhibitor peptide.
XX
KW Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX


```

OS Synthetic.
PN EP531080-A2.
XX
XX 10-MAR-1993.
XX
XX 01-SEP-1992; 92EP-0307905.
XX
XX 04-SEP-1991; 91US-0754829.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Oliff AI, Riemen MW;
XX
XX WPI; 1993-078581/10.
XX
XX New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
XX Claim 7; Page 15; 15pp; English.
XX
XX The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 14; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LOPE 4
XX ||||
XX 1 LOPE 4
XX
XX RESULT 41
XX AAR33170
XX ID AAR33170 standard; peptide; 9 AA.
XX
XX AC AAR33170;
XX
XX 25-MAR-2003 (updated)
XX 25-JUN-1993 (first entry)
XX
XX HPV E7 protein - RBG protein binding inhibitor peptide.
XX
XX Human papilloma virus; retinoblastoma gene; genital warts;
XX cervical cancer; treatment.
XX
XX Synthetic.
XX
XX EP531080-A2.
XX
XX 10-MAR-1993.
XX
XX 01-SEP-1992; 92EP-0307905.
XX
XX 04-SEP-1991; 91US-0754829.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Oliff AI, Riemen MW;
XX
XX WPI; 1993-078581/10.
XX
XX New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
XX Claim 7; Page 15; 15pp; English.
XX
XX The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 14; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LOPE 4
XX ||||
XX 2 LOPE 5
XX
XX RESULT 40
XX AAR33163
XX ID AAR33163 standard; peptide; 9 AA.
XX
XX AC AAR33163;
XX
XX 25-MAR-2003 (updated)
XX 25-JUN-1993 (first entry)
XX
XX HPV E7 protein - RBG protein binding inhibitor peptide.
XX
XX Human papilloma virus; retinoblastoma gene; genital warts;
XX cervical cancer; treatment.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /label= OTHER
XX /note= "N-acetyl-Leu"
XX
XX EP531080-A2.
XX
XX 10-MAR-1993.
XX
XX 01-SEP-1992; 92EP-0307905.
XX
XX 04-SEP-1991; 91US-0754829.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Oliff AI, Riemen MW;
XX
XX WPI; 1993-078581/10.
XX

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RESULT 42
 AAR43741
 ID AAR43741 standard; peptide; 9 AA.
 XX
 AC AAR43741;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-MAY-1994 (first entry)
 XX
 XX MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.
 DE
 XX Human papilloma virus; major histocompatibility complex; prevention;
 KW treatment; virus-related diseases; T cell response; cervical; human;
 KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.
 XX
 OS Synthetic.
 XX
 XX WO9322338-A1.
 XX
 PD 11-NOV-1993.
 XX
 XX 04-MAY-1993; 93WO-NL00093.
 XX
 PR 05-MAY-1992; 92EP-0201252.
 PR 10-DEC-1992; 92EP-0203870.
 PR 01-FEB-1993; 93EP-0200243.
 PR 05-MAR-1993; 93EP-0200621.
 XX
 XX (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX Kast WM, Melief CJM, Sette AD, Sidney JC;
 PI
 XX WPI; 1993-368718/46.
 DR
 XX Peptide(s) derived from human papilloma virus - which bind to a
 PT human major histocompatibility complex Class I molecule, used for
 PT prevention and treatment of virus-related diseases
 XX
 XX Claim 5; Page 51; 64pp; English.
 XX
 CC The sequence is that of a peptide, derived from the E7 protein of
 CC human papilloma virus (HPV) (residues 11-19), which is able to bind
 CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell
 CC response effective against HPV, in partic. a HLA class I-restricted
 CC CD8+ cytotoxic T cell response. It can be used for prevention and
 CC treatment of cervical carcinoma and/or adenoma and other HPV-related
 CC diseases. It can also be used as a screening tool and in diagnostic
 CC applications.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 9 AA;
 PS
 CC Query Match 22.2%; Score 4; DB 14; Length 9;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 LQPE 4
 Db 5 LQPE 8
 XX
 RESULT 43
 AAR43742
 ID AAR43742 standard; peptide; 9 AA.
 XX
 AC AAR43742;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-MAY-1994 (first entry)
 XX
 XX MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.
 DE

KW Human papilloma virus; major histocompatibility complex; prevention;
 KW treatment; virus-related diseases; T cell response; cervical; human;
 KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.
 OS Synthetic.
 XX
 XX WO9322338-A1.
 XX
 PD 11-NOV-1993.
 XX
 XX 04-MAY-1993; 93WO-NL00093.
 XX
 PR 05-MAY-1992; 92EP-0201252.
 PR 10-DEC-1992; 92EP-0203870.
 PR 01-FEB-1993; 93EP-0200243.
 PR 05-MAR-1993; 93EP-0200621.
 XX
 XX (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX Kast WM, Melief CJM, Sette AD, Sidney JC;
 PI
 XX WPI; 1993-368718/46.
 DR
 XX Peptide(s) derived from human papilloma virus - which bind to a
 PT human major histocompatibility complex Class I molecule, used for
 PT prevention and treatment of virus-related diseases
 XX
 XX Claim 5; Page 51; 64pp; English.
 XX
 CC The sequence is that of a peptide, derived from the E7 protein of
 CC human papilloma virus (HPV) (residues 12-20), which is able to bind
 CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell
 CC response effective against HPV, in partic. a HLA class I-restricted
 CC CD8+ cytotoxic T cell response. It can be used for prevention and
 CC treatment of cervical carcinoma and/or adenoma and other HPV-related
 CC diseases. It can also be used as a screening tool and in diagnostic
 CC applications.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 9 AA;
 PS
 CC Query Match 22.2%; Score 4; DB 14; Length 9;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 LQPE 4
 Db 4 LQPE 7
 XX
 RESULT 44
 AAR59257
 ID AAR59257 standard; peptide; 9 AA.
 XX
 AC AAR59257;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-MAY-1995 (first entry)
 XX
 XX Peptide fragment (1.0229) of HPV binds HLA-A2.1.
 DE
 XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
 KW HIV1; core antigen; surface antigen; pharmaceutical composition;
 KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
 KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
 KW human leukocyte antigen.
 XX
 XX Human papilloma virus.
 OS
 XX WO9420127-A1.
 XX
 PD 15-SEP-1994.
 XX

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PF 04-MAR-1994; 94WO-US02353.
XX
XX 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX (CYTE-) CYTEL CORP.
PA
XX Gray HM, Kast WM, Sette A, Sidney J;
XX WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Example 5; Page 106; 138pp; English.
XX
XX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59257
CC has an IC50 of <0.0003 and the sequence occurs at position 14 in the HPV
CC E7 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 15; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LQPE 4
XX ||||
XX 2 LQPE 5
XX
XX
XX RESULT 45
XX AAR59246
XX ID AAR59246 standard; peptide; 9 AA.
XX AC AAR59246;
XX
XX 25-MAR-2003 (updated)
XX 04-MAY-1995 (first entry)
XX
XX Peptide fragment (1.0316) of c-ERB2 binds HLA-A2.1.
XX
XX antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
XX HIV1; core antigen; surface antigen; pharmaceutical composition;
XX in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
XX major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO9420127-A1.
XX
XX 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US02353.
XX
XX 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX (CYTE-) CYTEL CORP.
PA
XX Gray HM, Kast WM, Sette A, Sidney J;
XX WPI; 1994-302678/37.
XX

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XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Example 5; Page 105; 138pp; English.
XX
XX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59246
CC has an IC50 of <0.0002 and the sequence occurs at position 391 in the
CC c-ERB2 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 15; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LQPE 4
XX ||||
XX 2 LQPE 5
XX
XX
XX RESULT 46
XX AAR73799
XX ID AAR73799 standard; peptide; 9 AA.
XX AC AAR73799;
XX
XX 25-MAR-2003 (updated)
XX 19-JUN-1995 (first entry)
XX
XX Antigen fragment 115, from HPV(a) has binding affinity for HLA-2.1.
XX
XX antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
XX HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
XX human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
XX MAGE-1; melanoma antigen-1; core antigen; surface antigen;
XX pharmaceutical composition; in vivo; ex vivo; therapeutic;
XX diagnostic; MHC class I molecule; major histocompatibility complex;
XX HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
XX algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
XX herpes simplex virus; influenza A; M1.
XX
XX Human papilloma virus strain 16(a).
XX
XX WO9420127-A1.
XX
XX 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US02353.
XX
XX 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX (CYTE-) CYTEL CORP.
PA
XX Gray HM, Kast WM, Sette A, Sidney J;
XX WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Disclosure; Page 84; 138pp; English.
XX

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CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from HPV(a) E7(a)
 CC antigen has a binding value of 1.9000. The peptides of the invention can
 CC induce cytotoxic T lymphocytes which can react with target cells. They
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db |||||
 5 LOPE 8

RESULT 47
 AAR73800
 ID AAR73800 standard; peptide; 9 AA.

AC AAR73800;
 XX
 XX 25-MAR-2003 (updated)
 DT 19-JUN-1995 (first entry)
 XX
 DE Antigen fragment 116, from HPV has binding affinity for HLA-A2.1.
 XX
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
 KW herpes simplex virus; influenza A; M1.

XX Human papilloma virus strain 16.

XX WO9420127-A1.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.

XX 04-JUN-1993; 93US-0073205.

XX 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Kast WM, Sette A, Sidney J;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.

XX Disclosure; Page 84; 138pp; English.

XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7
 CC antigen has a binding value of 0.0130. The peptides of the invention can

CC induce cytotoxic T lymphocytes which can react with target cells. They
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db |||||
 4 LOPE 7

RESULT 48
 AAR73796
 ID AAR73796 standard; peptide; 9 AA.

AC AAR73796;

XX 25-MAR-2003 (updated)

DT 19-JUN-1995 (first entry)

XX Antigen fragment 112, from HPV has binding affinity for HLA-A2.1.

XX
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
 KW herpes simplex virus; influenza A; M1.

XX Human papilloma virus strain 16.

XX WO9420127-A1.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.

XX 04-JUN-1993; 93US-0073205.

XX 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Kast WM, Sette A, Sidney J;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.

XX Disclosure; Page 84; 138pp; English.

XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7
 CC antigen has a binding value of 1.4000. The peptides of the invention can
 CC induce cytotoxic T lymphocytes which can react with target cells. They
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

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Query Match      22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
DB 5 LOPE 8

RESULT 49
AAR80939
ID AAR80939 standard; peptide; 9 AA.
AC AAR80939;
DT 03-MAY-1996 (first entry)
DE Peptide for increasing HLA-A2.1 cell expression.
KW Human melanoma-associated protein; MAGE-2; tumour rejection antigen;
KW precursor; major histocompatibility complex; MHC; class I; HLA-A2.1;
KW binding motif; cytolytic T cell; CTL; induction; peptide loading;
KW primary immune response.
OS Synthetic.
OS WO9525530-A1.
PN 28-SEP-1995.
FD 21-MAR-1995; 95WO-US03535.
PF 24-MAR-1994; 94US-0217188.
PR (LUDW-) LUDWIG INST CANCER RES.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX Boon-Falleur T, Kast WM, Melief CJM, Van Der Bruggen P;
PI Visseren NW;
XX WPI; 1995-344456/44.
DR New peptide(s) based on tumour rejection antigen precursor MAGE-2 -
PT which bind HLA-A2 molecules to provoke cytolytic T cell prodn., used
PT partic. for treating cancers
XX Example 3; Page 37; 44pp; English.
CC Expression of HLA-A2.1 (T2) cells is increased by incubating T2
CC cells in medium containing the present peptide. T2 cells will
CC present the peptide bound to HLA-A2.1 in high amount and are good
CC antigen presenting cells. The claimed MAGE-2 peptides (see AAR80878-
CC AAR80888) can induce a similar primary immune response.
XX Sequence 9 AA;
SQ
Query Match      22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
DB 4 LOPE 7

RESULT 50
AAR78889
ID AAR78889 standard; peptide; 9 AA.
XX AAR78889;
XX 25-MAR-2003 (updated)
DT
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DT 27-MAR-1996 (first entry)
XX
DE HPV16 E7 11-19 cytotoxic T lymphocyte epitope.
XX
KW HPV16 E7 11-19; cytotoxic T; CTL; epitope; helper T; HTL; cell;
KW lymphocyte; antigens; treatment; disease prevention;
XX
OS Human papillomavirus.
XX
PN WO9522317-A1.
XX
PD 24-AUG-1995.
PF 16-FEB-1995; 95WO-US02121.
XX
PR 16-FEB-1994; 94US-0197484.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;
DR WPI; 1995-302545/39.
XX
PT Compsn. inducing cytotoxic T lymphocyte response to pref. viral,
PT bacterial, parasitic or tumour antigens - useful in the treatment
PT and prevention of diseases associated with the antigen e.g.
PT hepatitis B
XX
PS Example 14; Page 72; 109pp; English.
XX
CC A compen. which induces a cytotoxic T lymphocyte (CTL) response to
CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a
CC HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a
CC lipid conjugated helper T cell inducing peptide. The compsn. is
CC useful in the treatment and prevention of HPV associated diseases.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 9 AA;
Query Match      22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
DB 5 LOPE 8

RESULT 51
AAR78894
ID AAR78894 standard; peptide; 9 AA.
XX
AC AAR78894;
XX
DT 25-MAR-2003 (updated)
DT 27-MAR-1996 (first entry)
XX
DE HPV16 E7 12-20 cytotoxic T lymphocyte epitope.
XX
KW HPV16 E7 12-20; cytotoxic T; CTL; epitope; helper T; HTL; cell;
KW lymphocyte; antigens; treatment; disease prevention;
XX
OS Human papillomavirus.
XX
PN WO9522317-A1.
XX
PD 24-AUG-1995.
XX
PF 16-FEB-1995; 95WO-US02121.
XX
PR 16-FEB-1994; 94US-0197484.
XX
PA (CYTE-) CYTEL CORP.
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XX AC AAR84331;
XX DT 25-JAN-1996 (first entry)
XX DE HPV derived peptide (h).
XX KW Human papilloma virus; HPV; cytotoxic T-cell; HLA-B35 antigen;
XX KW prevention; treatment; carcinoma; cervix; cervical cancer.
XX OS Synthetic.
XX PN JP07126289-A.
XX PD 16-MAY-1995.
XX PF 02-NOV-1993; 93JP-0297378.
XX PR 02-NOV-1993; 93JP-0297378.
XX PA (KENB//) KENBARA K.
XX PA (TAKI//) TAKIGUCHI M.
XX DR WPI; 1995-212956/28.
XX XX
XX PT Human papilloma virus derived peptide(s) of 9-11 amino acids in
XX PT length - which bind with HLA-B35 antigen and are useful in
XX PT prevention and treatment of cervical cancer
XX PS Claim 1; Page 2; 7pp; Japanese.
XX CC The sequences given in AAR84324-35 are synthetic peptides which are
XX CC derived from human papilloma virus. These peptides are represented
XX CC in cytotoxic T-cells by binding with HLA-B35 antigen. They are
XX CC prepared by standard methods of peptide synthesis and may be used
XX CC for the prevention and treatment of carcinoma of the cervix.
XX XX
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 16; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 8 VPKV 11
Db 1 VPKV 4
|||
|||

RESULT 55
AAR89363
ID AAR89363 standard; peptide; 9 AA.
XX AC AAR89363;
XX DT 18-SEP-1996 (first entry)
XX DE Immunogenic peptide, based on Y1 analog of 1054.05.
XX DE Immunogenic peptide; supermotif; HLA molecule; CTL response;
XX KW therapeutic; diagnostic; cancer; viral infection; hepatitis B;
XX KW hepatitis C.
XX OS Synthetic.
XX PN WO9603140-A1.
XX PD 08-FEB-1996.
XX PF 21-JUL-1995; 95WO-US09234.
XX PR 30-MAY-1995; 95US-0452843.
XX PR 21-JUL-1994; 94US-0278634.
XX PR 23-NOV-1994; 94US-0344824.

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XX PA (CYTE-) CYTEL CORP.
XX PI Sette A, Sidney J;
XX DR WPI; 1996-116784/12.
XX XX
XX PT Compsn. comprising immunogenic peptide with supermotif allowing more
XX PT than one HLA mol. to bind - used to induce CTL response in patient
XX PT and for in vivo and ex vivo therapeutic and diagnostic applications
XX PS Claim 2; Page 26; 32pp; English.
XX CC The sequences given in AAR89362-82 are immunogenic peptides which were
XX CC use in the composition of the invention. The composition comprises
XX CC an immunogenic peptide of 9-10 residues with a supermotif which
XX CC allows binding of more than one HLA molecule. It pref. comprises
XX CC two conserved residues, a first at the 2nd position from the N-
XX CC terminal is Pro, and a 2nd at the C-terminal is Met. These peptides
XX CC are used to induce a CTL response in a patient. They are also
XX CC useful in compositions for in vivo and ex vivo therapeutic and
XX CC diagnostic applications, e.g the treatment of cancer and viral
XX CC infections, e.g. hepatitis B and C.
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 9 PKVK 12
Db 2 PKVK 5
|||
|||

RESULT 56
AAR39661
ID AAR39661 standard; peptide; 9 AA.
XX AC AAW39661;
XX DT 11-JUN-1998 (first entry)
XX DE HPV16/18 E7 peptide (pos. 11-19).
XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
XX KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
XX KW disease; anti-tumour; anti-viral.
XX OS Human papillomavirus.
XX PN WO9741440-A1.
XX PD 06-NOV-1997.
XX PF 28-APR-1997; 97WO-NL00229.
XX PR 23-DEC-1996; 96EP-0203670.
XX PR 26-APR-1996; 96EP-0201145.
XX PA (UYLE-) RIJXSUNIV LEIDEN.
XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX PT Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
XX DR WPI; 1997-549891/50.
XX XX
XX PT Method of selecting T cell peptide epitope(s) - by measuring the
XX PT stability of HLA class I-peptide complexes on intact B cells
XX PS Example 3; Page 78; 109pp; English.
XX XX
XX CC Peptides AAW39430-W39734 are used in a novel method for the selection of

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CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
CC method involves the identification of peptide sequences capable of
CC binding to an HLA (human leukocyte antigen) class I molecule and
CC measuring the binding of this epitope peptide to the HLA class I
CC peptide. The stability of binding of the peptide and MHC (major
CC histocompatibility complex) class I molecule is measured on intact human
CC B cells carrying the MHC molecule at their cell surfaces. The method can
CC be used to select peptide epitopes for generating vaccines against a
CC disease associated with the polypeptide, e.g. cancers or AIDS. The
CC peptide epitopes are especially T-cell peptide epitopes with strong
CC anti-tumour and anti-viral immune responses. Peptide AAW39661 is derived
CC from the human papillomavirus E7 protein and is capable of binding to the
CC human MHC Class I allele HLA-A2.1.

XX SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
|||
DB 5 LQPE 8

RESULT 57
AAW39662
ID AAW39662 standard; peptide; 9 AA.

XX AC AAW39662;

DT 11-JUN-1998 (first entry)

XX HPV16/18 E7 peptide (pos. 12-20).

XX T cell epitope; immune response; human leukocyte antigen; HLA Class I;
XX vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
XX disease; anti-tumour; anti-viral.

XX Human papillomavirus.

XX WO9741440-A1.

XX 06-NOV-1997.

XX 28-APR-1997; 97WO-NL00229.

XX 23-DEC-1996; 96EP-0203670.

XX 26-APR-1996; 96EP-0201145.

XX (UYLE-) RIJKSUNIV LEIDEN.

PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

XX Kast WM, Melief CUM, Offringa R, Toes REM, Van Der Burg SH;

XX WPI; 1997-549891/50.

XX Method of selecting T cell peptide epitope(s) - by measuring the
XX stability of HLA class I-peptide complexes on intact B cells

XX Example 3; Page 78; 109pp; English.

XX Peptides AAW39430-W39734 are used in a novel method for the selection of
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
CC method involves the identification of peptide sequences capable of
CC binding to an HLA (human leukocyte antigen) class I molecule and
CC measuring the binding of this epitope peptide to the HLA class I
CC peptide. The stability of binding of the peptide and MHC (major
CC histocompatibility complex) class I molecule is measured on intact human
CC B cells carrying the MHC molecule at their cell surfaces. The method can
CC be used to select peptide epitopes for generating vaccines against a
CC disease associated with the polypeptide, e.g. cancers or AIDS. The
CC peptide epitopes are especially T-cell peptide epitopes with strong

CC anti-tumour and anti-viral immune responses. Peptide AAW39662 is derived
CC from the human papillomavirus E7 protein and is capable of binding to the
CC human MHC Class I allele HLA-A2.1.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 18; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4

|||

DB 4 LQPE 7

RESULT 58

AAW36590

ID AAW36590 standard; peptide; 9 AA.

XX AC AAW36590;

XX 25-MAR-2003 (updated)

DT 09-MAR-1998 (first entry)

XX Hepatitis B virus bulk antigen.

XX Melanoma protein; MAGE-2; tumour rejection antigen precursor; HBV;

XX binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell;

XX CTL; induce; production; Hepatitis B virus.

XX Hepatitis B virus.

XX US5686068-A.

XX 11-NOV-1997.

XX 25-JUL-1996; 96US-0687226.

XX 25-JUL-1996; 96US-0687226.

XX 24-MAR-1994; 94US-0217188.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX Boon-Falleur T, Melief CJM, Van Der Bruggen P, Van Der Burg S;

XX Visseren WM;

XX WPI; 1997-558084/51.

XX Induction of cytolytic T cell production in vivo - by administering
XX MAGE-2 peptide(s)

XX Example 3; Column 9; 24pp; English.

XX This peptide sequence represents a hepatitis B virus reference peptide
XX used in determining the primary induction of the immune response against
XX MAGE-2 (a tumour rejection antigen precursor) peptides. Only peptides
XX AAW36529-39 have the ability to bind to human leukocyte antigen (HLA)
XX A2.1 molecule with high affinity and are therefore the only candidates of
XX the MAGE-2 protein to be recognised by human cytolytic T cells (CTL),
XX because CTL recognise peptides only when bound to HLA molecules.
XX Production of CTL in a subject can be induced by administering a MAGE-2
XX peptide (particularly AAW36531, AAW36533 and AAW36537) to a subject who
XX presents HLA-A2 molecules on cells. The method can be used to treat
XX subjects in need of additional CTL.
XX (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 18; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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PN WO9813378-A1.
XX
PD 02-APR-1998.
XX
PF 25-SEP-1997; 97WO-NL00536.
XX
PR 26-SEP-1996; 96EP-0202701.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Drijfhout JW, Koning F;
XX
XX WPI; 1998-230631/20.
DR
XX
XX Increasing uptake and presentation of antigen(s) - by adding mannose
PT residue(s) to antigen for increasing T cell response, useful in,
PT e.g. vaccines against viral infection(s)
XX
PS Disclosure; Page 37; 47pp; English.
XX
XX The peptides AAW54559-W54809 are examples of peptides to which at least
CC 1 (preferably 2) mannose can be attached to increase their uptake as
CC antigens by antigen-presenting cells. Uptake of agonist mannosylated
CC peptides will increase the T cell response, whereas uptake of antagonist
CC peptides blocks the T cell response. Blocking binding of immunogenic
CC autoantigens can be used in treatment of type I diabetes, rheumatoid
CC arthritis, graft rejection etc., also to induce T-cell non-
CC responsiveness. Vaccines containing mannosylated antigen are used to
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
CC and parasites.
XX
XX Sequence 9 AA;
SQ
XX
XX Query Match 22.2%; Score 4; DB 19; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LOPE 4
XX ||||
XX Db 4 LOPE 7
XX
XX
XX RESULT 63
XX AAW53466
XX ID AAY53466 standard; Protein; 9 AA.
XX AC AAY53466;
XX
XX DT 18-JAN-2000 (first entry)
XX
XX DE HIV-1 RT protein (aa 185-193) binds HLA-B8.
XX
XX KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
XX KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
XX KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
XX KW melanoma; malaria; parasite.
XX
XX OS Synthetic.
XX OS Human immunodeficiency virus type 1.
XX
XX PN FR2776926-A1.
XX
XX PD 08-OCT-1999.
XX
XX PF 07-APR-1998; 98FR-0004323.
XX
XX PR 07-APR-1998; 98FR-0004323.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PA (INSP ) INST PASTEUR LILLE.
XX
XX Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;
XX WPI; 1999-583113/50.
XX
XX New lipopeptide containing lipid regions and two epitopes, all
PT separated by peptide spacers that impart hydrophilicity, useful in
PT vaccines -
XX
XX Disclosure; Page 21; 35pp; French.
XX
XX The invention relates to the generation of a lipopeptide comprising at
CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
CC epitope and at least one lipid residue with (i) the epitopes and lipid
CC portion and (ii) the epitopes, being separated independently by peptide
CC spacers. These spacers comprise sequences of amino acids which carry an
CC overall electrical charge in neutral media to ensure that the
CC lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents

```

CC examples of peptide epitopes used to generate the lipopeptides. These are
 CC used in therapeutic or prophylactic compositions and vaccines to induce
 CC specific immune responses against human immunodeficiency, hepatitis B or
 CC papilloma viruses; p53 of melanoma or the malaria parasite.

SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 PKVK 12
 ||||
 Db 2 PKVK 5

RESULT 64
 AAY55432
 ID AAY55432 standard; peptide; 9 AA.

XX AC AAY55432;

XX DT 17-JAN-2000 (first entry)

XX DE HLA binding plu-1 peptide.

XX KW Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
 KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
 KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9949034-A1.

XX PD 30-SEP-1999.

XX PF 19-MAR-1999; 99WO-GB00866.

XX PR 20-MAR-1998; 98GB-0005877.

XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX PI Taylor-papadimitriou J;

XX DR WPI; 1999-591090/50.

XX PT New nucleic acid encoding the cancer-associated polypeptide plu-1, for
 PT diagnosis, treatment and prevention of cancer, especially of breast and
 PT ovary -

XX PS Example 2; Fig 12; 173pp; English.

XX CC The invention relates to a human cancer-associated polypeptide plu-1.
 CC The plu-1 polypeptide can be recombinantly expressed by standard
 CC recombinant methodology. Detection of the plu-1 nucleic acid or the
 CC polypeptide is used for the following: (i) diagnosis (including imaging)
 CC and prognosis of, and determination of susceptibility to, cancer,
 CC specifically ovarian or breast cancer; and ii) treating cancer (by
 CC inducing an immune response against cancer cells, e.g. as a vaccine, or
 CC by antisense inhibition). Antigens derived from the polypeptide are used
 CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for
 CC subsequent return to the patient for treatment of cancer. The polypeptide
 CC may also be used to identify inhibitors of plu-1 activity. Fragments of
 CC the polypeptide, and antibodies raised against plu-1, are useful as assay
 CC and imaging agents, also therapeutically (to induce an anti-idiotype
 CC response or where conjugated to cytotoxic agents). The plu-1 antigen is
 CC expressed more commonly in breast tumors than some known tumor antigens.
 CC Sequences AAY55320-629 represent predicted peptides from the plu-1
 CC polypeptide which may bind to the human class I alleles B27, A2, A3 and
 CC A11.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQPE 4
 ||||
 Db 2 LQPE 5

RESULT 65

AAY40315

ID AAY40315 standard; Peptide; 9 AA.

XX AC AAY40315;

XX DT 19-NOV-1999 (first entry)

XX DE Amino acid sequence of a HIV-1 epitope.

XX KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
 KW vaccine; tumor; infection; immune response; cytokine profile;
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
 KW autoimmune disease.

XX OS Human immunodeficiency virus type 1.

XX PN FR2774687-A1.

XX PD 13-AUG-1999.

XX PF 06-FEB-1998; 98FR-0001439.

XX PR 06-FEB-1998; 98FR-0001439.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI (INSP) INST PASTEUR LILLE.

XX PT Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;
 XX WPI; 1999-510734/43.

XX PT New lipopeptide comprising C-terminal interferon-gamma fragment with
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating
 PT cancer or virus infection

XX PS Disclosure; Page 39; 53pp; French.

XX CC AAY40323-Y40379 represent epitopes that are able to activate cytotoxic
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
 CC B epitopes recognized by corresponding antibodies. The epitopes may be
 CC used in the composition of the invention. The specification describes a
 CC lipopeptide that has a peptide part derived from mammalian interferon
 CC gamma (IFNg) and one or more lipophilic parts comprising a linear or
 CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The
 CC lipopeptide mimics the activity of IFNg. Compositions comprising the
 CC lipopeptide are used to treat or prevent any condition that responds
 CC to IFNg, and as adjuvant for vaccines (particularly those directed
 CC against tumors, viral or parasitic infections), to stimulate or
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.
 CC Particular applications are treatment of infections (particularly
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
 CC (particularly of kidney, cutaneous T cells or ovary, chronic
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune
 CC diseases.

XX SQ Sequence 9 AA;

QY 9 PKVK 12
 DB 2 PKVK 5
 RESULT 66
 AAY26807
 ID AAY26807 standard; peptide; 9 AA.
 XX
 AC AAY26807;
 XX
 DT 14-SEP-1999 (first entry)
 XX
 DE HIV-derived lipopeptide epitope #77 for mixed micelles.
 XX
 KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
 KW melanoma; Plasmodium falciparum; malaria.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus type 1.
 XX
 FR2771640-A1.
 XX
 PD 04-JUN-1999.
 XX
 PF 03-DEC-1997; 97FR-0015246.
 XX
 PR 03-DEC-1997; 97FR-0015246.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INSP) INST PASTEUR LILLE.
 XX
 PI Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;
 PI Tartar A, Wieruszkeski JM;
 XX
 DR WPI; 1999-349509/30.
 XX
 PT Immunogenic lipopeptide micelles - comprising lipopeptides
 PT containing cytotoxic and helper T-lymphocyte epitopes
 XX
 PS Disclosure; Page 34; 60pp; French.
 XX
 CC The invention relates to the generation of mixed micelles or
 CC microaggregates for inducing an immune response comprise: (a) a first
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
 CC different from that of the first lipopeptide. This peptide represents
 CC an example of a lipopeptide epitope used in the invention and is derived
 CC from a human immunodeficiency virus type 1 (HIV-1) protein. The
 CC immunogenic lipopeptide micelles are used in vaccines, especially
 CC against HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma
 CC or Plasmodium falciparum malaria.
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PKVK 12
 DB 2 PKVK 5
 RESULT 67
 AAY10346
 ID AAY10346 standard; Peptide; 9 AA.
 XX
 AC AAY10346;
 XX
 DT 12-MAY-1999 (first entry)
 XX
 DE T cell epitope/MHC ligand SEQ ID NO:276.
 XX
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.
 XX
 OS Synthetic.
 OS Human papillomavirus.
 XX
 PN WO9902183-A2.
 XX
 PD 21-JAN-1999.
 XX
 PF 10-JUL-1998; 98WO-US14289.
 XX
 PR 10-DEC-1997; 97US-0988320.
 PR 10-JUL-1997; 97CA-2209815.
 XX
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Kuendig TM, Simard JLL;
 XX
 DR WPI; 1999-120514/10.
 XX
 PT Inducing a cytotoxic T lymphocyte response - by maintaining a level
 PT of antigen in the lymphatic system of a mammal so as to provide a
 PT sustained CTL response, used to treat, e.g. AIDS
 XX
 PS Disclosure; Page 34; 199pp; English.
 XX
 CC The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. AAY10071 to AAY10639 represent examples of peptide
 CC antigens given in the present invention.
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOPE 4
 DB 4 LOPE 7
 RESULT 68
 AAY10511
 ID AAY10511 standard; Peptide; 9 AA.
 XX
 AC AAY10511;
 XX
 DT 12-MAY-1999 (first entry)
 XX
 DE HLA Class I motif peptide SEQ ID NO:441.
 XX
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;

KW immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.

XX Synthetic.

OS Human papillomavirus.

XX WO9902183-A2.

XX PD 21-JAN-1999.

XX PF 10-JUL-1998; 98WO-US14289.

XX PR 10-DEC-1997; 97US-0988320.

XX PR 10-JUL-1997; 97CA-2209815.

XX PA (CTL1-) CTL IMMUNOTHERAPIES CORP.

XX PI Kuendig TM, Simard JUL;

XX DR WPI; 1999-120514/10.

XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
 of antigen in the lymphatic system of a mammal so as to provide a
 sustained CTL response, used to treat, e.g. AIDS

XX PS Disclosure; Page 44; 1999p; English.

XX The present invention describes a method of inducing and/or sustaining
 an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 method comprises: (a) delivering an antigen to the mammal at a level to
 induce an immunological CTL response in the mammal; and (b) maintaining
 the level of the antigen in the mammal's lymphatic system to maintain
 the immunologic CTL response. The method can be used for the delivery of
 e.g. a differentiation antigen, a tumour-specific multilineage antigen,
 an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 gene antigen, or a viral antigen. They can be used for the treatment of
 disease such as cancer, e.g. malignant melanoma or infectious disease,
 e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 to the lymphatic system provides for potent CTL stimulation that takes
 place in the milieu of the lymphoid organ, and it sustains stimulation
 that is necessary to keep CTL active, cytotoxic and recirculating
 through the body. AAY10071 to AAY10639 represent examples of peptide
 antigens given in the present invention.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4

DB 4 LQPE 7

RESULT 69

AAB33705

ID AAB33705 standard; Peptide; 9 AA.

XX AAB33705;

XX 26-JAN-2001 (first entry)

XX DE MHC class I associated immunogenic peptide SEQ ID 104.

XX Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
 KW major histocompatibility complex; vaginal tissue; mucosal tissue..

XX Unidentified.

XX WO200053161-A2.

XX 14-SEP-2000.

PD

XX

XX 10-MAR-2000; 2000WO-US06578.

XX 11-MAR-1999; 99US-0286463.

XX 27-MAY-1999; 99US-0321346.

XX PA (ZYCO-) ZYCOS INC.

XX PI Lunsford LB, Putnam D, Hedley ML;

XX DR WPI; 2000-638130/61.

XX Microparticles useful for administering a nucleic acid into the mucosal
 tissue preferably vaginal tissue of an animal, comprises a polymeric
 matrix, a lipid and a nucleic acid molecule -

XX PS Disclosure; Page 16; 96pp; English.

XX The present invention relates to microparticles which are less than 20
 microns in diameter, which comprise a polymeric matrix, a lipid and a
 nucleic acid molecule. The microparticle is specifically not
 encapsulated in a liposome and does not comprise a cell. The nucleotide
 sequence encodes an expression product that binds to major
 histocompatibility complex (MHC) type I or II molecules. Peptides
 AAB33602-B33647 represent MHC class II associated immunogenic peptides,
 and AAB33648-B33710 represent MHC class I associated immunogenic
 peptides. The peptides are examples of the expression products of the
 nucleotide sequences which can be included in the microparticles of the
 invention. Sequences AAB33711-B33716 represent alternative expression
 products and nuclear localisation signals also used in the invention. The
 microparticles are useful for administering a nucleic acid into the
 mucosal tissue preferably vaginal tissue of an animal.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4

DB 5 LQPE 8

RESULT 70

AAB18492

ID AAB18492 standard; peptide; 9 AA.

XX AC AAB18492;

XX DT 15-JAN-2001 (first entry)

XX DE Peptide substrate used to test prolyl-tripeptidyl peptidase activity.

XX KW Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
 KW gingivitis; periodontitis.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "hydrogen attached"

XX FN WO200052147-A2.

XX PD 08-SEP-2000.

XX PF 03-MAR-2000; 2000WO-US05551.

XX PR 05-MAR-1999; 99US-0123148.

XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.

XX (TRAV/) TRAVIS J.

PA (POTE/) POTEPA J.
 PA (BANE/) BANBULA A.
 XX
 PI Travis J, Potempa J, Banbula A;
 XX
 DR WPI; 2000-594181/56.
 XX
 PT Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
 PT for identifying its inhibitor which is useful for protecting an animal
 PT from a periodontal disease such as gingivitis and periodontitis -
 XX
 XX Claim 3; Page 37; 58pp; English.
 XX
 XX The present sequence represents a substrate which was used to test
 CC the activity of prolyl tripeptidyl-peptidases PTP-A and DPP IV. The
 CC prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves
 CC a peptide bond in a target polypeptide having at least 4 amino acids.
 CC This bond is between a proline and an amino acid attached to the
 CC alpha-carboxyl group end of the proline. The polypeptide is useful for
 CC identifying inhibitors. These inhibitors are then useful for reducing
 CC the growth of bacterium or for protecting an animal from a periodontal
 CC disease such as gingivitis and periodontitis caused by Porphyromonas
 CC gingivalis.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPK 10
 DB 1 GVPK 4
 |||||
 |||||

RESULT 71
 AAY96941
 ID AAY96941 standard; peptide; 9 AA.
 XX
 AC AAY96941;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Processed N-terminal peptide of human IL-1RA1L and IL-1RA1V.
 XX
 KW hIL-1RA1; human interleukin-1 receptor antagonist-1 long; IL-1lp;
 KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
 KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
 KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
 KW gene therapy; N-terminal.
 KW
 XX Homo sapiens.
 OS
 XX WO200039297-A2.
 PN
 XX 06-JUL-2000.
 PD
 XX 22-DEC-1999; 99WO-US30720.
 PF
 XX 23-DEC-1998; 98US-0113430.
 PR 22-JAN-1999; 99US-0116843.
 PR 13-APR-1999; 99US-0129122.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Goddard A, Pan J;
 PI
 XX WPI; 2000-452395/39.
 DR
 XX Nucleic acids encoding interleukin-1-like polypeptides, useful for
 PT preventing and treating e.g. inflammation, asthma and psoriasis
 PT
 XX Example 14; Page 94; 143pp; English.
 PS

XX An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-1lp) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (hIL-1RA1) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-1lp polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patients production of the polypeptide or to rectify
 CC mutations that lead to the production of in active peptides). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-1lp protein expression and activity which may be use
 CC to treat disorders associated with inappropriate IL-1lp expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 DB 5 PKVK 8
 |||||
 |||||

RESULT 72
 AAY66364
 ID AAY66364 standard; Peptide; 9 AA.
 XX
 AC AAY66364;
 XX
 DT 22-FEB-2000 (first entry)
 XX
 DE HLA-B7-binding HIV-1 Pol peptide #166.
 XX
 KW HIV-1; MHC; major histocompatibility complex; Class I; HLA;
 KW human leukocyte antigen; allele; binding; conserved; genome;
 KW peptide; targeting; toxic; drug; antibody; antigen; antigen;
 KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;
 KW localisation; quantification; detection; infection; drug resistance;
 KW immune response.
 KW
 OS Human immunodeficiency virus type 1.
 XX
 XX WO9949893-A1.
 PN
 XX 07-OCT-1999.
 PD
 XX 31-MAR-1999; 99WO-US07111.
 PF
 XX 31-MAR-1998; 98US-0052530.
 PR
 XX (UYBO-) UNIV BOSTON.
 PA
 XX Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;
 PI
 XX WPI; 2000-038361/03.
 DR
 XX Novel methods for designing molecular conjugate therapeutics which are
 PT used for diagnosis, imaging and treatment against pathogens -
 PT
 XX Example 3; Page 45; 62pp; English.
 PS
 XX AAY66199-Y66413 are peptides derived from conserved portions of the
 CC HIV-1 genome which bind to different HLA alleles of MHC (major
 CC histocompatibility complex) Class I molecules. The peptides are used to
 CC construct targetting antigens comprising one or more peptides bound to

CC the corresponding MHC Class I molecule, which can be used to raise
 CC antibodies. The antibody may then be used as a targeting vehicle to
 CC deliver a potentially toxic drug to its target site of action, rather
 CC than administering it systemically, which may result in adverse side
 CC effects. The invention relates to improved methods for the design of
 CC molecular conjugate therapeutics for the diagnosis and treatment of
 CC infections caused by pathogens with a high mutation rate (such as
 CC HIV-1). This method involves identifying conserved peptide-encoding
 CC regions among the genomes of multiple variants of a pathogen, identifying
 CC the Class I MHC molecules which occur with greatest frequency in a
 CC population of interest (e.g., human sub-populations), and determining
 CC which of the peptides bind to the Class I MHC molecules. The MHC-binding
 CC peptides and the corresponding Class I MHC molecules are selected and
 CC used to construct targeting antigens, which are in turn used to produce
 CC targeting antibodies. The methods may be used in localisation,
 CC quantification and in situ detection of specific peptide-MHC Class I
 CC complexes and also to detect and treat viral infection. The methods of
 CC the invention mitigate against the development of viral resistance to
 CC drugs and to the immune response, as well as providing a solution for
 CC targeting toxic compounds to destroy viruses sequestered in sites not
 CC accessible to T cells. In addition, the methods eliminate the virus,
 CC whereas current therapies only arrest viral replication.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 ||||
 Db 2 PKVK 5

RESULT 74
 AAY66378
 ID AAY66378 standard; Peptide; 9 AA.
 AC AAY66378;
 XX
 DT 22-FEB-2000 (first entry)
 XX
 DE HLA-B8-binding HIV-1 Pol peptide #180.
 XX
 KW HIV-1; MHC; major histocompatibility complex; Class I; HLA;
 KW human leukocyte antigen; allele; binding; conserved; genome;
 KW peptide; targeting; toxic; drug; antibody; antigen; antiviral;
 KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;
 KW localisation; quantification; detection; infection; drug resistance;
 KW immune response.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO5949893-A1.
 XX
 ED 07-OCT-1999.
 XX
 XX 31-MAR-1999; 99WO-US07111.
 XX
 XX 31-MAR-1998; 98US-0052530.
 XX
 XX (UYBO-) UNIV BOSTON.
 XX
 XX Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;
 XX Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WPI; 2000-038361/03.
 XX
 XX Novel methods for designing molecular conjugate therapeutics which are
 PT used for diagnosis, imaging and treatment against pathogens -
 XX
 XX Example 3; Page 46; 62pp; English.
 XX
 XX AAY66199-Y66413 are peptides derived from conserved portions of the

CC HIV-1 genome which bind to different HLA alleles of MHC (major
 CC histocompatibility complex) Class I molecules. The peptides are used to
 CC construct targeting antigens comprising one or more peptides bound to
 CC the corresponding MHC Class I molecule, which can be used to raise
 CC antibodies. The antibody may then be used as a targeting vehicle to
 CC deliver a potentially toxic drug to its target site of action, rather
 CC than administering it systemically, which may result in adverse side
 CC effects. The invention relates to improved methods for the design of
 CC molecular conjugate therapeutics for the diagnosis and treatment of
 CC infections caused by pathogens with a high mutation rate (such as
 CC HIV-1). This method involves identifying conserved peptide-encoding
 CC regions among the genomes of multiple variants of a pathogen, identifying
 CC the Class I MHC molecules which occur with greatest frequency in a
 CC population of interest (e.g., human sub-populations), and determining
 CC which of the peptides bind to the Class I MHC molecules. The MHC-binding
 CC peptides and the corresponding Class I MHC molecules are selected and
 CC used to construct targeting antigens, which are in turn used to produce
 CC targeting antibodies. The methods may be used in localisation,
 CC quantification and in situ detection of specific peptide-MHC Class I
 CC complexes and also to detect and treat viral infection. The methods of
 CC the invention mitigate against the development of viral resistance to
 CC drugs and to the immune response, as well as providing a solution for
 CC targeting toxic compounds to destroy viruses sequestered in sites not
 CC accessible to T cells. In addition, the methods eliminate the virus,
 CC whereas current therapies only arrest viral replication.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 ||||
 Db 2 PKVK 5

RESULT 74
 ABP11796
 ID ABP11796 standard; Peptide; 9 AA.
 AC ABP11796;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 XX HIV A01 super motif pol peptide #68.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 XX 05-OCT-2000; 2000WO-US27766.
 XX
 XX 05-OCT-1999; 99US-0412863.
 XX
 XX (EPIM-) EPIMMUNE INC.
 XX
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 XX
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 XX Claim 32; Page 110; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 Db 5 PKVK 8

RESULT 75

ABP16116
 ID ABP16116 standard; Peptide; 9 AA.

XX ABP16116;

DT 15-JUL-2002 (first entry)

XX HIV A24 super motif pol peptide #296.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 198; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
 Db 5 PKVK 8

Search completed: November 25, 2003, 19:27:08
 Job time : 46.9419 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 : Search time 28.8837 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVPKVKETMPVK 18

Scoring table: OIRGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-281-652-21
2	5	27.8	12	9	US-09-789-561-163
3	5	27.8	14	8	US-08-908-894-22
4	5	27.8	14	9	US-09-908-323-22
5	5	27.8	16	15	US-10-225-567A-1251
6	5	27.8	16	15	US-10-225-567A-1282
7	5	27.8	20	12	US-10-280-066-315
8	4	22.2	4	10	US-09-985-357A-12
9	4	22.2	4	12	US-10-353-767-12
10	4	22.2	5	12	US-10-302-817A-46
11	4	22.2	6	9	US-09-045-020-14
12	4	22.2	7	15	US-10-281-652-16
13	4	22.2	9	7	US-08-344-824-33
14	4	22.2	9	7	US-08-344-824-118
15	4	22.2	9	8	US-08-452-843A-2

Sequence 17, Appl	9	9	US-09-759-960-17	4	22.2	16
Sequence 104, Appl	9	10	US-09-909-460-104	4	22.2	17
Sequence 33, Appl	9	12	US-09-942-052-33	4	22.2	18
Sequence 39, Appl	9	12	US-09-942-052-39	4	22.2	19
Sequence 104, Appl	9	12	US-09-942-052-104	4	22.2	20
Sequence 218, Appl	9	12	US-09-942-052-218	4	22.2	21
Sequence 235, Appl	9	12	US-09-942-052-235	4	22.2	22
Sequence 236, Appl	9	12	US-09-942-052-236	4	22.2	23
Sequence 312, Appl	9	12	US-09-942-052-312	4	22.2	24
Sequence 329, Appl	9	12	US-09-942-052-329	4	22.2	25
Sequence 424, Appl	9	12	US-09-942-052-424	4	22.2	26
Sequence 548, Appl	9	12	US-09-942-052-548	4	22.2	27
Sequence 619, Appl	9	12	US-09-942-052-619	4	22.2	28
Sequence 2, Appl	9	12	US-10-365-908-3	4	22.2	29
Sequence 26, Appl	9	12	US-10-365-908-26	4	22.2	30
Sequence 634, Appl	9	12	US-10-200-708-634	4	22.2	31
Sequence 648, Appl	9	12	US-10-200-708-648	4	22.2	32
Sequence 669, Appl	9	12	US-10-200-708-669	4	22.2	33
Sequence 12, Appl	9	15	US-10-001-546-12	4	22.2	34
Sequence 28, Appl	9	15	US-10-128-711-28	4	22.2	35
Sequence 66, Appl	9	15	US-10-128-711-66	4	22.2	36
Sequence 71, Appl	9	15	US-10-128-711-71	4	22.2	37
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Sequence 167, Appl	9	15	US-10-133-210-167	4	22.2	39
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Sequence 183, Appl	10	10	US-09-922-261-283	4	22.2	41
Sequence 10, Appl	10	10	US-09-833-328-10	4	22.2	42
Sequence 22, Appl	10	10	US-09-835-853-22	4	22.2	43
Sequence 388, Appl	10	11	US-09-876-904A-388	4	22.2	44
Sequence 1436, Ap	10	11	US-09-572-404B-1436	4	22.2	45
Sequence 33, Appl	10	12	US-10-177-390-33	4	22.2	46
Sequence 54, Appl	10	12	US-09-942-052-54	4	22.2	47
Sequence 74, Appl	10	12	US-09-942-052-74	4	22.2	48
Sequence 256, Appl	10	12	US-09-942-052-256	4	22.2	49
Sequence 257, Appl	10	12	US-09-942-052-257	4	22.2	50
Sequence 360, Appl	10	12	US-09-942-052-360	4	22.2	51
Sequence 476, Appl	10	12	US-09-942-052-476	4	22.2	52
Sequence 573, Appl	10	12	US-09-942-052-573	4	22.2	53
Sequence 669, Appl	10	12	US-09-942-052-669	4	22.2	54
Sequence 688, Appl	10	12	US-09-942-052-688	4	22.2	55
Sequence 122, Appl	10	12	US-10-200-708-122	4	22.2	56
Sequence 223, Appl	10	12	US-10-200-708-223	4	22.2	57
Sequence 248, Appl	10	12	US-10-200-708-248	4	22.2	58
Sequence 338, Appl	10	12	US-10-200-708-338	4	22.2	59
Sequence 345, Appl	10	12	US-10-200-708-345	4	22.2	60
Sequence 520, Appl	10	12	US-10-200-708-520	4	22.2	61
Sequence 542, Appl	10	12	US-10-200-708-542	4	22.2	62
Sequence 635, Appl	10	12	US-10-200-708-635	4	22.2	63
Sequence 649, Appl	10	12	US-10-200-708-649	4	22.2	64
Sequence 670, Appl	10	12	US-10-200-708-670	4	22.2	65
Sequence 228, Appl	10	15	US-10-062-710-228	4	22.2	66
Sequence 271, Appl	10	15	US-10-133-210-271	4	22.2	67
Sequence 19, Appl	10	15	US-10-224-286-19	4	22.2	68
Sequence 13, Appl	10	15	US-10-054-968-13	4	22.2	69
Sequence 264, Appl	11	15	US-09-852-910-264	4	22.2	70
Sequence 206, Appl	11	15	US-10-062-710-206	4	22.2	71
Sequence 42, Appl	12	9	US-09-832-723-42	4	22.2	72
Sequence 42, Appl	12	12	US-10-303-331-42	4	22.2	73
Sequence 72, Appl	12	12	US-10-116-275-72	4	22.2	74
Sequence 26, Appl	12	15	US-10-185-815-26	4	22.2	75
Sequence 3, Appl	12	13	US-10-300-215-3	4	22.2	76
Sequence 7, Appl	12	13	US-10-300-215-7	4	22.2	77
Sequence 29, Appl	12	13	US-10-300-215-29	4	22.2	78
Sequence 36, Appl	12	13	US-10-300-215-36	4	22.2	79
Sequence 36, Appl	13	15	US-10-001-546-36	4	22.2	80
Sequence 2, Appl	14	12	US-10-221-125-2	4	22.2	81
Sequence 43, Appl	14	15	US-10-033-741-43	4	22.2	82
Sequence 44, Appl	15	10	US-09-909-460-44	4	22.2	83
Sequence 9, Appl	15	12	US-09-569-197-9	4	22.2	84
Sequence 16, Appl	15	12	US-10-229-567-16	4	22.2	85
Sequence 453, Appl	16	11	US-09-897-778-453	4	22.2	86
Sequence 228, Appl	16	11	US-09-876-904A-228	4	22.2	87
Sequence 453, Appl	16	12	US-10-117-982-453	4	22.2	88

89 Sequence 6, Appli
90 Sequence 7, Appli
91 Sequence 344, App
92 Sequence 114, App
93 Sequence 227, App
94 Sequence 10, Appl
95 Sequence 1531, Ap
96 Sequence 8, Appli
97 Sequence 173, App
98 Sequence 32381, A
99 Sequence 1545, Ap
100 Sequence 88, Appl

4 22.2 16 12 US-10-387-645-6
4 22.2 16 12 US-10-387-645-7
4 22.2 16 12 US-10-161-791-344
4 22.2 16 12 US-10-350-405-114
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4 22.2 19 15 US-10-225-567A-1545
4 22.2 19 15 US-10-163-198-88

ALIGNMENTS

RESULT 1
US-10-281-652-21
; Sequence 21, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-21

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Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPEIMGVPKVKETMVPK 18
Db 1 LOPEIMGVPKVKETMVPK 18

RESULT 2
US-09-789-561-163
; Sequence 163, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: PZ043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163

; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-163

Query Match 27.8%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPKV 11
Db 1 GVPKV 5

RESULT 3
US-08-908-884-22
; Sequence 22, Application US/08908884
; Publication No. US20020138872A1
; GENERAL INFORMATION:
; APPLICANT: Dong et al.
; TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,884
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/023,851
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: 60/035,166
; FILING DATE: January 10, 1997
; APPLICATION NUMBER: 60/046,769
; FILING DATE: May 16, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elbing, Karen L
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/339004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-908-884-22

Query Match 27.8%; Score 5; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPKVK 12
Db 9 VPKVK 13

RESULT 4
US-09-908-323-22
; Sequence 22, Application US/09908323


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Db      14 MGVPK 18

RESULT 8
US-09-985-357A-12
; Sequence 12, Application US/09985357A
; Patent No. US20020110913A1
; GENERAL INFORMATION:
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation
; FILE REFERENCE: HUBR 1151.1 CON PFF/MAS
; CURRENT APPLICATION NUMBER: US/09/985,357A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/463,380
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/EP98/04590
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: DE 19753681.1
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: EP 97112640
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: WordPerfect
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide start coded by
; OTHER INFORMATION: EX5
US-09-985-357A-12

Query Match      22.2%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVP 9
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Db      1 MGVP 4

RESULT 9
US-10-353-767-12
; Sequence 12, Application US/10353767
; Publication No. US20030166275A1
; GENERAL INFORMATION:
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans
; APPLICANT: KOLL
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene
; TITLE OF INVENTION: activation
; FILE REFERENCE: HUBR 1151.1 CON PFF/MAS
; CURRENT APPLICATION NUMBER: US/10/353,767
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/985,357A
; PRIOR FILING DATE: 2001-11-12
; PRIOR APPLICATION NUMBER: US 09/463,380
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/EP98/04590
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: DE 19753681.1
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: EP 97112640
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; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: WordPerfect
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide
; OTHER INFORMATION: start coded by primer
; OTHER INFORMATION: EX5
US-10-353-767-12

Query Match      22.2%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVP 9
      |||||
Db      1 MGVP 4

RESULT 10
US-10-302-817A-46
; Sequence 46, Application US/10302817A
; Publication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Thermus brockianus
US-10-302-817A-46

Query Match      22.2%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
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Db      2 PKVK 5

RESULT 11
US-09-045-020-14
; Sequence 14, Application US/09045020
; Patent No. US20020025942A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M., Roder, Hanno M.
; TITLE OF INVENTION: No. US20020025942A1e1 Tau/Neurofilament Protein
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 28 Carleton Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,020
; FILING DATE: 20-Mar-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,793
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 07/912,293
; FILING DATE: July 10, 1992
; APPLICATION NUMBER: 07/742,880
; FILING DATE: 9-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0656/7008
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14
US-09-045-020-14
;
; Query Match 22.2%; Score 4; DB 9; Length 6;
; Best Local Similarity 100.0%; Pred. No. 6e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 3 PEIM 6
Db 2 PEIM 5
;
RESULT 12
US-10-281-652-16
; Sequence 16, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: BOLDGOUGH, Istvan
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-16
;
; Query Match 22.2%; Score 4; DB 15; Length 7;
; Best Local Similarity 100.0%; Pred. No. 6e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 LQPE 4
Db 4 LQPE 7
;
RESULT 13
US-08-344-824-33
; Sequence 33, Application US/08344824
```

```
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-33
;
; Query Match 22.2%; Score 4; DB 7; Length 9;
; Best Local Similarity 100.0%; Pred. No. 6e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 9 PKVK 12
Db 2 PKVK 5
;
RESULT 14
US-08-344-824-118
; Sequence 118, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/344,824
;; FILING DATE: 23-NOV-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; FILING DATE: 21-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bastian, Kevin L.
;; REGISTRATION NUMBER: 34,774
;; REFERENCE/DOCKET NUMBER: 14137-80-1
;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 118:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-344-824-118

Query Match 22.2%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 PKVK 12
|||
DB 2 PKVK 5

RESULT 15
US-08-452-843A-2
;; Sequence 2, Application US/08452847A
;; Publication No. US20020098197A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
;; FILE REFERENCE: 3996322001321
;; CURRENT APPLICATION NUMBER: US/08/452,843A
;; CURRENT FILING DATE: 1995-05-03
;; PRIOR APPLICATION NUMBER: US 08/344,824
;; PRIOR FILING DATE: 1994-11-23
;; PRIOR APPLICATION NUMBER: US 08/278,634
;; PRIOR FILING DATE: 1994-07-21
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Y1 analog of 1054.05
US-08-452-843A-2

Query Match 22.2%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 PKVK 12
|||
DB 2 PKVK 5

RESULT 16
US-09-759-960-17
;; Sequence 17, Application US/09759960
;; Patent No. US20010006639A1
;; GENERAL INFORMATION:
;; APPLICANT: Urban, Robert G.
;; APPLICANT: Chiciz, Roman M.

;; APPLICANT: Collins, Edward J.
;; APPLICANT: Hedley, Mary Lynn
;; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
;; TITLE OF INVENTION: PROTEIN
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/759,960
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/169,425
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 08191/004002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-543-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-759-960-17

Query Match 22.2%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LOPE 4
|||
DB 5 LOPE 8

RESULT 17
US-09-909-460-104
;; Sequence 104, Application US/09909460
;; Publication No. US20020182258A1
;; GENERAL INFORMATION:
;; APPLICANT: Lunsford, Lynn B.
;; APPLICANT: Putnam, David
;; APPLICANT: Hedley, Mary Lynn
;; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
;; FILE REFERENCE: 08191/014001
;; CURRENT APPLICATION NUMBER: US/09/909,460
;; CURRENT FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
;; NUMBER OF SEQ ID NOS: 114
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 104
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Human papilloma virus
US-09-909-460-104

Query Match 22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;

```
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQPE 4
   ||||
Db 5 LQPE 8

RESULT 18
US-09-942-052-33
; Sequence 33, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-33

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQPE 4
   ||||
Db 2 LQPE 5

RESULT 19
US-09-942-052-39
; Sequence 39, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-39

Query Match 22.2%; Score 4; DB 12; Length 9;
```

```
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQPE 4
   ||||
Db 5 LQPE 8

RESULT 20
US-09-942-052-104
; Sequence 104, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-104

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQPE 4
   ||||
Db 2 LQPE 5

RESULT 21
US-09-942-052-218
; Sequence 218, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 218
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-218
```

```
Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 2 LOPE 5

RESULT 22
US-09-942-052-235
; Sequence 235, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 235
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-235

Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 1 LOPE 4

RESULT 23
US-09-942-052-236
; Sequence 236, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-236

Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 1 LOPE 4

RESULT 24
US-09-942-052-312
; Sequence 312, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 312
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-312

Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 5 LOPE 8

RESULT 25
US-09-942-052-339
; Sequence 339, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-339
```


US-09-942-052-339

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
|
|
|
|
Db 1 LOPE 4

RESULT 26

US-09-942-052-424
; Sequence 424, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-942-052-424

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
|
|
|
|
Db 1 LOPE 4

RESULT 27

US-09-942-052-548
; Sequence 548, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-548

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
|
|
|
|
Db 2 LOPE 5

RESULT 28

US-09-942-052-619
; Sequence 619, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 619
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-942-052-619

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
|
|
|
|
Db 1 LOPE 4

RESULT 29

US-10-365-908-3
; Sequence 3, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus

```
US-10-365-908-3
Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 5 LOPE 8

RESULT 30
US-10-365-908-26
; Sequence 26, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-25

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 1 LOPE 4

RESULT 31
US-10-200-708-634
; Sequence 634, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 634
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-634

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-365-908-3
Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 5 LOPE 8

RESULT 30
US-10-365-908-26
; Sequence 26, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-25

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
   ||||
Db 1 LOPE 4

RESULT 31
US-10-200-708-634
; Sequence 634, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 634
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-634

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-200-708-648
Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
   ||||
Db 2 PKVK 5

RESULT 32
US-10-200-708-648
; Sequence 648, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-648

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
   ||||
Db 2 PKVK 5

RESULT 33
US-10-200-708-669
; Sequence 669, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-669

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy      9 PKVK 12
      ||||
Db      6 PKVK 9

RESULT 34
US-10-001-546-12
; Sequence 12, Application US/10001546
; Publication No. US20030027766A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: FISK, BRYAN A.
; APPLICANT: IOANNIDES, MARIA G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: 1-LYMPHOCYTES
; FILE REFERENCE: UTSC:390USC2
; CURRENT APPLICATION NUMBER: US/10/001,546
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 08/403,459
; PRIOR FILING DATE: 1995-03-14
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-001-546-12

Query Match      22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LQPE 4
      ||||
Db      2 LQPE 5

RESULT 35
US-10-128-711-28
; Sequence 28, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, MARIA A.
; CHESTNUT, ROBERT W.
; SETTE, ALESSANDRO D.
; CELIS, ESTEBAN
; GRAY, HOWARD
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; City: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811

Qy      9 PKVK 12
      ||||
Db      6 PKVK 9

RESULT 36
US-10-128-711-66
; Sequence 66, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, MARIA A.
; CHESTNUT, ROBERT W.
; SETTE, ALESSANDRO D.
; CELIS, ESTEBAN
; GRAY, HOWARD
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; City: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-128-711-66

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 37
US-10-128-711-71
; Sequence 71, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793

; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-128-711-71

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 38
US-10-133-210-146
; Sequence 146, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-146

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 39
US-10-133-210-167
; Sequence 167, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 167
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-167

Query Match      22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
   ||||
Db 2 PKVK 5

RESULT 40
US-09-847-185-19
; Sequence 19, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1W 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19

Query Match      22.2%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
   ||||
Db 5 LQPE 8

RESULT 41
US-09-922-261-283
; Sequence 283, Application US/09922261
```

```
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-283

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVPK 18
   ||||
Db 1 MVPK 4

RESULT 42
US-09-833-328-10
; Sequence 10, Application US/09833328
; Patent No. US20020136713A1
; GENERAL INFORMATION:
; APPLICANT: Laemmle, Bernhard
; APPLICANT: Schwarz, Hans-Peter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Antoine, Gerhard
; APPLICANT: Kerschbaumer, Randolph
; APPLICANT: Tagliavacca, Luigina
; APPLICANT: Zimmermann, Klaus
; APPLICANT: Furlan, Miha
; APPLICANT: Turecek, Peter
; APPLICANT: Geritsen, Helena E.
; TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease F
; TITLE OF INVENTION: Comprising a Polypeptide Chain with the Amino Acid Sequence AF
; FILE REFERENCE: 247.00CIP
; CURRENT APPLICATION NUMBER: US/09/833,328
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 09/721,254
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human
US-09-833-328-10

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMVP 17
   ||||
Db 5 TMVP 8
```

RESULT 43

US-09-835-853-22
; Sequence 22, Application US/09835853
; Patent No. US20020165136A1
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/835,853

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/704,344

FILING DATE: 28-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, Henry N.

REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 104322.196

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 942-8459

TELEFAX: (202) 942-8484

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-835-853-22

Query Match 22.2%; Score 4; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4

Db 5 LOPE 8

RESULT 44

US-09-876-904A-388

; Sequence 388, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 388

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

; FEATURE:

; OTHER INFORMATION: C. elegans Sdc-3 protein.

US-09-876-904A-388

Query Match 22.2%; Score 4; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVKE 13

Db 7 KVKE 10

RESULT 45

US-09-572-404B-1436

; Sequence 1436, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 1436

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in SLC12A2 OR NKCC1 at 281-290 and may interact

; OTHER INFORMATION: Sequence 1435 in this patent.

US-09-572-404B-1436

Query Match 22.2%; Score 4; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12

Db 4 PKVK 7

RESULT 46

US-10-177-390-33

; Sequence 33, Application US/10177390

; Publication No. US20030143743A1

; GENERAL INFORMATION:

; APPLICANT: Schuler, Gerold

; APPLICANT: N.V. Antwerp Innovatiecentrum

; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear

; TITLE OF INVENTION: Polynucleotides by Electroporation

; FILE REFERENCE: 021505wo/JH/ml

; CURRENT APPLICATION NUMBER: US/10/177,390

; CURRENT FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 33

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Influenza virus

US-10-177-390-33

Query Match 22.2%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4

Db 5 LOPE 8

```

Db          6 LQPE 9

RESULT 47
US-09-942-052-54
; Sequence 54, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-54

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
   ||||
Db 2 LQPE 5

RESULT 48
US-09-942-052-74
; Sequence 74, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-74

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
   ||||

Db          6 LQPE 9

RESULT 49
US-09-942-052-256
; Sequence 256, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 256
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-256

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
   ||||
Db 6 LQPE 9

RESULT 50
US-09-942-052-257
; Sequence 257, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-257

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
   ||||
```

```
Db          1 LOPE 5
           ||||
           2 LOPE 5

RESULT 51
US-09-942-052-360
; Sequence 360, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 360
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-360

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LOPE 4
           ||||
           6 LOPE 9

RESULT 52
US-09-942-052-476
; Sequence 476, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 476
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-476

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LOPE 4
           ||||
           6 LOPE 9

RESULT 53
US-09-942-052-573
; Sequence 573, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 573
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-573

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LOPE 4
           ||||
           5 LOPE 8

RESULT 54
US-09-942-052-669
; Sequence 669, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-669

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1 LOPE 4
| | | |
Db 5 LQPE 8

RESULT 55
US-09-942-052-688
; Sequence 688, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-2002B.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 688
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-942-052-688

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
| | | |
Db 2 LOPE 5

RESULT 56
US-10-200-708-122
; Sequence 122, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus

US-10-200-708-122

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
| | | |
Db 6 PKVK 9

RESULT 57
US-10-200-708-223
; Sequence 223, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 223
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus

US-10-200-708-223

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
| | | |
Db 2 PKVK 5

RESULT 58
US-10-200-708-248
; Sequence 248, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus

US-10-200-708-248

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
| | | |
Db 2 PKVK 5

```
RESULT 59
US-10-200-708-338
; Sequence 338, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/200,708
; FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 338
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-338

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 60
US-10-200-708-345
; Sequence 345, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/200,708
; FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-345

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 61
US-10-200-708-635
; Sequence 635, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/200,708
; FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 520
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-520

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 62
US-10-200-708-542
; Sequence 542, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/200,708
; FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-542

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 7 PKVK 10

RESULT 63
US-10-200-708-635
; Sequence 635, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/200,708
; FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-542

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 7 PKVK 10
```

```

; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-635

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVK 12
Db      2 PKVK 5

RESULT 64
US-10-200-708-649
; Sequence 649, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 649
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-649

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVK 12
Db      2 PKVK 5

RESULT 65
US-10-200-708-670
; Sequence 670, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES

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; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 670
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-670

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVK 12
Db      6 PKVK 9

RESULT 66
US-10-062-710-228
; Sequence 228, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-062-710-228

Query Match      22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOPE 4
Db      5 LOPE 8

RESULT 67
US-10-133-210-271
; Sequence 271, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND

```

; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-271

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 5 LOPE 8

RESULT 68
US-10-224-286-19
; Sequence 19, Application US/10224286
; Publication No. US20030108517A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/224,286
; FILING DATE: 19-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4

Db 5 LOPE 8

RESULT 69
US-10-054-968-13
; Sequence 13, Application US/10054968
; Publication No. US20030119101A1
; GENERAL INFORMATION:
; APPLICANT: NEUTEC PHARMA PLC
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM
; TITLE OF INVENTION: POSITIVE
; TITLE OF INVENTION: COCCI
; FILE REFERENCE: PM 259204
; CURRENT APPLICATION NUMBER: US/10/054,968
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US/09/214,307
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01830
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: GB9614274.0
; PRIOR FILING DATE: 1996-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-054-968-13

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPK 10
Db 7 GVPK 10

RESULT 70
US-09-852-910-264
; Sequence 264, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 264
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11)
; OTHER INFORMATION: G11 library peptide
US-09-852-910-264

Query Match 22.2%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVKE 13
Db 4 KVKE 7

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RESULT 71
US-10-062-710-206
; Sequence 206, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T Cell epitopes
US-10-062-710-206

Query Match      22.2%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
      ||||
Db      6 LQPE 9

RESULT 72
US-09-832-723-42
; Sequence 42, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-42

Query Match      22.2%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.1e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TWVP 17
      ||||
Db      7 TWVP 10

RESULT 73
US-10-303-331-42
; Sequence 42, Application US/10303331
```

```
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-42

Query Match      22.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TWVP 17
      ||||
Db      7 TWVP 10

RESULT 74
US-10-116-275-72
; Sequence 72, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lamkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance I
; OTHER INFORMATION: take Across the GIT"
US-10-116-275-72

Query Match      22.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TWVP 17
      ||||
Db      7 TWVP 10

RESULT 75
US-10-185-815-26
; Sequence 26, Application US/10185815
; Publication No. US20030096354A1
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; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide ligand
US-10-185-815-26

Query Match 22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 14 TMVP 17
|||
Db 7 TMVP 10

Search completed: November 25, 2003, 20:36:59
Job time : 29.8837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-21
Perfect score: 18
Sequence: 1 LQPEIMGVVKVETWPK 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	4	US-09-641-803-21
2	4	22.2	4	4	US-09-985-357A-12
3	4	22.2	4	4	US-09-113-692B-9
4	4	22.2	4	4	US-09-607-277A-9
5	4	22.2	5	2	US-08-760-075A-29
6	4	22.2	5	3	US-09-338-546-29
7	4	22.2	5	4	US-09-659-084-29
8	4	22.2	6	2	US-08-480-793-14
9	4	22.2	6	5	PCT-US92-05925A-14
10	4	22.2	7	3	US-09-258-754-383
11	4	22.2	7	3	US-09-042-107-383
12	4	22.2	7	4	US-09-641-803-16
13	4	22.2	8	3	US-09-296-284-14
14	4	22.2	9	1	US-08-217-188A-62
15	4	22.2	9	1	US-08-687-226-62
16	4	22.2	9	1	US-08-467-083-2
17	4	22.2	9	1	US-08-615-181-79
18	4	22.2	9	1	US-08-787-547-104
19	4	22.2	9	1	US-08-414-417B-2
20	4	22.2	9	2	US-08-486-348A-2
21	4	22.2	9	2	US-08-468-545B-2
22	4	22.2	9	3	US-08-948-378A-17
23	4	22.2	9	3	US-08-667-725B-62
24	4	22.2	9	3	US-08-466-680B-2
25	4	22.2	9	3	US-09-007-748-62
26	4	22.2	9	3	US-09-169-425C-17
27	4	22.2	9	4	US-08-197-484-28
28	4	22.2	9	4	US-08-197-484-66
29	4	22.2	9	4	US-08-197-484-71
30	4	22.2	9	4	US-08-403-459-12
31	4	22.2	9	4	US-09-759-960-17
32	4	22.2	9	5	PCT-US95-02121-28
33	4	22.2	9	5	PCT-US95-02121-66
34	4	22.2	9	5	PCT-US95-02121-71
35	4	22.2	10	2	US-08-902-516-19
36	4	22.2	10	2	US-08-760-075A-34
37	4	22.2	10	3	US-08-704-344-22
38	4	22.2	10	3	US-09-338-546-34
39	4	22.2	10	3	US-09-461-697-283
40	4	22.2	10	4	US-09-659-084-34
41	4	22.2	10	4	US-09-847-185-19
42	4	22.2	10	4	US-08-760-075A-1
43	4	22.2	11	2	US-08-760-075A-13
44	4	22.2	11	3	US-09-101-886B-57
45	4	22.2	11	3	US-09-338-546-1
46	4	22.2	11	4	US-09-659-084-1
47	4	22.2	12	4	US-08-949-059A-29
48	4	22.2	12	4	US-08-949-059A-31
49	4	22.2	12	6	5460961-8
50	4	22.2	13	1	US-07-610-525-5
51	4	22.2	13	4	US-08-403-459-36
52	4	22.2	14	4	US-08-949-059A-26
53	4	22.2	14	4	US-08-949-059A-27
54	4	22.2	14	4	US-08-949-059A-28
55	4	22.2	15	1	US-07-610-525-4
56	4	22.2	15	1	US-08-097-997A-2
57	4	22.2	15	1	US-08-259-672-11
58	4	22.2	15	1	US-08-459-351-11
59	4	22.2	15	1	US-08-460-533-11
60	4	22.2	15	1	US-08-787-547-44
61	4	22.2	15	2	US-08-553-257A-62
62	4	22.2	15	3	US-08-660-347-3
63	4	22.2	15	3	US-09-041-889-16
64	4	22.2	15	3	US-08-837-058-16
65	4	22.2	15	3	US-08-685-574C-2
66	4	22.2	15	3	US-08-946-994-2
67	4	22.2	15	4	US-09-417-264-16
68	4	22.2	15	4	US-09-441-992-62
69	4	22.2	15	5	PCT-US94-06654-11
70	4	22.2	16	2	US-08-591-438-13
71	4	22.2	16	2	US-08-760-075A-2
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73	4	22.2	16	3	US-08-405-647B-11
74	4	22.2	16	3	US-08-602-999A-344
75	4	22.2	16	3	US-08-985-499-11
76	4	22.2	16	3	US-09-204-335-1
77	4	22.2	16	3	US-09-204-335-2
78	4	22.2	16	3	US-09-338-546-2
79	4	22.2	16	4	US-09-659-084-2
80	4	22.2	16	4	US-09-500-124-344
81	4	22.2	16	5	PCT-US96-03180-11
82	4	22.2	16	5	5200320-32
83	4	22.2	17	1	US-07-610-525-3
84	4	22.2	17	1	US-08-445-909A-14
85	4	22.2	17	2	US-08-733-982A-12
86	4	22.2	17	4	US-09-352-078-5
87	4	22.2	17	4	US-09-232-225-10
88	4	22.2	18	1	US-08-259-672-10
89	4	22.2	18	1	US-08-459-351-10
90	4	22.2	18	1	US-08-460-533-10
91	4	22.2	18	1	US-08-451-472-18
92	4	22.2	18	1	US-08-451-472-48
93	4	22.2	18	1	US-08-451-472-68
94	4	22.2	18	3	US-08-075-541D-34
95	4	22.2	18	3	US-08-075-541D-35
96	4	22.2	18	3	US-08-075-541D-45
97	4	22.2	18	5	PCT-US94-06654-10
98	4	22.2	19	1	US-07-610-525-2
99	4	22.2	20	1	US-07-678-974D-6
100	4	22.2	20	2	US-08-484-530-39

ALIGNMENTS

RESULT 1
US-09-641-803-21
; Sequence 21, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-21
Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOPEIMGVPKVKETMVPK 18
Db 1 LOPEIMGVPKVKETMVPK 18
RESULT 2
US-09-985-357A-12
; Sequence 12, Application US/09985357A
; Patent No. 6544748
; GENERAL INFORMATION:
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation
; FILE REFERENCE: HUBR 1151.1 CON PFF/WAS
; CURRENT APPLICATION NUMBER: US/09/985,357A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/463,380
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/EP98/04590
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: DE 19753681.1
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: EP 97112640
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Wordperfect
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide start coded by
; OTHER INFORMATION: EXS
US-09-985-357A-12
Query Match 22.2%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 MGVP 9
Db 1 MGVP 4
RESULT 3
US-09-113-692B-9
; Sequence 9, Application US/09113692B
; Patent No. 6548296
; GENERAL INFORMATION:
; APPLICANT: Stern, Anne
; APPLICANT: Brandt, Michael
; APPLICANT: Honold, Konrad
; APPLICANT: Auer, Johannes
; APPLICANT: Koll, Hans
; APPLICANT: Franze, Reinhard
; APPLICANT: Pessara, Ulrich
; TITLE OF INVENTION: Methods For Identifying Human Cell Lines Useful for
; TITLE OF INVENTION: Endogenous Gene Activation, Isolated Human Cell Lines
; TITLE OF INVENTION: Identified Thereby, And Uses Thereof
; FILE REFERENCE: Hubr 1126
; CURRENT APPLICATION NUMBER: US/09/113,692B
; CURRENT FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP/97 112 640
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: EP/97 121 073
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: EP/97 53 681
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-113-692B-9
Query Match 22.2%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 MGVP 9
Db 1 MGVP 4
RESULT 4
US-09-607-277A-9
; Sequence 9, Application US/09607277A
; Patent No. 6555373
; GENERAL INFORMATION:
; APPLICANT: Stern, Anne
; APPLICANT: Brandt, Michael
; APPLICANT: Honold, Konrad
; APPLICANT: Auer, Johannes
; APPLICANT: Koll, Hans
; APPLICANT: Franze, Reinhard
; APPLICANT: Pessara, Ulrich
; TITLE OF INVENTION: Methods For Identifying Human Cell Lines Useful for
; TITLE OF INVENTION: Endogenous Gene Activation, Isolated Human Cell Lines
; TITLE OF INVENTION: Identified Thereby, And Uses Thereof
; FILE REFERENCE: Hubr 1126.1
; CURRENT APPLICATION NUMBER: US/09/607,277A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/113,692
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP/97 112 640
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: EP/97 121 073
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: EP/97 53 681
; PRIOR FILING DATE: 1997-12-03


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; NUMBER OF SEQ ID NOS:      10
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-607-277A-9

Query Match          22.2%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy      6 MGVP 9
      .|.|.|
Db      1 MGVP 4

RESULT 5
US-08-760-075A-29
; Sequence 29, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08760,075
; FILING DATE: 04-DEC-1995
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-29

Query Match          22.2%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy      5 IMGV 8
      .|.|.|
Db      2 IMGV 5

RESULT 6
US-09-338-546-29
; Sequence 29, Application US/09338546
```

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; Patent No. 6251645
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,546
; FILING DATE:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: DB 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-338-546-29

Query Match          22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy      5 IMGV 8
      .|.|.|
Db      2 IMGV 5

RESULT 7
US-09-659-084-29
; Sequence 29, Application US/09659084
; Patent No. 6403299
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/659,084
; FILING DATE: 11-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/338,546
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-659-084-29

Query Match      22.2%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 IMGV 8
DB      2 IMGV 5

RESULT 8
US-08-480-793-14
; Sequence 14, Application US/08480793
; Patent No. 5955444
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M., Roder, Hanno M.
; TITLE OF INVENTION: Novel Tau/Neurofilament Protein
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 28 Carleton Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,793
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/912,293
; FILING DATE: July 10, 1992
; APPLICATION NUMBER: 07/742,880
; FILING DATE: 9-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0656/7008
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-793-14

Query Match      22.2%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PEIM 6
DB      2 PEIM 5

RESULT 9
PCT-US92-05825A-14
; Sequence 14, Application PC/TUS9205825A
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M., Roder, Hanno M.
; TITLE OF INVENTION: Novel Tau/Neurofilament Protein
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 28 Carleton Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05825A
; FILING DATE: 19920710
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/742,980
; FILING DATE: 9-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0656/7008
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-05825A-14

Query Match      22.2%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PEIM 6
DB      2 PEIM 5

RESULT 10
US-09-258-754-383
; Sequence 383, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
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```

; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 383
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-383

Query Match      22.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVK 12
      ||||
Db      1 PKVK 4

RESULT 11
US-09-042-107-383
; Sequence 383, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 383
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-383

Query Match      22.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVK 12
      ||||
Db      1 PKVK 4

RESULT 12
US-09-641-803-16
; Sequence 16, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-641-803-16

Query Match      22.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVK 12
      ||||
Db      1 PKVK 4

RESULT 13
US-09-296-284-14
; Sequence 14, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
; APPLICANT: Choi, Eun-Sung
; APPLICANT: Rhee, Sang-Ki
; APPLICANT: Lee, Eun-Hae
; TITLE OF INVENTION: Glucanobacter Suboxydans Sorbitol Dehydrogenase, Genes
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: 1533.0870000
; CURRENT APPLICATION NUMBER: US/09/296,284A
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Glucanobacter suboxydans
US-09-296-284-14

Query Match      22.2%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GVPK 10
      ||||
Db      5 GVPK 8

RESULT 14
US-08-217-188A-62
; Sequence 62, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994

```

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 15
US-08-687-226-62
; Sequence 62, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Meliet, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Pallieur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGS-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;

US-08-687-226-62

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 16
US-08-467-083-2
; Sequence 2, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-467-083-2

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 2 LQPE 5

RESULT 17
US-08-615-181-79
; Sequence 79, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; TITLE OF INVENTION: CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; US-08-615-181-79
```

ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,181
FILING DATE: 04-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01756
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261302/1993
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-796-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-79

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 2 PKVK 5

RESULT 18
US-08-787-547-104
; Sequence 104, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-104

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 5 LOPE 8

RESULT 19
US-08-414-417B-2
; Sequence 2, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-414-417B-2

Query Match 22.2%; Score 4; DB 1; Length 9;

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-378A-17

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 5 LQPE 8

RESULT 23

US-08-667-725B-62
; Sequence 62, Application US/08667725B
; Patent No. 6063900

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.

; APPLICANT: Visseren, M. J. W.

; APPLICANT: Kast, W. M.

; APPLICANT: van der Bruggen, Pierre

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Tumor Rejection Antigen

; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/667,725B

; FILING DATE: 21 June 1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6063900man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 318-3000

; TELEFAX: (212) 752-5958

; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acid residues

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-667-725B-62

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 4 LQPE 7

RESULT 24

US-08-466-680B-2

; Sequence 2, Application US/08466680B

; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,680B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; REFERENCE/DOCKET NUMBER: 920010.448C4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-466-680B-2

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 2 LQPE 5

RESULT 25

US-09-007-748-62

; Sequence 62, Application US/09007748

; Patent No. 6147187

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.

; APPLICANT: Visseren, M. J. W.

; APPLICANT: Kast, W. M.

; APPLICANT: van der Bruggen, Pierre

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Tumor Rejection Antigen

; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/007,748
FILING DATE: 15 January 1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6147187man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-007-748-62

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LOPE 4
|||
Db 4 LOPE 7

RESULT 26
US-09-169-425C-17
Sequence 17, Application US/09169425C
Patent No. 6183746
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chiciz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
NUMBER OF SEQUENCES: 33
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,425C
FILING DATE: 09-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/061,657
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-169-425C-17

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 1 LOPE 4
|||
Db 5 LOPE 8
RESULT 27
US-08-197-484-28
Sequence 28, Application US/08197484
Patent No. 6419931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
NUMBER OF SEQUENCES: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-28

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 PKVK 12
|||
Db 2 PKVK 5

RESULT 28

US-08-197-484-66
 ; Sequence 66, Application US/08197484
 ; Patent No. 6419931
 ; GENERAL INFORMATION:
 ; APPLICANT: VITIELLO, Maria A.
 ; APPLICANT: CHESTNUT, Robert W.
 ; APPLICANT: SETTE, Alessandro D.
 ; APPLICANT: CELIS, Esteban
 ; APPLICANT: GRAY, Howard
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 ; TITLE OF INVENTION: CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: Steuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/197,484
 ; FILING DATE: 16-FEB-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/935,811
 ; FILING DATE: 26-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/874,491
 ; FILING DATE: 27-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,682
 ; FILING DATE: 29-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/749,568
 ; FILING DATE: 26-AUG-1991
 ; FILING DATE: 27-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 14137-26-4
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (206) 623-6793
 ; INFORMATION FOR SEQ ID NO: 66:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-197-484-66

Query Match 22.2%; Score 4; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
 Db 5 LOPE 8

RESULT 29

US-08-197-484-71
 ; Sequence 71, Application US/08197484
 ; Patent No. 6419931
 ; GENERAL INFORMATION:

; APPLICANT: VITIELLO, Maria A.
 ; APPLICANT: CHESTNUT, Robert W.
 ; APPLICANT: SETTE, Alessandro D.
 ; APPLICANT: CELIS, Esteban
 ; APPLICANT: GRAY, Howard
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 ; TITLE OF INVENTION: CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: Steuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/197,484
 ; FILING DATE: 16-FEB-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/935,811
 ; FILING DATE: 26-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/874,491
 ; FILING DATE: 27-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,682
 ; FILING DATE: 29-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/749,568
 ; FILING DATE: 26-AUG-1991
 ; FILING DATE: 27-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 14137-26-4
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (206) 623-6793
 ; INFORMATION FOR SEQ ID NO: 71:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-197-484-71

Query Match 22.2%; Score 4; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
 Db 4 LOPE 7

RESULT 30

US-08-403-459-12
 ; Sequence 12, Application US/08403459
 ; Patent No. 6514942
 ; GENERAL INFORMATION:
 ; APPLICANT: Ioannides, Constantin G.
 ; APPLICANT: Fisk, Bryan A.
 ; APPLICANT: Ioannides, Maria G.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
 ; TITLE OF INVENTION: T-LYMPHOCYTES
 ; NUMBER OF SEQUENCES: 68
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,459
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSC:390/KIT
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-459-12

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 2 LQPE 5

RESULT 31
US-09-759-960-17
Sequence 17, Application US/09759960
Patent No. 6582704
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/169,425
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 'Fraser, Janis K.

REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-759-960-17

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 32
PCT-US95-02121-28
Sequence 28, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-28

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 2 PKVK 5

RESULT 33
PCT-US95-02121-66
; Sequence 66, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-66

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 5 LQPE 8

RESULT 34
PCT-US95-02121-71
; Sequence 71, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-71

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 4 LQPE 7

RESULT 35

US-08-902-516-19
; Sequence 19, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:

; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-902-516-19

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LOPE 4
DB 5 LOPE 8

RESULT 36
US-08-760-075A-34
Sequence 34, Application US/08760075A
Patent No. 5942429
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-760-075A-34

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 IMGV 8
DB 5 IMGV 8

RESULT 37
US-08-704-344-22
Sequence 22, Application US/08704344
Patent No. 6218363
GENERAL INFORMATION:
APPLICANT: BASERGA, Renato L.
APPLICANT: RESNICOFF, Mariana
APPLICANT: HUANG, Ziwei
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,344
FILING DATE: 28-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 942-8459
TELEFAX: (202) 942-8459
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-704-344-22

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LOPE 4
DB 5 LOPE 8

RESULT 38
US-09-338-546-34
Sequence 34, Application US/09338546
Patent No. 6251645
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: KIRSCHBAUM, Bernd
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-338-546-34

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IMGV 8
Db 5 IMGV 8

RESULT 39
US-09-461-697-283
Sequence 283, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Purnam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 283
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-461-697-283

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVPK 18

Db 1 MVPK 4
RESULT 40
US-09-659-084-34
Sequence 34, Application US/09659084
Patent No. 6403299
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
MUELLNER, Stefan
BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/659,084
FILING DATE: 11-Sep-2000
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/338,546
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-659-084-34

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IMGV 8
Db 5 IMGV 8

RESULT 41
US-09-847-185-19
Sequence 19, Application US/09847185
Patent No. 6482407
GENERAL INFORMATION:
APPLICANT: Soo Hoo, William
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/847,185
FILING DATE: 01-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,931
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
|||
DB 5 LQPE 8

RESULT 42
US-09-214-307A-13
Sequence 13, Application US/09214307A
Patent No. 6544516
GENERAL INFORMATION:
APPLICANT: NEUTEC PHARMA PLC
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM POSITIVE
FILE REFERENCE: PM 259204
CURRENT FILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: US/09/214,307A
PRIOR FILING DATE: 1997-07-07
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: GB9614274.0
PRIOR FILING DATE: 1996-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 10
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-214-307A-13

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPK 10
|||
DB 7 GVPK 10

RESULT 43

US-08-760-075A-1
Sequence 1, Application US/08760075A
Patent No. 5942429
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-760-075A-1

Query Match 22.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8
|||
DB 5 IMGV 8

RESULT 44
US-09-101-886B-57
Sequence 57, Application US/09101886B
Patent No. 6197507
GENERAL INFORMATION:
APPLICANT: BERG, THOMAS
APPLICANT: TOLLERSRUD, OLE K
APPLICANT: NILSEN, OIVIND
TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: BARBARA G. ERNST
STREET: 555 13TH STREET, NW SUITE 701E
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,886B
FILING DATE: 29-JANUARY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/00109
FILING DATE: 12-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-240
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: not relevant
ANTI-SENSE: not relevant
FRAGMENT TYPE: internal
US-09-101-886B-57

Query Match 22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 7 PKVK 10

RESULT 45
US-09-338-546-1
Sequence 1, Application US/09338546
Patent No. 6251645
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
MUELLNER, Stefan
BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-338-546-1

Query Match 22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8
DB 5 IMGV 8

RESULT 46
US-09-659-084-1
Sequence 1, Application US/09659084
Patent No. 6403299
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
MUELLNER, Stefan
BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/659,084
FILING DATE: 11-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/338,546
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-659-084-1

Query Match 22.2%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8
DB 5 IMGV 8

RESULT 47
US-08-949-059A-29
; Sequence 29, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhanev, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-29

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 8 PKVK 11

RESULT 48
US-08-949-059A-31
; Sequence 31, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhanev, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-29

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 8 PKVK 11

RESULT 49
US-08-949-059A-31
; Sequence 31, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhanev, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
US-08-949-059A-31

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 8 PKVK 11

RESULT 49
5460961-8
; Patent No. 5460961
; APPLICANT: DEBY, CAROL;PINCEMAIL, JOEL;BOLLEN, ALEX
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
; THERAPEUTIC APPLICATION
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,678
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 460,931

; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhanev, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
US-08-949-059A-31

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 8 PKVK 11

RESULT 49
5460961-8
; Patent No. 5460961
; APPLICANT: DEBY, CAROL;PINCEMAIL, JOEL;BOLLEN, ALEX
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
; THERAPEUTIC APPLICATION
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,678
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 460,931

; FILING DATE: 14-FEB-1990
 ; SEQ ID NO:8;
 ; LENGTH: 12
 ; 5460961-8

Query Match 22.2%; Score 4; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGVP 9
 Db 1 MGVP 4

RESULT 50

US-07-610-525-5

; Sequence 5, Application US/07610525

; Patent No. 5196512

; GENERAL INFORMATION:

; APPLICANT: BIANCHI Elisabetta

; APPLICANT: PESSI Antonello

; APPLICANT: CORRADIN Giampietro

; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS

; TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGATES

; TITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SHEA & GOULD

; STREET: 1251 AVENUE OF THE AMERICAS

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: UNITED STATES

; ZIP: 10020-1193

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/610,525

; FILING DATE: 19901108

; CLASSIFICATION: 424

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-827-3000

; TELEFAX: 212-840-6702

; TELEX: 423973

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acid residues

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: no

; FRAGMENT TYPE: internal fragment

US-07-610-525-5

Query Match 22.2%; Score 4; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPKV 11
 Db 4 VPKV 7

RESULT 51

US-08-403-459-36

; Sequence 36, Application US/08403459

; Patent No. 6514942

; GENERAL INFORMATION:

; APPLICANT: Ioannides, Constantine G.

; APPLICANT: Fisk, Bryan A.

; APPLICANT: Ioannides, Maria G.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
 ; TITLE OF INVENTION: T-LYMPHOCYTES

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/403,459

; FILING DATE: Concurrently Herewith

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: UTSC:390/KIT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (713) 789-2679

; TELEX: 79-0924

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-403-459-36

Query Match 22.2%; Score 4; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
 Db 1 LOPE 4

RESULT 52

US-08-949-059A-26

; Sequence 26, Application US/08949059A

; Patent No. 6358921

; GENERAL INFORMATION:

; APPLICANT: Kondejewski, Leslie H.

; APPLICANT: Hodges, Robert S.

; APPLICANT: Wishart, David S.

; APPLICANT: Hancock, Robert E.W.

; APPLICANT: McElhaney, Ronald N.

; APPLICANT: Prentner, Elmar J.

; APPLICANT: Lewis, Ruthven N.A.H

; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND

; TITLE OF INVENTION: METHOD

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/949,059A
;; FILING DATE: 10-OCT-1997
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 660081.412
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: cyclic
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 6
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 13
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; US-08-949-059A-26

Query Match 22.2%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
||||
Db 7 PKVK 10

RESULT 53
US-08-949-059A-27
; Sequence 27, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhanev, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963

;; REFERENCE/DOCKET NUMBER: 660081.412
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: cyclic
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Residue is a D-Lysine"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 6
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 13
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;; US-08-949-059A-27

Query Match 22.2%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
||||
Db 7 PKVK 10

RESULT 54
US-08-949-059A-28
; Sequence 28, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhanev, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

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; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /note= "Residue is a D-Valine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-28
;
; Query Match 22.2%; Score 4; DB 4; Length 14;
; Best Local Similarity 100.0%; Pred. No. 2.5e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 9 PKVK 12
; DB 7 PKVK 10
;
; RESULT 55
; US-07-610-525-4
; Sequence 4, Application US/07610525
; Patent No. 5196512
; GENERAL INFORMATION:
; APPLICANT: BIANCHI Eisabetta
; APPLICANT: PESSI Antonello
; APPLICANT: CORRADIN Giampietro
; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS
; TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGATES
; TITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHEA & GOULD
; STREET: 1251 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10020-1193
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/610,525
; FILING DATE: 19901108
; CLASSIFICATION: 424
; TELEPHONE: 212-827-3000
; TELEFAX: 212-840-6702
; TELEX: 423973
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no

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; FRAGMENT TYPE: internal fragment
; US-07-610-525-4
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; Query Match 22.2%; Score 4; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 2.7e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 8 VPKV 11
; DB 6 VPKV 9
;
; RESULT 56
; US-08-097-997A-2
; Sequence 2, Application US/08097997A
; Patent No. 5728536
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; APPLICANT: Quelle, Frederick W.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
; TITLE OF INVENTION: Transduction
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,997A
; FILING DATE: 29-JULY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0370000/SLF/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-097-997A-2
;
; Query Match 22.2%; Score 4; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 2.7e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 10 KVKK 13
; DB 10 KVKK 13
;
; RESULT 57
; US-08-259-672-11
; Sequence 11, Application US/08259672
; Patent No. 5736337
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN
; TITLE OF INVENTION: INTERACTIONS

```

```

; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,672
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-259-672-11

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 1 LOPE 4

RESULT 58
US-08-459-351-11
; Sequence 11, Application US/08459351
; Patent No. 5763571
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-Feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,351
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-259-672-11
```

```

; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-459-351-11

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 1 LOPE 4

RESULT 59
US-08-460-533-11
; Sequence 11, Application US/08460533
; Patent No. 5767075
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-Feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,533
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-460-533-11
```

US-08-460-533-11

Query Match 22.2%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
 ||||
 Db 1 LOPE 4

RESULT 60

US-08-787-547-44
 ; Sequence 44, Application US/08787547
 ; Patent No. 5783567
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Curley, Joanne M.
 ; APPLICANT: Langer, Robert S.
 ; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
 ; TITLE OF INVENTION: OF NUCLEIC ACID
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/787,547
 ; FILING DATE: 22-JAN-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 08191/003001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 44:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-787-547-44

Query Match 22.2%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPKV 11
 ||||
 Db 6 VPKV 9

RESULT 61

US-08-553-257A-62
 ; Sequence 62, Application US/08553257A
 ; Patent No. 5994083
 ; GENERAL INFORMATION:
 ; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
 ; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.

; APPLICANT: FELICI, Franco
 ; APPLICANT: LUZZAGO, Alessandra
 ; APPLICANT: NICOSIA, Alfredo
 ; APPLICANT: MONACI, Paolo
 ; APPLICANT: CORTESE, Riccardo
 ; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
 ; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
 ; TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
 ; NUMBER OF SEQUENCES: 68
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street N.W. Ste. 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/553,257A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/IT94/00054
 ; FILING DATE: 05-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: RM93A000301
 ; FILING DATE: 11-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Browdy, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: FELICI=1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-5197
 ; TELEFAX: (202) 737-3528
 ; INFORMATION FOR SEQ ID NO: 62:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-553-257A-62

Query Match 22.2%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
 ||||
 Db 7 PKVK 10

RESULT 62
 US-08-660-347-3
 ; Sequence 3, Application US/08660347
 ; Patent No. 6029335
 ; GENERAL INFORMATION:
 ; APPLICANT: Purchio, Anthony F.
 ; APPLICANT: New, Ligu
 ; APPLICANT: Liu, Kang
 ; APPLICANT: Kamali, Vafa
 ; APPLICANT: Naughton, Brian
 ; TITLE OF INVENTION: No. 6027935el Gene Up-Regulated in
 ; TITLE OF INVENTION: Regenerating Liver
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,347
FILING DATE: 05-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6261-0151-999
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6027935e
US-08-660-347-3

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
DB 4 VKET 7

RESULT 63
US-09-041-899-16
Sequence 16, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: 'Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-041-899-16

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 4 PKVK 7

RESULT 64
US-08-837-058-16
Sequence 16, Application US/08837058
Patent No. 6074835
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Targan, Stephan R.
APPLICANT: Eggena, Mark
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Histone H1
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-837-058-16

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 4 PKVK 7

RESULT 65

```

US-08-665-574C-2
; Sequence 2, Application US/08665574C
; Patent No. 6136595
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,574C
; FILING DATE: 18-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/282,012
; FILING DATE: 29-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/097,997
; FILING DATE: 29-JUL-1993
; APPLICATION NUMBER: 08/118,968
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-665-574C-2
Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVKE 13
Db 10 KVKE 13

RESULT 66
US-08-946-994-2
; Sequence 2, Application US/08946994
; Patent No. 6210654
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; APPLICANT: Quelle, Frederick W.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
; TITLE OF INVENTION: Transduction
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600

```

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,994
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,574
; FILING DATE: 18-JUN-1996
; APPLICATION NUMBER: 08/282,012
; FILING DATE: 29-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/097,997
; FILING DATE: 29-JUL-1993
; APPLICATION NUMBER: 08/118,968
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-946-994-2
Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVKE 13
Db 10 KVKE 13

RESULT 67
US-09-417-264-16
; Sequence 16, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC pANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-417-264-16

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 4 PKVK 7

RESULT 68
US-09-441-992-62
Sequence 62, Application US/09441992
Patent No. 6541210
GENERAL INFORMATION:
APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
MOLECOLARE P. ANGELETTI S.p.A.
FELICI, Franco
LUZZAGO, Alessandra
NICOSIA, Alfredo
MONACI, Paolo
CORTESE, Riccardo
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/441,992
FILING DATE: 18-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,257
FILING DATE: <Unknown>
APPLICATION NUMBER: RM93A000301
FILING DATE: 11-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI=1
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-441-992-62

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 7 PKVK 10

RESULT 69
PCT-US94-06654-11
Sequence 11, Application PC/TUS9406654
GENERAL INFORMATION:
APPLICANT: Joseph Avruch
APPLICANT: Xian-feng Zhang
APPLICANT: Mark S. Marshall
TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06654
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark, Esq.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/234001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-06654-11

Query Match 22.2%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
DB 1 LOPE 4

RESULT 70
US-08-591-438-13
Sequence 13, Application US/08591438

; Patent No. 5939063
; GENERAL INFORMATION:
; APPLICANT: Vadas, Mathew A.
; APPLICANT: Lopez, Angel F.
; APPLICANT: Shannon, Mary F.
; TITLE OF INVENTION: HAEMOPOIETIC GROWTH FACTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591.438
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio Esq., Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; US-08-591-438-13

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
| | | |
DB 3 VKET 6

RESULT 71
US-08-760-075A-2
; Sequence 2, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075A

; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-760-075A-2

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8
| | | |
DB 5 IMGV 8

RESULT 72
US-09-011-525-1
; Sequence 1, Application US/09011525
; Patent No. 6020172
; GENERAL INFORMATION:
; APPLICANT: BOTH, GERALD W.
; TITLE OF INVENTION: GENE THERAPY USING OVINE ADENOVIRAL VECTORS
; FILE REFERENCE: Gene Therapy Using Ovine Adenoviral Ve
; CURRENT APPLICATION NUMBER: US/09/011,525
; CURRENT FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00518
; EARLIER FILING DATE: 1996-08-14
; EARLIER APPLICATION NUMBER: AU PN4776
; EARLIER FILING DATE: 1995-08-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Ovine adenovirus
; US-09-011-525-1

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVPK 18
| | | |
DB 4 MVPK 7

RESULT 73
US-08-405-647B-11
; Sequence 11, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.
; APPLICANT: Crandall, Ian E.
; APPLICANT: Sholest, Stephen B.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
; NUMBER OF SEQUENCES: 50

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; FILING DATE: 17-MAR-1995
;; APPLICATION NUMBER: US/08/405,647B
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Kenneth A.
;; REGISTRATION NUMBER: 31,677
;; REFERENCE/DOCKET NUMBER: 02307E-068700US
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-405-647B-11

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 MVPK 18
Db 6 MVPK 9

RESULT 74
US-08-602-999A-344
;; Sequence 344, Application US/08602999A
;; Patent No. 6184205
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999A
;; FILING DATE: 16-FEB-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 344:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-602-999A-344

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 9 PKVK 12
Db 11 PKVK 14

RESULT 75
US-08-985-499-11
;; Sequence 11, Application US/08985499
;; Patent No. 6191103
;; GENERAL INFORMATION:
;; APPLICANT: Shohet, Stephen B.
;; APPLICANT: Sherman, Irwin
;; APPLICANT: von Andrian, Ulrich
;; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
;; TITLE OF INVENTION: Mammal
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/985,499
;; FILING DATE: 05-DEC-1997
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hyman, Laurence J.
;; REGISTRATION NUMBER: 35,551
;; REFERENCE/DOCKET NUMBER: 02307E-084500US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-985-499-11

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 MVPK 18
Db 11 PKVK 14

Db 6 MYPK 9

Search completed: November 25, 2003, 20:29:58
Job time : 15.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18
Sequence: 1 HKEMPPFKVPVPTTSQ 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	22.2	14	2	H64008
2	4	22.2	16	2	PC4371
3	3	16.7	5	2	PQ0009
4	3	16.7	5	2	J70520
5	3	16.7	6	2	A61049
6	3	16.7	6	2	I51317
7	3	16.7	7	1	XYDGD
8	3	16.7	7	2	S33244
9	3	16.7	8	2	A32523
10	3	16.7	8	2	S20162
11	3	16.7	9	2	PD0443
12	3	16.7	10	2	A60410
13	3	16.7	10	2	S65728
14	3	16.7	10	2	A37268
15	3	16.7	11	2	P58501
16	3	16.7	11	2	PA0028
17	3	16.7	11	2	PC4267
18	3	16.7	11	2	PQ0731
19	3	16.7	11	2	I54193
20	3	16.7	11	2	A54348
21	3	16.7	13	2	PQ0491
22	3	16.7	13	2	A4818
23	3	16.7	13	2	A28953
24	3	16.7	13	2	S21152
25	3	16.7	13	2	A60458
26	3	16.7	13	2	PC2371
27	3	16.7	13	2	D56661
28	3	16.7	13	2	B61620
29	3	16.7	13	2	D61458

30	3	16.7	13	2	B61458
31	3	16.7	13	2	PH1772
32	3	16.7	14	2	PT0026
33	3	16.7	14	2	E33098
34	3	16.7	15	2	PA0024
35	3	16.7	15	2	PS0452
36	3	16.7	15	2	PA0062
37	3	16.7	15	2	B61457
38	3	16.7	15	2	A36527
39	3	16.7	15	2	A49480
40	3	16.7	15	2	PT0205
41	3	16.7	15	2	B45115
42	3	16.7	16	2	B42324
43	3	16.7	16	2	C45133
44	3	16.7	16	2	I40065
45	3	16.7	16	2	C53113
46	3	16.7	17	2	S05671
47	3	16.7	17	2	S05033
48	3	16.7	17	2	B31769
49	3	16.7	17	2	G85956
50	3	16.7	18	2	S29264
51	3	16.7	18	2	H64711
52	3	16.7	18	2	S58377
53	3	16.7	18	2	S71592
54	3	16.7	18	2	I46853
55	3	16.7	18	2	A59137
56	3	16.7	19	1	EWSMCN
57	3	16.7	19	2	S59485
58	3	16.7	19	2	S43641
59	3	16.7	19	2	C56661
60	3	16.7	19	2	PQ0492
61	3	16.7	19	2	A61144
62	3	16.7	19	2	C39305
63	3	16.7	19	2	I46654
64	3	16.7	19	2	S69166
65	3	16.7	19	2	S11611
66	3	16.7	20	2	S06466
67	3	16.7	20	2	JP0059
68	3	16.7	20	2	PL0145
69	3	16.7	20	2	PQ0046
70	3	16.7	20	2	S29635
71	3	16.7	20	2	B30208
72	3	16.7	20	2	S58382
73	3	16.7	20	2	I46652
74	3	16.7	20	2	A41439
75	2	11.1	3	3	GKHU
76	2	11.1	3	3	A33802
77	2	11.1	3	3	A43391
78	2	11.1	3	3	I78890
79	2	11.1	4	2	A32039
80	2	11.1	4	2	S53508
81	2	11.1	4	2	PT0240
82	2	11.1	4	2	I54357
83	2	11.1	5	2	JN0862
84	2	11.1	5	2	C41225
85	2	11.1	5	2	B60274
86	2	11.1	5	2	T14908
87	2	11.1	5	2	PQ0689
88	2	11.1	5	2	B37988
89	2	11.1	5	2	JS0319
90	2	11.1	5	2	S53595
91	2	11.1	5	2	S11127
92	2	11.1	5	2	PT0308
93	2	11.1	5	2	PT0610
94	2	11.1	5	2	PT0644
95	2	11.1	6	2	JN0861
96	2	11.1	6	2	S14835
97	2	11.1	6	2	S11556
98	2	11.1	6	2	B60110
99	2	11.1	6	2	A31263
100	2	11.1	6	2	B31263

Ig kappa chain V-I
T cell receptor al
calotropin DI - mu
214K exoantigen (v
protein QA300050 -
32K protein 3306 -
fumarate hydratase
alpha-glucosidase
juvenile-hormone e
major immunophilin
insulin-like growth
peptidylprolyl iso
cytochrome P450c27
casein kinase II (c
shikimate 5-dehydr
lys-gingipain form
hirudin Ia - medic
photosystem II pro
T-cell receptor de
hypothetical prote
ovoemerythrin - d
hypothetical prote
insulin-like growth
serine proteinase
T-cell receptor de
protein PII - gold
cinnamycin - Strep
hydroxyproline-rich
carboxylesterase (c
S-locus specific g
self-incompatibili
probable flagellar
neurotoxin Tx3 - s
T-cell receptor de
ferredoxin b - Jap
ribosomal protein
T-cell receptor al
ribosomal protein
carbon-monoxide de
citrate (si)-synth
jacalin beta chain
hypothetical prote
hypothetical prote
T-cell receptor de
acid ribonuclease
growth-modulating
thyrotropin-releas
TRH-like tripeptid
tyrosine protein k
tyrosine-melanocyt
starvation-induced
Ig heavy chain CRD
schwannomin - mous
peptidyl-dipeptida
copper resistance
major protein anti
hypothetical prote
photosystem I 10.4
acid proteinase li
subesophageal gang
hypothetical prote
phosphoprotein, bo
Ig heavy chain CRD
T-cell receptor be
T-cell receptor be
peptidyl-dipeptida
dnaA protein - Pse
hydrogensulfite re
repetitive protein
dihydrofolate redu
dihydrofolate redu

ALIGNMENTS

RESULT 1

H64008
 Hypothetical protein H10492 - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64008
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: H64008
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-14 <TIGR>
 A:Cross-references: GB:U32731; GB:142023; NID:g1573465; PID:g1573478; TIGR:H10492

Query Match 22.2%; Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKYP 10
 ||||
 DB 3 PKYP 6

RESULT 2

PC4371
 Telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C:Accession: PC4371
 R:Sarig, G.; Weisman-Shoner, P.; Fry, M. Biochem. Biophys. Res. Commun. 237, 617-623, 1997
 A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the C/A:Reference number: PC4371; MUID:97445086; PMID:9299414
 A:Accession: PC4371
 A:Molecule type: protein
 A:Residues: 1-16 <SAR>
 C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 22.2%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
 ||||
 DB 5 PVEP 8

RESULT 3

PQ0009
 angiotensin-converting enzyme inhibitor (FLP-2) - common fig
 N:Alternate names: ficus latex peptide 2
 C:Species: Ficus carica (common fig)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
 C:Accession: PQ0009
 R:Maruyama, S.; Miyoshi, S.; Tanaka, H. Agric. Biol. Chem. 53, 2763-2767, 1989
 A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
 A:Reference number: PQ0008
 A:Accession: PQ0009
 A:Molecule type: protein
 A:Residues: 1-5 <MAR>
 A:Experimental source: latex
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 16.7%; Score 3; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
 ||||
 DB 2 YPV 4

RESULT 4

JT0520
 IG kappa chain V-III region (SD1) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
 C:Accession: JT0520
 R:Anker, R.; Conley, M.E.; Pollok, B.A. J. Exp. Med. 169, 2109-2119, 1989
 A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
 A:Reference number: JT0511; MUID:89279157; PMID:2786547
 A:Accession: JT0520
 A:Molecule type: mRNA
 A:Residues: 1-5 <ANK>
 A:Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
 A:Note: a stop codon terminates the sequence in the V region
 C:Keywords: heterotetramer; immunoglobulin
 P:1-5/Domain: V kappa region <VRE>

Query Match 16.7%; Score 3; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 DB 1 TES 3

RESULT 5

A61049
 halo-toxin - Pseudomonas syringae pv. mori
 C:Species: Pseudomonas syringae pv. mori
 A:Note: host mulberry tree
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
 C:Accession: A61049
 R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, Chem. Lett. 00, 679-680, 1989
 A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syringae pv. mori
 A:Reference number: A61049
 A:Accession: A61049
 A:Molecule type: protein
 A:Residues: 1-6 <KAJ>
 A:Note: sequence confirmed by synthesis
 C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry

Query Match 16.7%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
 ||||
 DB 1 PFP 3

RESULT 6

I51317
 bHLH transcription factor inhibitor - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: I51317
 R:Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G. Mech. Dev. 50, 119-130, 1995
 A:Title: Id gene activity during Xenopus embryogenesis.
 A:Reference number: I51316; MUID:95344988; PMID:7619724
 A:Accession: I51317

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
 A;Residues: 1-6 <ZHA>
 A;Cross-references: GB:S79038; NID:gl042006; PIDN:AAD14294.1; PID:g4261994
 C;Genetics:
 A;Gene: XID1b

Query Match 16.7%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
 ||||
 Db 4 EPF 6

RESULT 7

XEYDGD

galactose oxidase inhibitor - fungus (Cladobotryum dendroides)

C;Species: Cladobotryum dendroides
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
 C;Accession: A01341

R;Avigad, G.; Markus, Z.

Red. Proc. 31, 447, 1972

A;Reference number: A01341

A;Accession: A01341

A;Molecule type: protein

A;Residues: 1-7 <AVI>
 A;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, may inactivate the enzyme by binding to its prosthetic copper group.
 C;Superfamily: galactose oxidase inhibitor
 C;Keywords: copper

Query Match 16.7%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 5 TES 7

RESULT 8

S33244

neuromodulatory peptide Wamide-1 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S33244

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FBS Lett. 323, 104-108, 1993

A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of b
 A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33244

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

Query Match 16.7%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
 ||||
 Db 2 KEM 4

RESULT 9

A32523

peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)

N;Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I

C;Species: Bos primigenius taurus (cattle)

C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 11-May-2000

C;Accession: A32523

R;Harris, R.B.

Adv. Exp. Med. Biol. 198, 513-521, 1986

A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-conver
 A;Reference number: A32523; MUID:87123961; PMID:3028071

A;Accession: A32523

A;Molecule type: protein

A;Residues: 1-8 <HAR>

C;Superfamily: mammalian peptidyl-dipeptidase A

C;Keywords: alternative splicing; blood pressure control; peptidyl-dipeptide hydrolase

Query Match 16.7%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
 ||||
 Db 1 FTE 3

RESULT 10

S20162

leghemoglobin III - Sesbania rostrata (fragment)

C;Species: Sesbania rostrata

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 04-Mar-2000

C;Accession: S20162

R;Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.

Mol. Gen. Genet. 214, 181-191, 1988

A;Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-n
 A;Reference number: S08322; MUID:89181515; PMID:3237206

A;Accession: S20162

A;Molecule type: DNA

A;Residues: 1-8 <MET>

A;Cross-references: EMBL:X13504; NID:g21383; PIDN:CAA31858.1; PID:g579482

C;Genetics:

A;Gene: glb3

C;Superfamily: globin; globin homology

C;Keywords: heme; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
 ||||
 Db 3 FTE 5

RESULT 11

PD0443

3-oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999

C;Accession: PD0443

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Contents: Striatum

A;Accession: PD0443

A;Molecule type: protein

A;Residues: 1-9 <KAW>

C;Keywords: CoA-transferase

Query Match 16.7%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
 ||||
 Db 7 PVE 9

RESULT 12

A60410
beta-neoendorphin / dynorphin precursor - guinea pig
N;Alternate names: alpha-neoendorphin; proenkephalin B precursor
C;Species: Cavia porcellus (guinea pig)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000
C;Accession: A60410
R;Murphy, R.; Turner, C.A.
Peptides 11, 65-68, 1990
A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.
A;Reference number: A60410; MUID:90259864; PMID:2342991
A;Accession: A60410
A;Molecule type: protein
A;Residues: 1-10 <MUR>
C;Superfamily: proenkephalin
C;Keywords: neuropeptide; opioid peptide

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
|||
DB 7 KYP 9

RESULT 13
S65728
hemoglobin, extracellular, chain d1 - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65728
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A;Reference number: S65721; MUID:96176855; PMID:8597573
A;Accession: S65728
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <FUS>

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
|||
DB 5 TES 7

RESULT 14
A37268
Ig heavy chain C region (129) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: A37268
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A37268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <RUF>

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
|||
DB 1 ESQ 3

RESULT 15
F58501
43.5K bile stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: F58501
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: F58501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BIN>
A;Experimental source: human bile with stones
A;Note: 6-Asn and 8-Ala were also found

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
|||
DB 9 PVE 11

RESULT 16
PA0028
protein QA300042 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0028
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimens
A;Reference number: PA0001
A;Accession: PA0028
A;Molecule type: protein
A;Residues: 1-11 <KAM>
A;Experimental source: seed
C;Keywords: seed

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
|||
DB 6 PFP 8

RESULT 17
PC4267
ribosomal protein L12.1 - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: PC4267
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIPID, April 1997
A;Reference number: PC4267
A;Accession: PC4267
A;Molecule type: protein
A;Residues: 1-11 <KAW>
A;Experimental source: strain Japonica Nihonbare

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
|||
DB 4 TES 6

```
RESULT 18
PQ0731
unidentified 5.7/35K protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0731
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: PQ0696
A:Accession: PQ0731
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <KOM>

Query Match      16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
   |||
Db 6 PKY 8

RESULT 19
I54193
Rhesus blood group CcBe protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I54193
R:Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.
Genomics 19, 68-74, 1994
A:Title: Organization of the gene (RHCE) encoding the human blood group RhCcBe antigens
A:Reference number: I54193; MUID:94245182; PMID:8188244
A:Accession: I54193
A:Status: preliminary; translated from GB/ENBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S70456; NID:G546795; PIDN:AAD14061.1; PID:94261761
C:Genetics:
A:Gene: GDB:RHCE
A:Cross-references: GDB:229957; OMIM:111700
A:Map position: lp36.2-lp34

Query Match      16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
   |||
Db 4 KYP 6

RESULT 20
A54348
N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C:Accession: A54348
R:Shillatiffard, A.; Cummings, R.D.
Biochemistry 33, 4273-4282, 1994
A:Title: Purification and characterization of N-acetylglucosamine-6-sulfate sulfatase fr
A:Reference number: A54348; MUID:94206936; PMID:8155645
A:Accession: A54348
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <SHI>
C:Keywords: sulfuric ester hydrolase

Query Match      16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 12 RPF 14
   |||
Db 2 RPF 4

RESULT 21
PQ0491
self-incompatibility locus glycoprotein delta - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Oct-1997
C:Accession: PQ0491
R:Gaude, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
Plant Cell 5, 75-86, 1993
A:Title: Expression of a self-incompatibility gene in a self-compatible line of Brass
A:Reference number: JQ1733; MUID:93177215; PMID:8439745
A:Accession: PQ0491
A:Molecule type: protein
A:Residues: 1-13 <GAU>
A:Experimental source: stigma, var. acephala p578i
C:Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot
C:Keywords: glycoprotein

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
   |||
Db 7 TES 9

RESULT 22
A44818
extracellular lipase - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C:Accession: A44818
R:Gilbert, E.J.; Cornish, A.; Jones, C.W.
J. Gen. Microbiol. 137, 2223-2229, 1991
A:Title: Purification and properties of extracellular lipase from Pseudomonas aerugin
A:Reference number: A44818; MUID:92085040; PMID:1748875
A:Accession: A44818
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-13 <GIL>
A:Experimental source: strain TB3285
A>Note: sequence extracted from NCBI backbone (NCBIP:70395)
C:Superfamily: Pseudomonas triacylglycerol lipase

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
   |||
Db 7 KYP 9

RESULT 23
A28953
alpha-conotoxin SI - cone shell (Conus striatus)
C:Species: Conus striatus (striated cone)
C>Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
C:Accession: A28953
R:Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.
Biochemistry 27, 7102-7105, 1988
A:Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.
A:Reference number: A28953; MUID:89062448; PMID:3196703
A:Accession: A28953
A:Molecule type: protein
A:Residues: 1-13 <ZAF>
A>Note: this sequence was confirmed by chemical synthesis
```


C;Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin
C;Superfamily: alpha-conotoxin
A;Title: Identification of DNA-binding proteins changed after induction of sporulation
F;2-7,3-13/Disulfide bonds: #status experimental
F;13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PKY 9
Db 9 PKY 11

RESULT 24

S21152
tryptophyllin-related peptide - two-colored leaf frog
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S21152

R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of the
A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21152
A;Molecule type: protein
A;Residues: 1-13 <MIG>
A;Experimental source: skin
C;Superfamily: unassigned animal peptides

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11
Db 11 YPV 13

RESULT 25

A60458
protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain GU2)
N;Alternate names: protocatechuate oxygenase
C;Species: Moraxella sp.
C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
C;Accession: A60458

R;Sterjades, R.; Pelmont, J.
Appl. Environ. Microbiol. 55, 340-347, 1989
A;Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Morax
A;Reference number: A60458; MUID:89245845; PMID:2541659
C;Accession: A60458

A;Molecule type: protein
A;Residues: 1-13 <STR>
A;Note: two forms P and G of the alpha subunit yielded identical amino terminal sequence
C;Keywords: iron; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11
Db 11 YPV 13

RESULT 26

PC2371
probable, endopeptidase Clp ATP-binding chain C [similarity] - Bacillus cereus (strain te
N;Contains: adenosinetriphosphatase (EC 3.6.1.3)

C;Species: bacillus cereus
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PC2371

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Saved, M.A.; Kajiwara, T.; Hatanoto, S.
Biochem. Biotechnol. Biochem. 59, 231-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of sporulation
A;Reference number: PC2369; MUID:95218265; PMID:7766022
C;Accession: PC2371

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <MAS>
C;Keywords: ATP; hydrolase; nucleotide binding

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16
Db 6 FTE 8

RESULT 27

D56661
S-locus specific glycoprotein (allele S3) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: D56661

R;Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal
A;Reference number: A56661; MUID:92090397; PMID:1752245

A;Accession: D56661
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <GAU>

A;Experimental source: stigma extracts, var. acephala
A;Note: sequence extracted from NCBI backbone (NCBIP:72300)
C;Comment: This glycoprotein, expressed only in stigmas, plays an important role in t
C;Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
Db 7 TES 9

RESULT 28

B61620
locustamyotropin IV - migratory locust

C;Species: Locusta migratoria (migratory locust)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C;Accession: B61620

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two
A;Reference number: A61620

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <SCH>
C;Keywords: amidated carboxyl end; neuropeptide
F;13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPF 6
Db 7 MPF 9

RESULT 29

D61458
 IG kappa chain V-IV region (FUE) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
 C:Accession: D61458; PI0158
 R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A>Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-associated glycoprotein
 A:Reference number: A61458; MUID:90039128; PMID:2478651
 A:Accession: D61458
 A:Molecule type: protein
 A:Residues: 1-13 <BRO>
 C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycoprotein
 C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17

Db 5 TES 7
 |||

RESULT 30

E61458
 IG kappa chain V-IV region (FUE) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
 C:Accession: E61458
 R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A>Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-associated glycoprotein
 A:Reference number: A61458; MUID:90039128; PMID:2478651
 A:Accession: E61458
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <BRO>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17

Db 5 TES 7
 |||

RESULT 31

PH1772
 T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: PH1772
 R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
 J. Exp. Med. 178, 1-16, 1993
 A>Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057
 A:Accession: PH1772
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <POR>

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

Db 4 VEP 6
 |||

RESULT 32

PT0026
 calotropin DI - mudar (fragment)
 C:Species: Calotropis gigantea (mudar, madar)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
 C:Accession: PT0026
 R:Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
 Phytochemistry 26, 633-636, 1987
 A>Title: Chemical modification and amino terminal sequence of calotropin DI from Calo
 A:Reference number: PT0026
 A:Accession: PT0026
 A:Molecule type: protein
 A:Residues: 1-14 <SHA>
 C:Comment: This enzyme is classified as a plant cysteine protease.
 C:Keywords: pyrrolidone carboxylic acid (Gln) #status experimental
 F:1/Modified site: pyrrolidone carboxylic acid (Gln)

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11

Db 5 YPV 7
 |||

RESULT 33

E33098
 214K exoantigen (version 2) - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: E33098
 R:Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: E33098
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11

Db 12 YPV 14
 |||

RESULT 34

PA0024
 protein QA300050 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0024
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
 A:Reference number: PA0001
 A:Accession: PA0024
 A:Molecule type: protein
 A:Residues: 1-15 <XAM>
 A:Experimental source: seed

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7

Db 6 PFP 8
 |||

Db 4 PFT 6

RESULT 35

PS0452 32K protein 3306 - rice (strain Nihonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C;Accession: PS0452

R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A;Reference number: PS0208

A;Accession: PS0452

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: bran, strain Nihonbare

C;Comment: molecular weight 32K, pI 5.3.

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFT 7

Db 6 PFT 8

RESULT 36

PA0062

fumarate hydratase (EC 4.2.1.2) - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0062

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PA0051

A;Accession: PA0062

A;Molecule type: protein

A;Residues: 1-15 <CHO>

C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17

Db 5 TES 7

RESULT 37

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999

C;Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification

A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457

A;Molecule type: protein

A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SGC5

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monomer

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFT 15

Db 11 PFT 13

Db

RESULT 38

A36527

juvenile-hormone esterase (EC 3.1.1.59) - tobacco hornworm (fragment)

C;Species: Manduca sexta (tobacco hornworm)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 03-Feb-1994

C;Accession: A36527

R;Venkatesh, K.; Abdel-Aal, Y.A.I.; Armstrong, F.B.; Roe, R.M.

J. Biol. Chem. 265, 21727-21732, 1990

A;Title: Characterization of affinity-purified juvenile hormone esterase from the ple

A;Reference number: A36527; MUID:91072375; PMID:2254326

A;Accession: A36527

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <VEN>

C;Keywords: carboxylic ester hydrolase

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17

Db 12 TES 14

RESULT 39

A49480

major immunophilin hsp56 - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995

C;Accession: A49480

R;Yen, A.W.; Reardon, I.M.; Leone, J.W.; Heinrichson, R.L.; Deibel Jr., M.R.

Biochemistry 32, 12571-12576, 1993

A;Title: An active FK506-binding domain of 17,000 daltons is isolated following limit

A;Reference number: A49480; MUID:94072550; PMID:7504525

A;Accession: A49480

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <YEM>

A;Experimental source: thymus

A;Note: sequence extracted from NCBI backbone (NCBIP:142438)

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17

Db 7 TES 9

RESULT 40

PT0205

insulin-like growth factor-binding protein, bone - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 08-Dec-1994

C;Accession: PT0205; A33175

R;Bautista, C.M.; Baylink, D.J.; Mohan, S.

Biochem. Biophys. Res. Commun. 176, 756-763, 1991

A;Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from l

A;Reference number: PT0205; MUID:91222244; PMID:11709017

A;Accession: PT0205

A;Molecule type: protein

A;Residues: 1-15 <BAU>

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

Db 7 VEP 9

RESULT 41

B45115

peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)

N:Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP51

C:Species: Homo sapiens (man)

C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997

C:Accession: B45115

R:Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton, D.

J. Biol. Chem. 267, 21753-21760, 1992

A:Title: Characterization of high molecular weight FK-506 binding activities reveals a new protein

A:Reference number: A45115; MUID:93016131; PMID:13833226

A:Accession: B45115

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <WIE>

A:Experimental source: JURKAT cells

A>Note: sequence extracted from NCBI backbone (NCBIP:116748)

C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
|||

Db 2 TES 4

RESULT 42

B42324

cytochrome P450c27/25 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Mar-1999

C:Accession: B42324

R:Shayiq, R.M.; Avadhani, N.G.

J. Biol. Chem. 267, 2421-2428, 1992

A:Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mitochondrial cytochrome P450c27/25 and P450c27/25

A:Reference number: A42324; MUID:92129322; PMID:1733943

A:Accession: B42324

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-16 <SHA>

A>Note: sequence extracted from NCBI backbone (NCBIN:78408, NCBIP:88990)

C:Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology

C:Keywords: heme; transmembrane protein

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
|||

Db 10 KYP 12

RESULT 43

C45133

casein kinase II (EC 2.7.1.-) alpha chain - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 03-Jun-1996

C:Accession: C45133

R:Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.

J. Biol. Chem. 267, 23789-23796, 1992

A:Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the associated protein

A:Reference number: A45133; MUID:93054738; PMID:1331100

A:Accession: C45133

A>Status: preliminary

A:Molecule type: protein

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
|||

Db 3 FTE 5

RESULT 46

S05671

hirudin Ia - medicinal leech (fragment)

A:Residues: 1-16 <OU1>

A:Experimental source: endoplasmic reticulum, pancreas

A>Note: sequence extracted from NCBI backbone (NCBIP:118799)

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protein

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
|||

Db 6 EPF 8

RESULT 44

I40065

shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)

C:Species: Buchnera aphidicola

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999

C:Accession: I40065

R:Roubbakhsh, D.; Baumann, P.

Gene 155, 107-112, 1995

A:Title: Characterization of a putative 23S-SS rRNA operon of Buchnera aphidicola (em)

A:Reference number: I40061; MUID:95212914; PMID:7535281

A:Accession: I40065

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <RES>

A:Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718

C:Genetics:

A:Gene: aroE

C:Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPK 8
|||

Db 9 FPK 11

RESULT 45

C53113

Lys-gingipain form 2, 17K - Porphyromonas gingivalis (fragment)

N:Alternate names: lysine-specific cysteine proteinase 2, 17K

C:Species: Porphyromonas gingivalis

C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995

C:Accession: C53113

R:Pike, R.; McGraw, W.; Potempa, J.; Travis, J.

J. Biol. Chem. 269, 406-411, 1994

A:Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis

A:Reference number: A53113; MUID:94103245; PMID:8276827

A:Accession: C53113

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <PIK>

A:Experimental source: H66

A>Note: sequence extracted from NCBI backbone (NCBIP:141693)

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
|||

Db 3 FTE 5

RESULT 46

S05671

hirudin Ia - medicinal leech (fragment)

N;Alternate names: thrombin inhibitor
 C;Species: Hirudo medicinalis (medicinal leech)
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Jul-1998
 C;Accession: S05671
 R;Scharf, M.; Engels, J.; Tripiet, D.
 FEBS Lett. 255, 105-110, 1989
 A;Title: Primary structures of new 'iso-birudins'.
 A;Reference number: S05671; MUID:80005945; PMID:2792365
 A;Accession: S05671
 A;Molecule type: protein
 A;Residues: 1-17 <SCH>
 C;Superfamily: thrombin inhibitor
 C;Keywords: anticoagulant; serine proteinase inhibitor; sulfoxoprotein
 F;6-14/Disulfide bonds: #status predicted

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
 ||||
 Db 7 TES 9

RESULT 47

S05033
 Photosystem II protein psbL - Synechococcus sp. (strain Copeland) (fragment)
 N;Alternate names: photosystem II 5K protein
 C;Species: Synechococcus sp.
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C;Accession: S05033
 R;Ikemuchi, M.; Koike, H.; Inoue, Y.
 FEBS Lett. 251, 155-160, 1989
 A;Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II
 A;Reference number: S05030
 A;Accession: S05033
 A;Molecule type: protein
 A;Residues: 1-17 <IKE>
 A;Note: the source is designated as Synechococcus vulcanus
 C;Genetics:
 A;Gene: psbL
 C;Keywords: photosynthesis; photosystem II; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
 ||||
 Db 9 PVE 11

RESULT 48

B31769
 T-cell receptor delta-2 chain J region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Nov-1999
 C;Accession: B31769
 R;Loh, E.Y.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988
 A;Title: Human T-cell receptor delta chain: genomic organization, diversity, and expression
 A;Reference number: A94221; MUID:89071766; PMID:2974163
 A;Accession: B31769
 A;Molecule type: DNA
 A;Residues: 1-17 <LOH>
 A;Cross-references: GB:L36386; NID:9540455; PIDN:AAA61108.1; PID:g540456
 C;Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

Db ||||
 15 VEP 17

RESULT 49

G85956
 hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain E)
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: G85956
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: G85956
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-17 <STO>
 A;Cross-references: GB:AE005174; NID:g12517539; PIDN:AAG58115.1; GSPDB:GN00145; UMG:
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z4331

Query Match 16.7%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
 ||||
 Db 6 PFP 8

RESULT 50

S29264
 ovohemerythrin - duck leech (fragment)
 N;Alternate names: 14K yolk protein
 C;Species: Theromyzon tessulatam (duck leech)
 C;Date: 19-Mar-1997 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: S29264
 R;Baert, J.L.; Britel, M.; Sautiere, P.; Malecha, J.
 Eur. J. Biochem. 209, 563-569, 1992
 A;Title: Ovohemerythrin, a major 14-kDa yolk protein distinct from vitellogenin in le
 A;Reference number: S29264; MUID:93049299; PMID:1425663
 A;Accession: S29264
 A;Molecule type: protein
 A;Residues: 1-18 <BAE>
 A;Cross-references: PIDN:AA23969.1; PID:g258980
 C;Superfamily: hemerythrin
 C;Keywords: egg yolk; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EFP 14
 ||||
 Db 5 EFP 7

RESULT 51

H64711
 hypothetical protein HP1536 - Helicobacter pylori (strain 26695)
 C;Species: Helicobacter pylori
 C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C;Accession: H64711
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, F
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glöck, A.; McK
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
 Nature 388, 539-547, 1997
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
 A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: H64711
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-18 <TOM>
A;Cross-references: GB:AE000651; GB:AE000511; NID:g2314708; PIDN:AA08578.1; PID:g231471

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
|||
Db 15 PKY 17

RESULT 52
S58277
insulin-like growth factor receptor type II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S58277
R;Smrzka, O.W.; Stoger, R.; Kurzbaue, R.; Pae, I.; Fischer, G.F.; Barlow, D.P.
submitted to the EMBL Data Library, January 1995
A;Description: Conservation of a methylation imprint and a putative imprinting box at th
A;Reference number: S58277
A;Accession: S58277
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <SMR>
A;Cross-references: EMBL:X83702; NID:g929644; PIDN:CAA58675.1; PID:g929645
C;Keywords: growth factor receptor

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
|||
Db 5 TES 7

RESULT 53
S71592
serine proteinase inhibitor, 31K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
C;Accession: S71592
R;Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.
Arch. Biochem. Biophys. 317, 311-314, 1995
A;Title: Novel extracellular matrix-associated serine proteinase inhibitors from human s
A;Reference number: S71592; MUID:95177688; PMID:7872799
A;Accession: S71592
A;Molecule type: protein
A;Residues: 1-18 <RAO>
C;Function:
A;Description: involved in turnover of connective tissues
C;Keywords: serine proteinase inhibitor

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
|||
Db 5 EPF 7

RESULT 54
I46653
T-cell receptor delta-chain J-delta-2 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 30-May-1997
C;Accession: I46653

R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-o
A;Reference number: I46623; MUID:95363165; PMID:7636249
A;Accession: I46653
A;Status: preliminary; translated from GB/EMBL/DBSJ
A;Molecule type: mRNA
A;Residues: 1-18 <YAN>
A;Cross-references: GB:D49561; NID:g1041174; PID:g1041175
C;Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
|||
Db 16 VEP 18

RESULT 55
A59137
protein P11 - golden needle mushroom (fragment)
C;Species: Flammulina velutipes (golden needle mushroom)
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: A59137
R;Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A;Description: Differences of proteins expressed in the fruiting dikaryon and the non
A;Reference number: A59137
A;Accession: A59137
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <SAK>

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
|||
Db 15 PFT 17

RESULT 56
EW5MCM
cinnamycin - Streptovorticillium cinnamoneum
N;Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C;Species: Streptovorticillium cinnamoneum
C;Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 07-May-1999
C;Accession: A45767
R;Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase,
J. Antibiot. 42, 837-845, 1989
A;Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and properie
A;Reference number: A45767; MUID:89291558; PMID:2544544
A;Accession: A45767
A;Molecule type: protein
A;Residues: 1-19 <NAR>
R;Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A;Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structu
A;Reference number: A53359
A;Contents: annotation; strain L337-2
C;Superfamily: cinnamycin precursor
C;Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F;1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F;4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F;5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F;6-19/Cross-link: (2Xi,9S)-lysinoalanine (Ser-Lys) #status experimental
F;15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
|||
Db 9 PFT 11

RESULT 57

S59485
hyoxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 05-Dec-1998
C:Accession: S59485; S59484; S59483
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A:Title: Specificity in the immobilisation of cell wall proteins in response to different
A:Reference number: S59481; MUID:96011753; PMID:7548825
A:Accession: S59485
A:Molecule type: protein
A:Residues: 1-19 <WOJ>
A:Note: hyoxyproline-rich cell wall glycoprotein, 42K
A:Accession: S59484
A:Molecule type: protein
A:Residues: 1-15 <WOW>
A:Note: hyoxyproline-rich cell wall glycoprotein, 84K
A:Accession: S59483
A:Molecule type: protein
A:Residues: 1-14 <WOP>
A:Note: hyoxyproline-rich cell wall glycoprotein, 136K, minor component
C:Superfamily: proline-rich protein 3
C:Keywords: Glycoprotein; hydroxyproline
P;6,11,16/Modified site: hydroxyproline (pro) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
|||
Db 6 PVE 8

RESULT 58

S43641
carboxylesterase (EC 3.1.1.1), thermostable - Alicyclobacillus acidocaldarius (fragment)
C:Species: Alicyclobacillus acidocaldarius
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C:Accession: S43641
R:Manco, G.; di Gennaro, S.; de Rosa, M.; Rossi, M.
Eur. J. Biochem. 221, 965-972, 1994
A:Title: Purification and characterization of a thermostable carboxylesterase from the
A:Reference number: S43641; MUID:94237161; PMID:8181479
A:Accession: S43641
A:Molecule type: protein
A:Residues: 1-19 <MAN>
A:Experimental source: strain MT3
A:Note: the source is designated as Bacillus acidocaldarius
C:Keywords: carboxylic ester hydrolase; monomer

Query Match 16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
|||
Db 4 PVE 6

RESULT 59

C56661
S-locus specific glycoprotein (allele S9) - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C:Accession: C56661
R:Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal
A:Reference number: A56661; MUID:92090397; PMID:1752245
A:Accession: C56661
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <GAU>
A:Experimental source: stigma extracts, var. acephala
A:Note: sequence extracted from NCBI backbone (NCBIP:72301)
C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in t
C:Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
|||
Db 7 TES 9

RESULT 60

PQ0492
self-incompatibility locus glycoprotein epsilon - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-1995
C:Accession: PQ0492
R:Gaude, T.; Frity, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
Plant Cell 5, 75-86, 1993
A:Title: Expression of a self-incompatibility gene in a self-compatible line of Brass
A:Reference number: JQ1733; MUID:93177215; PMID:8439745
A:Accession: PQ0492
A:Molecule type: protein
A:Residues: 1-19 <GAU>
A:Experimental source: stigma, var. acephala P57S1
C:Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
|||
Db 7 TES 9

RESULT 61

A61144
probable flagellar protein (clone FCH-F8-4) - Trypanosoma cruzi (fragment)
C:Species: Trypanosoma cruzi
C:Date: 10-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 24-Feb-1995
C:Accession: A61144
R:Bua, J.; Bontempi, E.J.; Levin, M.; Orn, A.; Velasco, D.; Moreno, M.; Levi-Yeyati,
Exp. Parasitol. 72, 54-62, 1991
A:Title: Trypanosoma cruzi: cellular and antibody response against the parasite in m
A:Reference number: A61144; MUID:91130571; PMID:1993465
A:Accession: A61144
A:Molecule type: mRNA
A:Residues: 1-19 <BUA>

Query Match 16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
|||
Db 17 VEP 19

RESULT 62

C39305

neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)
 C:Species: Phoneutria nigriventer
 C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-Feb-1997
 C:Accession: C39305
 R:Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
 Toxicol 29, 1225-1233, 1991
 A:Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria nigriventer
 A:Reference number: A39305; PMID:92196803; PMID:1801316
 A:Accession: C39305
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <REZ>
 C:Keywords: neurotoxin

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
 ||||
 Db 7 ESQ 9

RESULT 63
 I46654
 T-cell receptor delta-chain J-delta-3 - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
 C:Accession: I46654
 R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
 J. Immunol. 155, 1981-1993, 1995
 A:Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old pig
 A:Reference number: I46623; PMID:95363165; PMID:7636249
 A:Accession: I46654
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-19 <YAN>
 A:Cross-references: GB:D49562; NID:G1041176; PIDN:BA08506.1; PID:G1041177
 C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
 ||||
 Db 17 VEP 19

RESULT 64
 S69166
 ferredoxin b - Japanese radish (fragments)
 C:Species: Kaiware daikon (Japanese radish)
 C:Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
 C:Accession: S69166
 R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
 Arch. Biochem. Biophys. 316, 797-802, 1995
 A:Title: Four ferredoxins from Japanese radish leaves.
 A:Reference number: S69164; PMID:95168867; PMID:7864635
 A:Accession: S69166
 A:Molecule type: protein
 A:Residues: 1-19 <OBA>
 C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
 ||||
 Db 13 HKE 15

neurotoxin protein S2 [validated] - Halobacterium salinarum (fragment)
 N:Alternate names: ribosomal protein HS5A
 C:Species: Halobacterium salinarum
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
 C:Accession: S11611
 R:Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
 Zbl. Bakt. Hyg. 1. Abt. Orig. C 3, 200-208, 1982
 A:Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archa
 A:Reference number: S11609
 A:Accession: S11611
 A:Molecule type: protein
 A:Residues: 1-19 <YAG>
 A>Note: The protein is designated as ribosomal protein HS5A
 C:Keywords: protein biosynthesis; ribosome

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TBS 17
 ||||
 Db 7 TBS 9

RESULT 66
 S06466
 T-cell receptor alpha chain J segment (DO) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 06-Jun-1997
 C:Accession: S06466
 R:Yague, J.; Blackman, M.; Born, W.; Marrack, P.; Kappler, J.; Palmer, E.
 Nucleic Acids Res. 16, 11355-11364, 1988
 A:Title: The structure of V-alpha and J-alpha segments in the mouse.
 A:Reference number: S06466; PMID:89083566; PMID:2849763
 A:Accession: S06466
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-20 <YAG>
 A:Experimental source: strain Balb/c
 C:Genetics:
 A:Map position: 14
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein; heterodimer; T-cell receptor
 F:1-18/Domain: J segment <JSE>
 F:19-20/Domain: C region (fragment) <CRE>

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
 ||||
 Db 16 VEP 18

RESULT 67
 JP0059
 ribosomal protein L30 - Thermoactinomyces intermedius (fragment)
 C:Species: Thermoactinomyces intermedius
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03-May-1996
 C:Accession: JP0059
 R:Ochi, K.
 submitted to JIPID, February 1994
 A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
 A:Reference number: JP0042
 A:Accession: JP0059
 A:Molecule type: protein
 A:Residues: 1-20 <OCH>
 C:Superfamily: Escherichia coli ribosomal protein L30
 C:Keywords: protein biosynthesis; ribosome

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 ESQ 18
Db 17 ESQ 19

RESULT 68
PL0145
carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydoflava (fr
C:Species: Pseudomonas carboxydoflava
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: PL0145
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop
A:Reference number: PL0138; MUID:90055678; PMID:2818128
A:Accession: PL0145
A:Molecule type: protein
A:Residues: 1-20 <KRA>
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C:Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 VEP 13
Db 18 VEP 20

RESULT 69
PQ0046
citrate (si)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)
A:Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme; oxaloaceta
C:Species: Streptomyces hygroscopicus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-May-2000
C:Accession: PQ0046
R:Shimotobno, K.W.; Imai, S.; Murakami, T.; Seto, H.
Agric. Biol. Chem. 54, 463-470, 1990
A:Title: Purification and characterization of citrate synthase from Streptomyces hygrosc
A:Reference number: PQ0106; MUID:90334852; PMID:1368511
A:Accession: PQ0046
A:Molecule type: protein
A:Residues: 1-20 <SHI>
A:Experimental source: strain SF-1293
C:Comment: This enzyme catalyzes the synthesis of citric acid.
C:Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid cycle

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 YPV 11
Db 16 YPV 18

RESULT 70
S29635
jacalin beta chain - Artocarpus tonkinensis
C:Species: Artocarpus tonkinensis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S29635
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
A:Reference number: S29635; MUID:93152601; PMID:8427879
A:Accession: S29635
A:Status: preliminary

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 YPV 11
Db 16 YPV 18

RESULT 71
B30208
Hypothetical protein 1 (cpc-1.5' region) - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C:Accession: B30208
R:Paluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988
A:Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protei
A:Reference number: A30208; MUID:88234499; PMID:2967496
A:Accession: B30208
A:Molecule type: DNA
A:Residues: 1-20 <PAL>
A:Cross-references: GB:J03262

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PPP 7
Db 6 PFP 8

RESULT 72
S58382
Hypothetical protein 1 - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C:Accession: S58382
R:Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Res. 23, 2815-2822, 1995
A:Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis in
A:Reference number: S58382; MUID:95388493; PMID:7659502
A:Accession: S58382
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-20 <DIR>
A:Cross-references: EMBL:X83705; NID:g951023; PIDN:CAAS8678.1; PID:g951024

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PPP 7
Db 12 PFP 14

RESULT 73
I46652
T-cell receptor delta-chain J-delta-1 segment - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46652
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A:Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-ol
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46652
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-20 <YAN>
A:Cross-references: GB:D49560; NID:g1041172; PIDN:BAA08504.1; PID:g1041173
C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
|||
Db 18 VEP 20

RESULT 74
A41439
acid ribonuclease [EC 3.1.1.-] - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
C:Accession: A41439
R:Ohgi, K.; Sanda, A.; Takizawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A:Title: Purification of acid ribonucleases from bovine spleen.
A:Reference number: A41439; MUID:88227899; PMID:3131316
A:Accession: A41439
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <OHG>
C:Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPK 8
|||
Db 12 FPK 14

RESULT 75
GRHU
growth-modulating peptide - human
C:Species: Homo sapiens (man)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A01421
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A:Reference number: A01421; MUID:77162369; PMID:858356
A:Accession: A01421
A:Molecule type: protein
A:Residues: 1-3 <SCH>
A>Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit
C:Superfamily: unassigned animal peptides

Query Match 11.1%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HK 2
|||
Db 2 HK 3

Search completed: November 25, 2003, 19:36:08
Job time : 12.3488 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMFPKYPVEPFRESQ 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	16.7	7	1	IGAO DACDE
2	3	16.7	7	1	WVA3 ACHFU
3	3	16.7	10	1	UHA3_HUMAN
4	3	16.7	11	1	EFQ_CLOPA
5	3	16.7	13	1	LMT4 LOCOMI
6	3	16.7	13	1	UHA3 CANFA
7	3	16.7	13	1	YPE2 LACLC
8	3	16.7	14	1	CALI_CALGI
9	3	16.7	15	1	ESTJ_MANSE
10	3	16.7	15	1	UC08_MAIZE
11	3	16.7	15	1	UC16_MAIZE
12	3	16.7	15	1	UC25_MAIZE
13	3	16.7	16	1	H5_COTJA
14	3	16.7	16	1	ODEB_SOLTU
15	3	16.7	17	1	ITHE_HIRME
16	3	16.7	17	1	PSBL_SYNVO
17	3	16.7	18	1	D7A1 ACASC
18	3	16.7	18	1	HEMH_THETS
19	3	16.7	18	1	LCTN_LANGL
20	3	16.7	19	1	DURA_STRGV
21	3	16.7	19	1	TX3_PHONI
22	3	16.7	20	1	CISY_STRHY
23	3	16.7	20	1	SB60_MAIZE
24	3	16.7	20	1	GRWM_HUMAN
25	2	11.1	5	1	PAP2_PARMA
26	2	11.1	5	1	RE31_LITRU
27	2	11.1	5	1	RE32_LITRU
28	2	11.1	5	1	SUGA_ACHDO
29	2	11.1	6	1	ASP2_LACSN
30	2	11.1	7	1	ALL3_CARMA
31	2	11.1	7	1	CARP_MYTED
32	2	11.1	7	1	EIO5_LITRU
33	2	11.1	7	1	FARI_HELTI

34	2	11.1	7	1	FAR5_HIRME
35	2	11.1	7	1	UF04_MOUSE
36	2	11.1	7	1	UN06_PINPS
37	2	11.1	7	1	WVA1_ACHFU
38	2	11.1	8	1	AKH_LITAU
39	2	11.1	8	1	AKH_TABAT
40	2	11.1	8	1	ANG2_BOTJA
41	2	11.1	8	1	CLP_THICU
42	2	11.1	8	1	HTF2_PERAM
43	2	11.1	8	1	LMT2_LOCOMI
44	2	11.1	8	1	LPK_LEUMA
45	2	11.1	8	1	ORNY_ORCLI
46	2	11.1	8	1	PPK2_PERAM
47	2	11.1	8	1	PPK3_PERAM
48	2	11.1	8	1	RS7_MYCIT
49	2	11.1	8	1	UC26_MAIZE
50	2	11.1	8	1	UF06_MOUSE
51	2	11.1	8	1	UPA1_HUMAN
52	2	11.1	8	1	UPAA_HUMAN
53	2	11.1	8	1	CCAP_CARMA
54	2	11.1	9	1	CONO_CONGE
55	2	11.1	9	1	COXE_THUOB
56	2	11.1	9	1	FAR2_CALVO
57	2	11.1	9	1	FAR3_CALVO
58	2	11.1	9	1	FAR4_PENMO
59	2	11.1	9	1	FAR5_PENMO
60	2	11.1	9	1	FIBB_MACFU
61	2	11.1	9	1	FRF1_SARBU
62	2	11.1	9	1	HUTU_KLEAE
63	2	11.1	9	1	KNL3_BOMVA
64	2	11.1	9	1	LMT3_LOCOMI
65	2	11.1	9	1	OXYA_SCYCA
66	2	11.1	9	1	OXYF_SCYCA
67	2	11.1	9	1	OXYV_SQUAC
68	2	11.1	9	1	SAMP_MUSCA
69	2	11.1	9	1	THYF_PIG
70	2	11.1	9	1	UHA2_HUMAN
71	2	11.1	9	1	UN19_CLOPA
72	2	11.1	9	1	UPA3_HUMAN
73	2	11.1	10	1	ANG1_BOTJA
74	2	11.1	10	1	ANGT_BOVIN
75	2	11.1	10	1	ANGT_CHICK
76	2	11.1	10	1	BPF_VIPAS
77	2	11.1	10	1	COXA_ONCMY
78	2	11.1	10	1	FAR6_PANRE
79	2	11.1	10	1	GATJ_HUMAN
80	2	11.1	10	1	GON2_CHICK
81	2	11.1	10	1	HTR1_ROMMI
82	2	11.1	10	1	HTF2_CARMO
83	2	11.1	10	1	HTF_TABAT
84	2	11.1	10	1	LPK2_LOCOMI
85	2	11.1	10	1	ODP2_BOVIN
86	2	11.1	10	1	PNEU_HUMAN
87	2	11.1	10	1	PSNU_RAT
88	2	11.1	10	1	PPCK_FASHE
89	2	11.1	10	1	PKV_LOCOMI
90	2	11.1	10	1	Q2OB_COMTE
91	2	11.1	10	1	RL16_ACHLA
92	2	11.1	10	1	RT02_BOVIN
93	2	11.1	10	1	SLAP_BACTG
94	2	11.1	10	1	SYK_CAMUP
95	2	11.1	10	1	TKNB_CHICK
96	2	11.1	10	1	TKNB_ONCMY
97	2	11.1	10	1	TKNB_RANRI
98	2	11.1	10	1	TKU1_UREUN
99	2	11.1	10	1	UH05_RAT
100	2	11.1	10	1	UPA5_HUMAN

ALIGNMENTS

RESULT 1

```

IGAO_DACDE
ID _IGAO_DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides."
RL Fed. Proc. 31:447-447(1972).
CC -1- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
CC BINDING TO ITS PROSTHETIC COPPER GROUP.
DR PIR; A01341; KEYDGD.
KW Copper; Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17
Db 5 TES 7

RESULT 2
ID _WMA3_ACHFV STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wwamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica."
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AMIDATION.
SQ SEQUENCE 7 AA; 965 MW; 7362D5B698132310 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEM 4
Db 2 KEM 4

RESULT 3
ID _UHA3_HUMAN STANDARD; PRT; 10 AA.
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994."
RL Electrophoresis 15:1459-1465(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.
FT NON TER 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEP 13
Db 2 VEP 4

RESULT 4
ID _EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum WS."
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYP 10
Db 1 KYP 3

RESULT 5
ID _LMT4_LOCMI STANDARD; PRT; 13 AA.

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AC P41490;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 4 (LOM-MT-4).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE
CC STIMULATOR THAN LOM-MT I, II AND III.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; B61620;
DR InterPro; PS001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6
Db 7 MPF 9

RESULT 6
UHA3 CANFA
ID UHA3 CANFA STANDARD; PRT; 13 AA.
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE-98163340; PubMed-9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.9, ITS MW IS: 55.4 KDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
Db 7 PVE 9

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RESULT 7
YPE2_LACLC
ID YPE2_LACLC STANDARD; PRT; 13 AA.
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PEPT 5' region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94245610; PubMed-8188586;
RA Mierau I., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pept) of Lactococcus lactis: molecular cloning
RT and nucleotide sequencing of pept and construction of a chromosomal
RT deletion mutant.";
RL J. Bacteriol. 176:2854-2861(1994).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; L27596; AAA20625.1; --
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
Db 5 EPF 7

RESULT 8
CAL1 CALGI
ID CAL1 CALGI STANDARD; PRT; 14 AA.
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calotropin DI (EC 3.4.22.-) (Fragment).
OS Calotropis gigantea (Madar) (Bowstring hemp).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Gentianales; Apocynaceae; Asclepiadoideae;
OC Asclepiadeae; Calotropis.
OX NCBI_TaxID=4066;
RN [1]
RP SEQUENCE.
RA Bhattacharya D., Sengupta A., Sinha N.K.;
RT "Chemical modification and amino terminal sequence of calotropin DI
RT from Calotropis gigantea.";
RL Phytochemistry 26:633-636(1987).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR PIR; PT0026; PT0026.
DR MEROPS; C01.011; --
DR InterPro; IPR000169; SHprot.acsite.
DR PROSITE; PS00139; THIOLESTERASE CYS; PARTIAL.
DR PROSITE; PS00639; THIOLESTERASE HIS; PARTIAL.
DR PROSITE; PS00640; THIOLESTERASE ASN; PARTIAL.
KW Hydrolase; Thiol protease; Pyroliidone carboxylic acid.
FT MOD_RES 1 1

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FT NON TER 14 14
SQ SEQUENCE 14 AA; 1715 MW; D993F0276CDA4662 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
DB 5 YPV 7

RESULT 9
ESTJ_MANSE STANDARD; PRT; 15 AA.
ID ESTJ_MANSE STANDARD; PRT; 15 AA.
AC P19985;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Juvenile hormone esterase (EC 3.1.1.59) (JH esterase) (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.

TISSUE=Larval plasma;
RX MEDLINE=91072375; PubMed=2254326;
RC Venkatesh K., Abdel-Aal Y.A.I., Armstrong F.B., Roe R.M.;
RT "Characterization of affinity-purified juvenile hormone esterase from
the plasma of the tobacco hornworm, Manduca sexta.";
RL J. Biol. Chem. 285:21727-21732(1990).
CC -!- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF
JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
CC -!- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-
epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR PIR; A36527; A36527.
DR InterPro; IP002018; Carboxylesterase.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW Hydrolase; Serine esterase.
FT NON TER 15
SQ SEQUENCE 15 AA; 1659 MW; D321BA432E58B848 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
DB 12 TES 14

RESULT 10
UC08_MAIZE STANDARD; PRT; 15 AA.
ID UC08_MAIZE STANDARD; PRT; 15 AA.
AC P80614;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC PACCAD clade; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.

TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family.
CC Maize-2DPAGE; P80614; COLEOPTILE.
DR MaizedB; 123934; -.
FT NON TER 15
SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
DB 8 YPV 10

RESULT 11
UC16_MAIZE STANDARD; PRT; 15 AA.
ID UC16_MAIZE STANDARD; PRT; 15 AA.
AC P80622;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 308)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC PACCAD clade; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.

TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.9, ITS MW IS: 18.6 kDa.
CC Maize-2DPAGE; P80622; COLEOPTILE.
DR MaizedB; 123948; -.
FT NON TER 15
SQ SEQUENCE 15 AA; 1796 MW; D331A518F7440BE7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
DB 12 VEP 14

RESULT 12
UC25_MAIZE STANDARD; PRT; 15 AA.
ID UC25_MAIZE STANDARD; PRT; 15 AA.
AC P80631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE (Fragment).
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OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Toullet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Fernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:957-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC Maize-2DPAGE; P80631; COLEOPTILE.
 DR MaizeDB; 123957; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PVE 12
 DB 10 PVE 12
 RESULT 13
 H5_CONJA
 ID H5_CONJA STANDARD; PRT; 16 AA.
 AC P18638;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Histone H5 (Fragment).
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277939; PubMed=962913;
 RA Seligy V., Roy C., Dove M., Yaguchi M.;
 RT "Species variability of N-terminal sequence of avian erythrocyte-
 RT specific histone H5.";
 RL Biochem. Biophys. Res. Commun. 71:196-202(1976).
 CC -!- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING
 CC NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER
 CC ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: ERYTHROID CELLS.
 CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
 KW Chromosomal protein; Nuclear protein; DNA-binding; DNA condensation.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1665 MW; DB528219B3074D3C CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TES 17
 DB 1 TES 3
 RESULT 14
 ODPE_SOLTU
 ID ODPE_SOLTU STANDARD; PRT; 16 AA.
 AC P81419;

DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
 DE (EC 1.2.4.1) (PDHE1-B) (Fragment).
 OX Solanum tuberosum (Potato).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
 OC Asteridae; Lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Romano; TISSUE=Tuber;
 RX MEDLINE=98399821; PubMed=9729464;
 RA Millar A.H., Knorpp C., Leaver C.J., Hill S.A.;
 RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and
 RT identification of catalytic components in potato.";
 RL Biochem. J. 334:571-576(1998).
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
 CC multiple copies of three enzymatic components: pyruvate
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
 CC lipoamide dehydrogenase (E3).
 CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
 CC acetyldihydrolipoamide + CO(2).
 CC -!- COFACTOR: THIAMINE PYROPHOSPHATE.
 CC -!- SUBUNIT: Tetramer of two alpha and two beta subunits (by
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
 KW Phosphorylation; Mitochondrion.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1705 MW; FF6ED808C804F797 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEM 4
 DB 5 KEM 7
 RESULT 15
 ITHB_HIRME
 ID ITHB_HIRME STANDARD; PRT; 17 AA.
 AC P28502;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hirudin IA (Fragment).
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'.";
 RL FEBS Lett. 255:105-110(1989).
 CC -!- FUNCTION: Hirudin is a potent thrombin-specific protease
 CC inhibitor. It forms a stable non-covalent complex with alpha-
 CC thrombin, thereby abolishing its ability to cleave fibrinogen.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR PIR; S05671; S05671.
 DR HSP; P01050; IHIC.
 DR InterPro; IPR000429; Hirudin.
 DR Pfam; PF00713; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1877 MW; 8904C6786C301CE7 CRC64;

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Query Match      16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TES 17
      |||
Db      7 TES 9

RESULT 16
PSBL SYNNU
ID PSBL SYNNU STANDARD; PRT; 17 AA.
AC P12241;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II reaction center L protein (PSII 5 kDa protein)
DE (Fragment).
GN PSBL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RA Ikeuchi M., Koike H., Inoue Y.;
RT "Identification of psbI and psbL gene products in cyanobacterial
RT photosystem II reaction center preparation.";
RL FEBS Lett. 251:155-160(1989).
CC -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
CC B559.
CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.
DR PIR; S05033; S05033.
DR InterPro; IPR003372; PSII_Psbl.
DR Pfam; PF02419; PsbL; 1.
KW Photosynthesis; Photosystem II.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVE 12
      |||
Db      9 PVE 11

RESULT 17
D7AI ACASC
ID D7AI ACASC STANDARD; PRT; 18 AA.
AC P83402;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)
DE (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT.
RC TISSUE=Liver;
RX MEDLINE=21956475; PubMed=11959129;
RA Tang W.-K., Cheng C.H.K., Fong W.-P.;
RT "First purification of the antiquitin protein and demonstration of its
RT enzymatic activity.";
RL FEBS Lett. 516:183-186(2002).
CC -!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid +
      NADH.

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CC -!- SUBUNIT: Homotetramer.
CC -!- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is
CC 2.0 mM and Vmax is 1.3 micromol/min x mg enzyme.
CC -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
DR GO; 0004029; F:aldehyde dehydrogenase (NAD+) activity; IDA.
DR GO; 0006081; P:aldehyde metabolism; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PARTIAL.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; PARTIAL.
KW Oxidoreductase; NAD.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EF1A9B4047 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PKY 9
      |||
Db      8 PKY 10

RESULT 18
HEMH THETS
ID HEMH THETS STANDARD; PRT; 18 AA.
AC P80155;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ovohemerythrin (YPI4) (Fragment).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzom.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RT TISSUE=Oocyte;
RX MEDLINE=93049299; PubMed=1425663;
RA Baert J.-L., Britel M., Sautiere P., Malecha J.;
RT "Ovohemerythrin, a major 14-kDa yolk protein distinct from
RT vitellogenin in leech.";
RL Eur. J. Biochem. 209:563-569(1992).
CC -!- FUNCTION: MAJOR YOLK PROTEIN. THIS IRON PROTEIN MAY PLAY A ROLE
CC IN THE DETOXIFICATION OF FREE IRON AFTER A BLOOD MEAL.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the hemerythrin family.
DR PIR; S29264; S29264.
DR HSSP; P02247; 2MHR.
DR InterPro; IPR002063; Hemerythrin.
DR Pfam; PF01814; Hemerythrin; 1.
DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
KW Oxygen transport; Metal-binding; Iron; Yolk.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 2368 MW; 33397EEE587C81F1 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EPF 14
      |||
Db      5 EPF 7

RESULT 19
LCFN LAMGL
ID LCFN LAMGL STANDARD; PRT; 18 AA.
AC P83315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lactophorin (Whey protein) (Fragment).
OS Lama glama (Llama).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=20000588; PubMed=10531593;
 RA Kappeler S., Farah Z., Puhon Z.;
 RT "Alternative splicing of lactophorin mRNA from lactating mammary gland
 of the camel (Camelus dromedarius).";
 RL J. Dairy Sci. 82:1-10(1999).
 CC -!- SIMILARITY: BELONGS TO THE PP3 / GLYCAM-1 FAMILY.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR Pfam; PF05242; GLYCAM-1; 1.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2079 MW; CD59616E5B236AC6 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ESQ 18
 DB |||
 15 ESQ 17

RESULT 20
 DURA_STRGV STANDARD; PRT; 19 AA.
 AC P36504;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Lantibiotic duramycin (Leucopeptin) (Antibiotic PA48009).
 OS Streptococcus thermophilus (Leuconostoc).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 RN NCBI_TaxID=68215;
 RP SEQUENCE, AND STRUCTURE BY NMR.
 RC STRAIN=PA-48009;
 RX MEDLINE=91107438; PubMed=2272918;
 RA Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,
 RA Itazaki H.;
 RT "The structure of PA48009: the revised structure of duramycin.";
 RL J. Antibiot. 43:1421-1430(1990).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=91107436; PubMed=2125590;
 RA Fredenhagen A., Fendrich G., Marki F., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RT "Duramycins B and C, two new lantibiotics containing antibiotics as
 inhibitors of phospholipase A2. Structural revision of duramycin and
 cinnamycin.";
 RL J. Antibiot. 43:1403-1412(1990).
 CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
 Thr, and Ser into dehydrated AA and the formation of thioether
 bonds with cysteine or the formation of dialkylamine bonds with
 lysine. This is followed by membrane translocation and cleavage of
 the modified precursor.
 CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 CC Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
 FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
 FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
 FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
 FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
 SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PFT 15

Db |||
 9 PFT 11

RESULT 21
 TX3_PHONI STANDARD; PRT; 19 AA.
 AC P31010;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotoxin Tx3 (Fragment).
 OS Phoneutria nigriventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
 OX NCBI_TaxID=6918;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=92196803; PubMed=1801316;
 RA Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;
 RT "Isolation of neurotoxic peptides from the venom of the 'armed'
 spider Phoneutria nigriventer.";
 RL Toxicon 29:1225-1233(1991).
 CC -!- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.
 DR PIR; C39305; C39305.
 KW Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2244 MW; 3214E89CF10F7587 CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ESQ 18
 DB |||
 7 ESQ 9

RESULT 22
 C15Y_STRHY STANDARD; PRT; 20 AA.
 AC P20903;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Citrate synthase (EC 2.3.3.1) (Fragment).
 GN GLTA.
 OS Streptomyces hygroscopicus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1912;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=SF1293;
 RX MEDLINE=90334852; PubMed=1368511;
 RA Shimotohno K.W., Imai S., Murakami T., Seto H.;
 RT "Purification and characterization of citrate synthase from
 Streptomyces hygroscopicus SF-1293 and comparison of its properties
 with those of 2-phosphoenolpyruvate carboxykinase.";
 RL Agric. Biol. Chem. 54:463-470(1990).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
 CoA.
 CC -!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.
 CC -!- PATHWAY: Tricarboxylic acid cycle.
 CC -!- SUBUNIT: Homohexamer.
 CC -!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
 CAPABLE OF OXIDATIVE METABOLISM.
 CC -!- SIMILARITY: Belongs to the citrate synthase family.
 DR PIR; PQ0046; PQ0046.

DR InterPro; IPR002020; Citrate_synt.
DR PROSITE; PS00480; CITRATE SYNTHASE; PARTIAL.
KW Transferase; Tricarboxylic acid cycle; Allosteric enzyme.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2234 MW; C527ECTA87119597 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
||
Db 16 YPV 18

RESULT 23
SB60_MAIZE
ID SB60_MAIZE STANDARD; PRT; 20 AA.
AC P82868;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Putative 60 kDa spermidine-binding protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RC STRAIN=cv. Cecilia; TISSUE=Coleoptile;
RX MEDLINE=21948208; PubMed=11950979;
RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Bagni N.;
RT "Spermidine-binding proteins. Purification and expression analysis in
maize.";
RL Plant Physiol. 128:1303-1312(2002).
CC -!- FUNCTION: May have spermidine-binding activity.
CC -!- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).
CC -!- SUBCELLULAR LOCATION: Microsomal membrane.
CC -!- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.
DR GO; GO:0005792; C:Microsome; NAS.
KW Membrane; Microsome.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2093 MW; 7FD730C0C391579A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YEP 13
||
Db 6 YEP 8

RESULT 24
GRWM_HUMAN
ID GRWM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Growth-modulating serum tripeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE

CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR GO; GO:0001558; P:regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HK 2
||
Db 2 HK 3

RESULT 25
PAP2_PARMA
ID PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81874;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidi; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea moses sole (Pardachirus
marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
properties. Forms voltage-dependent, ion-permeable channels
in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
||
Db 4 FP 5

RESULT 26
RE31_LITRU
ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;

RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
Db 4 FT 5

RESULT 27
RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9CB862A00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
Db 4 FT 5

RESULT 28
SUGA_ACHDO STANDARD; PRT; 5 AA.
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Subesophageal ganglion pentapeptide.
OS Acheta domesticus (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]

RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT subesophageal ganglion of Acheta domesticus (Orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC GANGLIA.
DR PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
Db 4 PF 5

RESULT 29
ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CBI;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
FT NON TER 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
Db 2 KE 3

RESULT 30
ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Rucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatoestatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EP 13
 ||
 Db 1 EP 2

RESULT 31
 CARP MYTED STANDARD; PRT; 7 AA.
 ID _FAR5_HIRME
 AC P41020;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE Catch-relaxing peptide (CARP).
 OS Mytilus edulis (Blue mussel).
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
 CC Mytiloida; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88052022; PubMed=3676797;
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
 RA Muneoka Y.;
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
 RL Brain Res. 422:374-376(1987).
 CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
 AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
 RETRACTOR MUSCLE.
 CC PIR; A29342; ECMUCR.
 DR Hormone; Amidation.
 KW MOD RES 7
 FT SEQUENCE 7 AA; 831 MW; 673407268769DB0 CRC64;
 SQ

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
 ||
 Db 2 MP 3

RESULT 32
 EI05 LITRU STANDARD; PRT; 7 AA.
 ID _FAR5_HIRME
 AC P82101;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 5.
 OS Litoria rubella (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EP 13
 ||
 Db 3 EP 4

RESULT 33
 FAR1 HELTI STANDARD; PRT; 7 AA.
 ID _FAR1_HELTI
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GDPFLRF-amide.
 OS Helisoma trivolvis (Snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 CC Lymnaeidae; Planorbidae; Helisoma.
 OX NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RA "FMRFamide-related peptides from the kidney of the snail, Helisoma
 RT trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD RES 7
 FT SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;
 SQ

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
 ||
 Db 3 PF 4

RESULT 34
 FAR5 HIRME STANDARD; PRT; 7 AA.
 ID _FAR5_HIRME
 AC P42564;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GGYMRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobdallida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD RES 7
 FT SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;
 SQ

SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KY 9
 ||
 3 KY 4

Db

RESULT 35
 UF04 MOUSE
 ID UF04_MOUSE STANDARD; PRT; 7 AA.
 AC P38642;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Fibroblast; PubMed=7523108;
 RX MEDLINE=9500907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PK 8
 ||
 1 PK 2

Db

RESULT 36
 UN06 PINPS
 ID UN06_PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Fionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON TER 1
 FT NON TER 7
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;

SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KY 9
 ||
 3 KY 4

Db

RESULT 37
 WWAL ACHFU
 ID WWAL_ACHFU STANDARD; PRT; 7 AA.
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE WWamide-1.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
 CC PIR: S33245; S33245.
 DR Neuropeptide; Amidation.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
 ||
 3 EM 4

Db

RESULT 38
 AKH LIBAU
 ID AKH_LIBAU STANDARD; PRT; 8 AA.
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
 OX NCBI_TaxID=6966;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-
 RT concentrating hormone family isolated and sequenced from a
 RT dragonfly.";
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR: S10596; S10596.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FT 15
 Db 4 FT 5

RESULT 39
 AKH_TABAT
 ID_AKH_TABAT STANDARD; PRT; 8 AA.
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC I).
 DE Tabanus atratus (Horse fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae; Tabanus.
 OC NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046759; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J., Vogel V.W., Zhang Y.-S., Hayes D.K.
 RA "Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera).";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
 RL CC
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 CC PIR; A33995; A33995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FT 15
 Db 4 FT 5

RESULT 40
 ANG2_BOTJA
 ID_ANG2_BOTJA STANDARD; PRT; 8 AA.
 AC Q10582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide II (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 OC NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.

RN [1]
 RP SEQUENCE.
 RX TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca";
 RL Comp. Biochem. Physiol. 113B:467-473 (1996).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro; IPR00215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 8 8
 FT SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PF 6
 Db 7 PF 8

RESULT 41
 CLP_THICU
 ID_CLP_THICU STANDARD; PRT; 8 AA.
 AC P80488;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Chemolithotroph-specific protein (Fragment).
 OS Thiobacillus cuprinus.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Thiomonas.
 OC NCBI_TaxID=36860;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED CHEMOLITHOTROPHICALLY.
 CC NON_TER 8 8
 FT SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PV 11
 Db 2 PV 3

RESULT 42
 HTF2_PERAM
 ID_HTF2_PERAM STANDARD; PRT; 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypertrahaloaemic factor II (Neuropeptide M-II) (Periplanetin CC-2) (Pea-CAH-II) (LeD-CC-II) (Hypertrahaloaemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea; Blattidae; Periplaneta.
 OC NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.

RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L.; Schaffer M.H.; O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M.; Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of *Periplaneta americana*.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90236559; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrihaloasemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
RT *Gromphadorhina portentosa*, *Blattella germanica* and *Blatta orientalis*
RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TRISALOSE IN THE HEMOLymph (TRISALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLymph OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 FT 15
DB 4 FT 5

RESULT 43
LMT2 LOCM1 STANDARD; PRT; 8 AA.
AC P22396;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustanoytrotropin 2 (LOM-WT-2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustanoytrotropin II, an
RT additional neuropeptide of *Locusta migratoria*. Member of the
RT cephalomyototropic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; PYROKININ.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 FT 15
DB 4 FT 5

RESULT 44
LFP LEUMA STANDARD; PRT; 8 AA.
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucopyrokinin (LPK) (LEM-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86269041; PubMed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RT leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN [2]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RT neuropeptide isolated from the cockroach, *Leucophaea maderae*.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (14%) THAN THE
CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
CC PENTAPEPTIDE FRAGMENT FTPL.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A23967; A23967.
DR InterPro; IPR001484; PYROKININ.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
||
Db 4 FT 5

RESULT 45

ORMY ORCLI
ID - ORMY ORCLI STANDARD; PRT; 8 AA.
AC P82455;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orcomytropin (OMT).
OS Orcomytes limosus (Spinycreek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacidea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]

RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.

RC TISSUE=Hindgut;
RX MEDLINE=20411310; PubMed=10952880;
RA Dirksen H., Burdzik S., Sauter A., Keller R.;
RT "Two orcomyins and the novel octapeptide orcomytropin in the hindgut
of the crayfish Orconectes limosus: identified myostimulatory
neuropeptides originating together in neurones of the terminal
abdominal ganglion.";
RL J. Exp. Biol. 203:2807-2818(2000).
CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
BY ABDOMINAL GANGLIONIC NEURONS.
CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
KW Amidation; Neuropeptide.
FT MOD RES 8
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
||
Db 4 FT 5

RESULT 46

PK2 PERAM
ID - PK2 PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]

RP TISSUE SPECIFICITY.
RA MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tegma-specific distribution of FXPRLamides in the nervous system of
the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).

CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
||
Db 3 PF 4

RESULT 47

PK3 PERAM
ID - PK3 PERAM STANDARD; PRT; 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212459; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]

RP TISSUE SPECIFICITY.

RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tegma-specific distribution of FXPRLamides in the nervous system of
the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).

CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).

CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
||
Db 3 PF 4

RESULT 48

RS7 MYCIT
ID - RS7 MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 30S ribosomal protein S7 (Fragment).
 GN RPSG.
 OS Mycobacterium intracellulare.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 CX NCBI_TaxID=1767;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93197130; PubMed=8451173;
 RA Nair J., Rouse D.A., Morris S.L.;
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of
 RT Mycobacterium intracellulare."
 RL Nucleic Acids Res. 21:1039-1039(1993).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center, probably blocks exit of the E-site
 CC tRNA (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
 CC and S11 (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L08171; AAA25376.1; --
 DR PIR; S35538; S35538.
 DR HAMAP; MF_00480; --; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; P800952; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; rRNA-binding; rRNA-binding; tRNA-binding.
 FT INIT MET 0 0 BY SIMILARITY.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PK 8
 Db 7 PK 8

RESULT 49
 UC26_MAIZE
 ID UC26_MAIZE STANDARD; PRT; 8 AA.
 AC P80632;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
 DE (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 CX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.

DR Maize-2DPAGE; P80632; COLEOPTILE.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EP 13
 Db 2 EP 3

RESULT 50
 UF06_MOUSE
 ID UF06_MOUSE STANDARD; PRT; 8 AA.
 AC P38644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis."
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EP 13
 Db 3 EP 4

RESULT 51
 UPAL_HUMAN
 ID UPAL_HUMAN STANDARD; PRT; 8 AA.
 AC P30087;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP TISUE=Plasma;
 RC TISUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
 DR SWISS-2DPAGE; P30087; HUMAN.
 FT NON_TER 1 1

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FT UNSURE      8      8
FT NON TER     8      8
SQ SEQUENCE    8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ES 17
DB 3 ES 4

RESULT 52
UPAA HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma; PubMed=1459097;
RX MEDLINE=9302937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 KDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON TER 1 1
FT VARIANT 5 5 F -> P.
FT /FTID=VAR_000004.
FT NON TER 8 8
FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YP 10
DB 6 YP 7

RESULT 53
CCAP_CARMA
ID CCAP_CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangler J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual Cardioactive peptide (CCAP) from pericardial organs of the

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RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta; PubMed=1426284;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL PEBB Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD RES 9 9 AMIDATION.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
DB 1 PF 2

RESULT 54
CONO CONGE
ID CONO CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6

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FT MOD RES 9 9 AMIDATION
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PK 8
DB 7 PK 8
RESULT 55
COXE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunmus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song B., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and liver."
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferrocycochrome c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR PIR; S77984; S77984.
DR -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KE 3
DB 1 KE 2
RESULT 56
FAR2_CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]

RP SEQUENCE.
RC TISSUE=thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated callifMRFamides) from the blowfly Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
DR PIR; C41978; B41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1128 MW; 29D0699CAB6C5A7 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 SQ 18
DB 3 SQ 4
RESULT 57
FAR3_CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated callifMRFamides) from the blowfly Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
DR PIR; C41978; C41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 SQ 18
DB 3 SQ 4
RESULT 58
FAR4_PENMO STANDARD; PRT; 9 AA.
ID FAR4_PENMO
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLP4 (SQPSWLRF-amide).
 OS Pnaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn *Penaeus monodon*.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;
 AMIDATION.
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 17 SQ 18
 Db 1 SQ 2
 RESULT 59
 FARP_PENMO STANDARD; PRT; 9 AA.
 ID FARP_PENMO
 AC P83320;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLP5 (SMPSLRLRF-amide).
 OS Pnaeus monodon (penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn *Penaeus monodon*.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;
 AMIDATION.
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 MP 5
 Db 2 MP 3

RESULT 60
 FIBB_MACFU STANDARD; PRT; 9 AA.
 ID FIBB_MACFU
 AC P19375;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Macaca fuscata fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9543;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85289140; PubMed=3928610;
 RA Nakamura S., Takenaka O., Takahashi K.;
 RA "Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and
 RT patas monkey (*Brythrocebus patas*): their amino acid sequences,
 RT restricted mutations, and a molecular phylogeny for macaques,
 RT guenons, and baboons.";
 RL J. Biochem. 97:1487-1492(1985).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR; C24180; C24180.
 DR InterPro; IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1038 MW; 69FE5B9C735BB1B CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 16 ES 17
 Db 3 ES 4
 RESULT 61
 FRFI_SARBU STANDARD; PRT; 9 AA.
 ID FRFI_SARBU
 AC P83350;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FMRamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (*Neobellieria bullata*).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AMIDATION, AND FUNCTION.
 RC TISSUE=CNS;
 RX MEDLINE=22342733; PubMed=12438685;
 RA Meusen T., Merrens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
 RT "Identification in *Drosophila melanogaster* of the invertebrate G
 RT protein-coupled FMRamide receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
 CC junctions.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 SQ 18
 DB 3 SQ 4
 RESULT 62
 HUTU_KLEAE STANDARD; PRT; 9 AA.
 AC P12381;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate hydrolase) (Fragment).
 GN HUTU.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=28451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88198018; PubMed=2834335;
 RA Newkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;
 RT "Bidirectional promoter in the hut(p) region of the histidine utilization (hut) operons from Klebsiella aerogenes.";
 RL J. Bacteriol. 170:2240-2246(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90368611; PubMed=2203754;
 RA Schwacha A., Bender R.A.;
 RT "Nucleotide sequence of the gene encoding the repressor for the histidine utilization genes of Klebsiella aerogenes.";
 RL J. Bacteriol. 172:5477-5481(1990).
 CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-yl)propanoate = urocanate + H(2)O.
 CC -!- COFACTOR: Binds 1 NAD per subunit (By similarity).
 CC -!- PATHWAY: Histidine degradation; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M19665; AAA25078.1; -;
 DR EMBL; W34604; AAA25076.1; -;
 DR HAMAP; MF_00577; -; 1.
 DR InterPro; IPR000193; Urocanase.
 DR PROSITE; PS01233; UROCANASE; PARTIAL.
 KW Histidine metabolism; Lyase; NAD.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KY 9
 DB 5 KY 6
 RESULT 63
 KNL3_BOMVA STANDARD; PRT; 9 AA.
 ID KNL3_BOMVA
 AC P83058;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE [Thr6]bradykinin.
 OS Bombina variegata (Yellow-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=8348;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
 RT "Cloning and post-translational processing of frog skin kininogens.";
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat arterial smooth muscle and constriction of intestinal smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
 KW Amphibian defense peptide; Vasodilator; Bradykinin.
 SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PF 6
 DB 7 PF 8
 RESULT 64
 LMT3_LOCMI STANDARD; PRT; 9 AA.
 ID LMT3_LOCMI
 AC P41489;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamyotropin 3 (LOM-MT-3).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P., de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamyotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC PIR; A61620; A61620.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
 DB 4 PF 5

RESULT 65
 OXYA-SCYCA STANDARD; PRT; 9 AA.
 AC P42996;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Asvatocin.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pituitary;
 RX MEDLINE=95062247; PubMed=7972045;
 RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
 RT "Special evolution of neurohypophysial hormones in cartilaginous
 fishes: asvatocin and phasvatocin, two oxytocin-like peptides
 RT isolated from the spotted dogfish (Scyliorhinus canicula).";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
 CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurohyp_horm.
 DR Pfam: PF00220; hormone4; 1
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PV 11
 DB 7 PV 8

RESULT 66
 OXYF-SCYCA STANDARD; PRT; 9 AA.
 AC P42997;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Phasvatocin.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pituitary;
 RX MEDLINE=95062247; PubMed=7972045;
 RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
 RT "Special evolution of neurohypophysial hormones in cartilaginous
 fishes: asvatocin and phasvatocin, two oxytocin-like peptides
 RT isolated from the spotted dogfish (Scyliorhinus canicula).";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
 CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurohyp_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PV 11
 DB 7 PV 8

RESULT 67
 OXYV-SQUAC STANDARD; PRT; 9 AA.
 AC P43000;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Valitocin.
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 OX NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73031727; PubMed=5083097;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
 RT isolated from a cartilaginous fish, Squalus acanthias.";
 RL Eur. J. Biochem. 29:12-19(1972).
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurohyp_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PV 11
 DB 7 PV 8

RESULT 68
 SAMP-MUSCA STANDARD; PRT; 9 AA.
 AC P19095;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum amyloid P-component (SAP) (Fragment).
 OS Mustelus canis (Smooth dogfish).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Blombranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RA MEDLINE=83160932; PubMed=6403520;
RX Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
dogfish, *Mustelus canis*, C-reactive protein and amyloid P
component.";
RT component.";
RL J. Biol. Chem. 258:3889-3894 (1983).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1 >9 PENTAXIN.
FT NON_TER 9 >9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
DB 2 FP 3

RESULT 69
THYF_PIG
ID THYF_PIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047 (1977).
CC -!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR; A01523; YPFG.
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SQ 18
DB 4 SQ 5

RESULT 70
UHA2_HUMAN
ID UHA2_HUMAN STANDARD; PRT; 9 AA.
AC P40929;

OC Blombranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RA MEDLINE=83160932; PubMed=6403520;
RX Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
dogfish, *Mustelus canis*, C-reactive protein and amyloid P
component.";
RT component.";
RL J. Biol. Chem. 258:3889-3894 (1983).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1 >9 PENTAXIN.
FT NON_TER 9 >9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
DB 2 FP 3

RESULT 69
THYF_PIG
ID THYF_PIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047 (1977).
CC -!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR; A01523; YPFG.
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SQ 18
DB 4 SQ 5

RESULT 70
UHA2_HUMAN
ID UHA2_HUMAN STANDARD; PRT; 9 AA.
AC P40929;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RL Electrophoresis 15:1459-1465 (1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1104 MW; 8874B1BB5B01B2CA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TE 16
DB 4 TE 5

RESULT 71
UNI9_CLOPA
ID UNI9_CLOPA STANDARD; PRT; 9 AA.
AC P81355;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from *Clostridium pasteurianum* W5.";
RL Electrophoresis 19:802-806 (1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
FT VARIANT 8 8 M -> D.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1128 MW; E33E9B0AF5BB19DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 7 EM 8

RESULT 72
UPA3_HUMAN
ID UPA3_HUMAN STANDARD; PRT; 9 AA.
AC F30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6. ITS MW IS: 46 kDa.
CC SWISS-2DPAGE; P30089; HUMAN.
DR
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
DB 4 FP 5

RESULT 73
ANG1 BOTJA
ID -ANG1 BOTJA STANDARD; PRT; 10 AA.
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Luca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
DB 7 PF 8

RESULT 74
ANGT BOVIN
ID -ANGT BOVIN STANDARD; PRT; 10 AA.
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPINAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin.";
RL Biochem. J. 65:246-254(1957).
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
CC plasma.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A90345; A90345.
DR PDB; 3ER5; 15-JUL-92.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
DB 7 PF 8

RESULT 75
ANGT CHICK
ID -ANGT CHICK STANDARD; PRT; 10 AA.
AC P01018;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPINAS.
OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE.
RX SPECIES=Chicken;
RX MEDLINE=74127845; PubMed=4361802;
RA Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
RT angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C. c. japonica;
RX MEDLINE=90284684; PubMed=2191893;

```


RA Takei Y., Hasegawa Y.:
RT "Vasopressor and depressor effects of native angiotensins and
inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol. 79:12-22(1990).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A60624; A60624.
DR PIR; A90917; A90917.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
Db 7 PF 8

Search completed: November 25, 2003, 19:28:22
Job time : 7.45515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMPPKYPVPEPTESQ 18

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mbc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertibrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	22.2	8	11	P82598
2	4	22.2	13	5	Q9TWR4
3	4	22.2	15	2	Q9R5Z5
4	4	22.2	18	11	Q8CJD4
5	3	16.7	8	2	Q9J4S4
6	3	16.7	10	4	Q8WXB5
7	3	16.7	10	6	Q9N1X1
8	3	16.7	10	10	Q9FS93
9	3	16.7	10	11	Q9QVJ5
10	3	16.7	10	11	Q9QVJ6
11	3	16.7	10	13	Q73588
12	3	16.7	11	3	Q9UR95
13	3	16.7	11	5	P82700
14	3	16.7	12	4	Q9HBU4
15	3	16.7	12	10	Q9FSA9
16	3	16.7	12	11	Q9WUX1

17	3	16.7	12	15	O12036
18	3	16.7	13	4	Q9H4C1
19	3	16.7	13	5	Q9W5Q6
20	3	16.7	13	10	Q9FSA8
21	3	16.7	13	10	Q9FS94
22	3	16.7	13	10	Q8SAT3
23	3	16.7	13	10	Q8SAT3
24	3	16.7	13	10	Q8SAT4
25	3	16.7	14	2	P83159
26	3	16.7	14	10	Q9FS95
27	3	16.7	14	10	Q9FSB1
28	3	16.7	14	10	Q9FS91
29	3	16.7	15	2	Q9R4U7
30	3	16.7	15	2	Q9R4U7
31	3	16.7	15	4	Q9UBK0
32	3	16.7	15	4	Q9BXQ0
33	3	16.7	15	4	Q8IZK4
34	3	16.7	15	6	Q8HZ79
35	3	16.7	15	8	Q9T2G9
36	3	16.7	15	9	Q38574
37	3	16.7	15	10	Q9FSA5
38	3	16.7	15	10	Q9FSB2
39	3	16.7	15	10	Q9FS98
40	3	16.7	15	10	Q9FE13
41	3	16.7	15	10	Q9FSA0
42	3	16.7	15	10	Q9FS99
43	3	16.7	15	10	Q9FE15
44	3	16.7	15	10	Q9FE14
45	3	16.7	15	10	Q9FS80
46	3	16.7	15	10	Q9FS80
47	3	16.7	15	13	Q9PRM3
48	3	16.7	16	2	Q9R4J0
49	3	16.7	16	2	Q9R4J4
50	3	16.7	16	2	Q44610
51	3	16.7	16	2	Q9R514
52	3	16.7	16	2	Q8KLP7
53	3	16.7	16	2	P82597
54	3	16.7	16	4	Q9UBQ9
55	3	16.7	16	6	Q9SM73
56	3	16.7	16	6	Q9TRK9
57	3	16.7	16	8	Q8HU42
58	3	16.7	16	8	Q8HU29
59	3	16.7	16	10	P83511
60	3	16.7	16	11	Q8CIS2
61	3	16.7	17	2	Q9R9C3
62	3	16.7	17	4	Q9Y3F6
63	3	16.7	17	4	Q9UC43
64	3	16.7	17	6	Q9TRH5
65	3	16.7	17	6	Q9SM49
66	3	16.7	17	8	Q36741
67	3	16.7	17	10	Q9S8F2
68	3	16.7	17	11	Q9QV57
69	3	16.7	17	12	Q9IHG7
70	3	16.7	17	12	Q9IHG9
71	3	16.7	17	12	Q9IHG4
72	3	16.7	17	12	Q9IH17
73	3	16.7	17	12	Q9IH14
74	3	16.7	17	12	Q9IH19
75	3	16.7	17	12	Q9IH14
76	3	16.7	17	12	Q9IHG9
77	3	16.7	17	12	Q9IH55
78	3	16.7	17	12	Q9IH11
79	3	16.7	17	12	Q9IHG8
80	3	16.7	17	12	Q9IHG5
81	3	16.7	17	12	Q9IH18
82	3	16.7	17	12	Q9IH10
83	3	16.7	17	12	Q9IH16
84	3	16.7	17	12	Q9IH88
85	3	16.7	17	12	Q9IH82
86	3	16.7	17	12	Q9IHG3
87	3	16.7	17	12	Q9IHJ0
88	3	16.7	17	12	Q9IHG6
89	3	16.7	17	12	Q9IH11

O12036	caprine art
Q9H4C1	homo sapien
Q9W5Q6	drosophila
Q9FSA8	silene bacc
Q9FS94	silene pent
Q8SAT3	flaveria ro
Q8SAT3	brassica ol
Q8SAT4	flaveria an
P83159	anabaena sp
Q9FS95	silene pent
Q9FSB1	silene aega
Q9FS91	silene sedo
Q9R4U7	bacillus fi
Q9R4U7	acinetobact
Q9UBK0	homo sapien
Q9BXQ0	homo sapien
Q8IZK4	homo sapien
Q8HZ79	bos taurus
Q9T2G9	solanum tub
Q38574	bacterioph
Q9FSA5	silene cryp
Q9FSB2	silene aega
Q9FS98	silene laco
Q9FE13	silene aega
Q9FSA0	silene haus
Q9FS99	silene inte
Q9FE15	silene sedo
Q9FE14	silene pent
Q9FS80	silene zawa
Q9FSB0	silene aega
Q9PRM3	gallus gall
Q9R4J0	arthrobacte
Q9R4J4	pseudomon
Q44610	buchnera ap
Q9R514	porphyrom
Q8KLP7	streptomyce
P82597	bacillus sp
Q9UBQ9	homo sapien
Q9SM73	pan troglod
Q9TRK9	canis fami
Q8HU42	passiflora
Q8HU29	passiflora
P83511	delonix reg
Q8CIS2	mus muscu
Q9R9C3	borrelia bu
Q9Y3F6	homo sapien
Q9UC43	homo sapien
Q9TRH5	bos taurus
Q9SM49	bos taurus
Q36741	homo sapien
Q9S8F2	lupinus arb
Q9QV57	mus sp. lac
Q9IHG7	human polio
Q9IHG9	human polio
Q9IH55	human polio
Q9IH11	human polio
Q9IHG8	human polio
Q9IHG5	human polio
Q9IH18	human polio
Q9IH10	human polio
Q9IH16	human polio
Q9IH88	human polio
Q9IH82	human polio
Q9IHG3	human polio
Q9IHJ0	human polio
Q9IHG6	human polio
Q9IH11	human polio

90 Q91hi3 human polio 17 12 Q91H13
91 Q91hh0 human polio 17 12 Q91HH0
92 Q91hh6 human polio 17 12 Q91HH6
93 Q91hh7 human polio 17 12 Q91HH7
94 Q91hi5 human polio 17 12 Q91HI5
95 Q91hi2 human polio 17 12 Q91HI2
96 Q91h3 human polio 17 12 Q91HH3
97 Q91hg2 human polio 17 12 Q91HG2
98 Q8x4a4 escherichia 17 16 Q8X4A4
99 Q9uc87 homo sapien 18 4 Q9UC87
100 Q98365 myosurus mi 18 8 Q98365

ALIGNMENTS

RESULT 1

P82598
ID P82598 PRELIMINARY; PRT; 8 AA.
AC P82598;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 38kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RA MEDLINE=20198203; PubMed=10731662;
RA Kim K.-Y., Choi I., Kim S.-S.;
RT "Purification and characterization of a novel inhibitor of the
RT proliferation of hepatic stellate cells.";
RL J. Biochem. 127:23-27(2000).
CC -/- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
CC -/- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
CC PROTEIN.
FT NON TER
SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match 22.2%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
Db 3 PVEP 6

RESULT 2

Q9TWR4
ID Q9TWR4 PRELIMINARY; PRT; 13 AA.
AC Q9TWR4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Peptide T=BRADYKININ potentiator.
OS Tityus serrulatus (Brazilian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butchoidea; Butidae; Tityus.
ON NCBI_TaxID=6887;
RX [1]
RP SEQUENCE.
RX MEDLINE=94024945; PubMed=8212046;
RA Ferreira L.A., Alves E.W., Henriques O.B.;
RA "Peptide T, a novel bradykinin potentiator isolated from Tityus
RT serrulatus scorpion venom.";
RL Toxicon 31:941-947(1993).
SQ SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;

Query Match 22.2%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVE 12
Db 5 YPVE 8

RESULT 3

Q9R5Z5
ID Q9R5Z5 PRELIMINARY; PRT; 15 AA.
AC Q9R5Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Streptolysin O (Fragment).
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
ON NCBI_TaxID=119602;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273535; PubMed=8500915;
RA Gerlach D., Kohler W., Gunther E., Mann K.;
RT "Purification and characterization of streptolysin O secreted by
RT Streptococcus equisimilis (group C).";
RL Infect. Immun. 61:2727-2731(1993).
SQ SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEMP 5
Db 3 KEMP 6

RESULT 4

Q8CJD4
ID Q8CJD4 PRELIMINARY; PRT; 18 AA.
AC Q8CJD4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Podocin (Fragment).
GN NP8S2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RA Morita H., Yoshimura A., Makino R., Inui K., Nakao N., Usami T.,
RA Roselli S., Antignac C., Matsuyama M., Ideura T.;
RT "Rat genome fragment containing a part of exons and all of the 3'UTR
RT of Nphe2 as well as as microsatellite sites.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AB094124; BAC23094.1; -.
DR NON TER
FT NON TER
SQ SEQUENCE 18 AA; 2033 MW; D47829DCFF0EF4B CRC64;

Query Match 22.2%; Score 4; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
Db 4 PVEP 7

```

RESULT 5
Q934S4 ID Q934S4 PRELIMINARY; PRT; 8 AA.
AC Q934S4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Merd protein (Fragment).
GN MERD.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]_TaxID=920;
RP SEQUENCE FROM N.A.
RC STRAIN=G66; TRANSPOSON=Th5037;
RA Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,
RA Nikiforov V.G.;
RT "Th5037, a Tn21-like mercury resistance transposon from Thiobacillus
RT ferrooxidans."
RL Russ. J. Genet. 37:972-975 (2001).
DR EMBL; AJ251743; CAC69252.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 937 MW; ED15A2D77B5DD446 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
DB 4 YPV 6

RESULT 6
Q8WXB5 ID Q8WXB5 PRELIMINARY; PRT; 10 AA.
AC Q8WXB5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE EYA2B (Fragment).
GN EYA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Fee B.E., Doyle C.A., Cleveland J.L.;
RT "A novel eyes absent protein is expressed in the human eye."
RL Gene 0:0-0(2002).
DR EMBL; AF455148; AAL57875.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1298 MW; 18021202C69B132B CRC64;

Query Match 16.7%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
DB 4 KEM 6

RESULT 7
Q9N1X1 ID Q9N1X1 PRELIMINARY; PRT; 10 AA.
AC Q9N1X1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Alcohol dehydrogenase 3 (Fragment).
GN ADH3.

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OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]_TaxID=9796;
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=106113847;
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249 (1999).
DR EMBL; AF134056; AAF31299.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;

Query Match 16.7%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
DB 5 VEP 7

RESULT 8
Q9FS93 ID Q9FS93 PRELIMINARY; PRT; 10 AA.
AC Q9FS93;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Caryophyllaceae; Silene.
OX NCBI_TaxID=49735;
RN [1]_TaxID=49735;
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296133; CAC13025.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1108 MW; CF1AB6D1B2CAB1A9 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
DB 2 PPT 4

RESULT 9
Q9QVJ5 ID Q9QVJ5 PRELIMINARY; PRT; 10 AA.
AC Q9QVJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myo-inositol hexakisphosphate phosphohydrolase (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]_TaxID=10118;
RP SEQUENCE.

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RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal
RL mucosa.";
RT Blochim. Biophys. Acta 1075:75-82(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1096 MW; 37ABEA4B1B1B02D7 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVE 12
Db 3 PVE 5

RESULT 10
Q9QVJ6 PRELIMINARY; PRT; 10 AA.
AC Q9QVJ6
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE MYO-inositol hexakisphosphate phosphohydrolase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal
RL mucosa.";
RT Blochim. Biophys. Acta 1075:75-82(1991).
SQ SEQUENCE 10 AA; 1124 MW; 28B8EA4B1B1B02D7 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVE 12
Db 3 PVE 5

RESULT 11
O73588 PRELIMINARY; PRT; 10 AA.
AC O73588;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Engrailed-3 (Fragment).
GN EN-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryo;
RX MEDLINE=98141813; PubMed=9473273;
RA Peale F.V. Jr., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U26148; AAC06186.1; -.
FT NON_TER 1
FT NON_TER 10

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SQ SEQUENCE 10 AA; 1118 MW; 73C0BE144735B72B CRC64;

Query Match 16.7%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ESQ 18
Db 8 ESQ 10

RESULT 12
Q9UR95 PRELIMINARY; PRT; 11 AA.
AC Q9UR95;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Heat shock protein 60 homolog (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE.
RX MEDLINE=33233840; PubMed=8096822;
RA Evers M.E., Hulse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast Hansenula
RT polymorpha using immobilized denatured alcohol oxidase.";
RL FEBS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 16.7%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
Db 2 HKE 4

RESULT 13
P82700 PRELIMINARY; PRT; 11 AA.
AC P82700;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Periviscerokinin-3 (LEM-PVK-3).
OS Leucophaea maderae (Madeira cockroach);
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach);
OS Blaberus craniifer,
OS Blaptica dubia (Argentinian wood cockroach), and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinins from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
KW Neuropeptide; Amidation.
FT MOD_RES 11
FT MOD_RES 11 AMIDATION.

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SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
Db 7 PFP 9

RESULT 14
Q9HBU4 PRELIMINARY; PRT; 12 AA.
AC Q9HBU4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE Caspase 8 isoform i (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eckhart L., Fischer H., Bach J., Henry M., Ban J., Tschaachler E.;
RT "Identification and characterization of novel splice variants of human
caspase-8.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207672; AAG10682.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 12 AA; 1343 MW; 80F055095B6802D1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 6 VEP 8

RESULT 15
Q9FSA9 PRELIMINARY; PRT; 12 AA.
AC Q9FSA9;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296130; CAC33014.1; -.
FT NON TER 1
FT NON TER 1
FT NON TER 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1304 MW; 83269695B441B2CA CRC64;

Query Match 16.7%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
Db 13 PPT 15

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Db 2 PPT 4

RESULT 16
Q9WUX1 PRELIMINARY; PRT; 12 AA.
AC Q9WUX1;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE APOBEC-1 protein (Fragment).
GN APOBEC-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98335789; PubMed=9672068;
RA Greeve J., Axelos D., Welker S., Schipper M., Greten H.;
RT "Distinct promoters induce APOBEC-1 expression in rat liver and
intestine.";
RL Arterioscler. Thromb. Vasc. Biol. 18:1079-1092(1998).
DR EMBL; AJ006695; CAB44439.1; -.
FT NON TER 1
FT NON TER 1
FT NON TER 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1357 MW; 70FB1679699325BB CRC64;

Query Match 16.7%; Score 3; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 4 TES 6

RESULT 17
OL2036 PRELIMINARY; PRT; 12 AA.
AC OL2036;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296261; PubMed=9151845;
RA Turelli P., Guiguen F., Mornex J.F., Vigne R., Querat G.;
RT "dUTPase-minus caprine arthritis-encephalitis virus is attenuated for
pathogenesis and accumulates G-to-A substitutions.";
RL J. Virol. 71:4522-4530(1997).
DR EMBL; U81390; AAC57905.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 12 AA; 1398 MW; 8D24228CA3733455 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
Db 2 HKE 4

RESULT 18
Q9H4C1 PRELIMINARY; PRT; 13 AA.
AC Q9H4C1;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Angiopoietin-2B (Fragment).
 GN ANGIOPOIETIN-2B
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422311; PubMed=10964717;
 RA Mezquita J., Mezquita P., Montseriat P., Mezquita B., Francone V.,
 RA Vilagrasa X., Mezquita C.
 RT "Genomic structure and alternative splicing of chicken angiopoietin-
 RT 2";
 RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
 DR ENBL; AJ289780; CAC08179.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1548 MW; C3A19DA93BE95B02 CRC64;

 Query Match 16.7%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 KEM 4
 DB |||
 3 KEM 5

 RESULT 19
 Q9WSQ6 PRELIMINARY; PRT; 13 AA.
 AC Q9WSQ6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2001 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Snap25 protein.
 GN SNAP25 OR CG17676 OR CG17884.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Avril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtak R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR ENBL; AE002931; AAF43394.2; -.
 DR FlyBase; Fgn0011288; Snap25.
 SQ SEQUENCE 13 AA; 1483 MW; 47FD7CC5C0AF9B13 CRC64;

 Query Match 16.7%; Score 3; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 KEM 4
 DB |||
 6 KEM 8

 RESULT 20
 Q9FSA8 PRELIMINARY; PRT; 13 AA.
 AC Q9FSA8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene baccifera (Berry catchfly) (Cucubalus baccifer).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=54818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AJ296139; CAC13015.1; -.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1437 MW; D931E2CF1AB6D1B2 CRC64;

 Query Match 16.7%; Score 3; DB 10; Length 13;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 13 PFT 15
 DB |||
 2 PFT 4

 RESULT 21
 Q9FS94 PRELIMINARY; PRT; 13 AA.
 AC Q9FS94;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene pentelica.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.

OX NCBI_TaxID=49735;
RN SEQUENCE FROM N.A.
RP Popp M., Oxelman B.;
RT "Inferring the history of the polyploid silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296132; CAC13024.1; -;
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; D931E2CF1AB6D1B2 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 22
Q8SAT3 PRELIMINARY; PRT; 13 AA.
AC Q8SAT3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Non-C4 chloroplastic NADP-malic enzyme (Fragment).
GN CHLM2-2.
OS Flaveria robusta.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Tageteae;
OC Flaveria.
OX NCBI_TaxID=163089;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21648948; PubMed=11788758;
RA Lai L.B., Wang L., Nelson T.M.;
RT "Distinct But Conserved Functions for Two Chloroplastic NADP-Malic
RT Enzyme Isoforms in C(3) and C(4) Flaveria Species.";
RL Plant Physiol. 128:125-139(2002).
DR EMBL; AF288914; AAL74058.1; -;
FT NON_TER 1
SQ SEQUENCE 13 AA; 1697 MW; 95393F9D91422775 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
Db 7 PKY 9

RESULT 23
Q9S922 PRELIMINARY; PRT; 13 AA.
AC Q9S922;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE S3 SGP=S-locus specific glycoprotein (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=37112;
RN [1]
RP SEQUENCE.
RX MEDLINE=92090397; PubMed=1752245;
RA Gaudet T., Denoroy L., Dumas C.;

RT "Use of a fast protein electrophoretic purification procedure for N-
RT terminal sequence analysis to identify S-locus related proteins in
RT stigmas of Brassica oleracea.";
RL Electrophoresis 12:646-653(1991).
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1351 MW; 9C23EDFF999601B5 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 7 TES 9

RESULT 24
Q8SAT4 PRELIMINARY; PRT; 13 AA.
AC Q8SAT4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Non-C4 chloroplastic NADP-malic enzyme (Fragment).
GN CHLM2.
OS Flaveria angustifolia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Tageteae;
OC Flaveria.
OX NCBI_TaxID=163088;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21648948; PubMed=11788758;
RA Lai L.B., Wang L., Nelson T.M.;
RT "Distinct But Conserved Functions for Two Chloroplastic NADP-Malic
RT Enzyme Isoforms in C(3) and C(4) Flaveria Species.";
RL Plant Physiol. 128:125-139(2002).
DR EMBL; AF288996; AAL74057.1; -;
FT NON_TER 1
SQ SEQUENCE 13 AA; 1697 MW; 95393F9D91422775 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
Db 7 PKY 9

RESULT 25
P83159 PRELIMINARY; PRT; 14 AA.
AC P83159;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated,
DE rod (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER
CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION
CC OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME
CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A
CC DIRECTED AND OPTIMAL ENERGY TRANSFER.

CC -/- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS
 CC ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).
 CC -/- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
 KW Phycobilisome; Photosynthesis.
 FT NON_TER 14 14

SQ SEQUENCE 14 AA; 1405 MW; 96823844F60A3115 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
 Db 12 EPF 14

RESULT 26
 Q9FS95

ID Q9FS95 PRELIMINARY; PRT; 14 AA.

AC Q9FS95;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.

OS Silene pentelica.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=49735;

RN [1]
 RP SEQUENCE FROM N.A.

RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296131; CAC13023.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14

SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;
 Query Match 16.7%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
 Db 2 PFT 4

RESULT 27
 Q9FSB1

ID Q9FSB1 PRELIMINARY; PRT; 14 AA.

AC Q9FSB1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.

OS Silene aegaea.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=49732;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296122; CAC13007.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14

SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
 Db 2 PFT 4

RESULT 28
 Q9FS91

ID Q9FS91 PRELIMINARY; PRT; 14 AA.

AC Q9FS91;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.

OS Silene sedoides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=39790;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296105; CAC13028.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14

SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;
 Query Match 16.7%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
 Db 2 PFT 4

RESULT 29
 Q9R4M8

ID Q9R4M8 PRELIMINARY; PRT; 15 AA.

AC Q9R4M8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Catalase isozyme I (Fragment).
 OS Bacillus firmus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1399;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=95267795; PubMed=7748885;

RT "Purification of three catalase isozymes from facultatively
 RT alkaliphilic *Bacillus firmus* OF4.";
 RL Blochim. Biophys. Acta 1229:347-355 (1995).
 OX NCBI_TaxID=15 AA; 1677 MW; 12B47DC8F66876ED CRC64;

SQ SEQUENCE 15 AA; 1677 MW; 12B47DC8F66876ED CRC64;

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
 Db 13 PFT 15

```
RESULT 30
Q9R4U7 ID Q9R4U7 PRELIMINARY; PRT; 15 AA.
AC Q9R4U7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Malonate decarboxylase gamma subunit (Fragment).
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE
RX MEDLINE=95050812; PubMed=7961952;
RA Kim Y.S., Byun H.S.;
RT "Purification and properties of a novel type of malonate decarboxylase
from Acinetobacter calcoaceticus.";
RL J. Biol. Chem. 269:29636-29641(1994).
SQ SEQUENCE 15 AA; 1816 MW; 4E14F10E389F9FEA CRC64;

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPK 8
DB 11 FPK 13

RESULT 31
Q9UBK0 ID Q9UBK0 PRELIMINARY; PRT; 15 AA.
AC Q9UBK0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Renal tissue-nonspecific alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
kidney";
RL Clin. Chem. 38:2539-2542(1992).
SQ SEQUENCE 15 AA; 1931 MW; 9A28FDE13F01F716 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
DB 9 PKY 11

RESULT 32
Q9BXQ0 ID Q9BXQ0 PRELIMINARY; PRT; 15 AA.
AC Q9BXQ0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tissue transglutaminase (EC 2.3.2.13) (Fragment).
OS TGM2.
GN TGM2.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Festoff B.W.;
RT "Intron-exon swapping of transglutaminase mRNA and neuronal tau
aggregation in Alzheimer's disease.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF311286; AAK15272.1; -.
KW Acyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1641 MW; C340982AFEFBF851 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
DB 2 EPF 4

RESULT 33
Q8IZK4 ID Q8IZK4 PRELIMINARY; PRT; 15 AA.
AC Q8IZK4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Breast and ovarian cancer susceptibility protein (Fragment).
GN BRCAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Valarmathi M.T., Agarwal A., Deo S.S.V., Shukla N.K., Das S.N.;
RT "BRCAL germline mutations in Indian breast cancer families.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDSI databases.
DR EMBL; AV093484; AAM18218.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1807 MW; D1E6E8F11AB530FB CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
DB 10 ESQ 12

RESULT 34
Q8HZ79 ID Q8HZ79 PRELIMINARY; PRT; 15 AA.
AC Q8HZ79;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha-synuclein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Tompkins M.M., Gai W.P., Douglas S., Bunn S.J.;
RT "Alpha-synuclein expression localizes to the Golgi apparatus in bovine
adrenal medullary chromaffin cells.";
```

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY124580; AA94359.1; -.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1774 MW; 17154333C9115DADA CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMP 5
 Db 1 EMP 3

RESULT 35

ID Q9T2G9 PRELIMINARY; PRT; 15 AA.
 AC Q9T2G9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE Carbonic anhydrase (EC 4.2.1.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96327808; PubMed=9680307;
 RA Rumeau D., Cuine S., Fina L., Gault N., Nicole M., Peltier G.;
 RT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum
 L. leaves: characterization of two compartment-specific isoforms.";
 RL Planta 199;79-88(1996).
 SQ SEQUENCE 15 AA; 1647 MW; CA5B7063CDD32976 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVE 12
 Db 10 PVE 12

RESULT 36

ID Q38574 PRELIMINARY; PRT; 15 AA.
 AC Q38574;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Lysis protein (Fragment).
 OS Bacteriophage Kuf.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Levivirus.
 OX NCBI_TaxID=12021;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96207403; PubMed=8615017;
 RA Groeneveld H., Oudot F., van Duin J.V.;
 RT "RNA phage Kuf has an insertion of 18 nucleotides in the start codon
 of its lysis gene.";
 RL Virology 218;141-147(1996).
 DR EMBL; S81763; AAD14372.1; -.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1736 MW; EA4430EAC749D708 CRC64;

Query Match 16.7%; Score 3; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
 Db 8 HKE 10

RESULT 37

ID Q9FSA5 PRELIMINARY; PRT; 15 AA.
 AC Q9FSA5;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene cryptoneura.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=39877;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296138; CAC13016.1; -.
 FT NON TER 1
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CFIAB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFT 15
 Db 2 PFT 4

RESULT 38

ID Q9FSB2 PRELIMINARY; PRT; 15 AA.
 AC Q9FSB2;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS Silene aegaea.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=49732;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid Silene aegaea
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296115; CAC13000.1; -.
 FT NON TER 1
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1633 MW; D3420931E2CFIAB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFT 15
 Db 2 PFT 4

```
RESULT 39
Q9FS98          PRELIMINARY;      PRT;      15 AA.
ID Q9FS98;
AC Q9FS98;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene laconica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49734;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296136; CAC13020.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1596 MW; 2C2EBDCD299DD887C CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFT 15
Db      2 PFT 4

RESULT 40
Q9FE13          PRELIMINARY;      PRT;      15 AA.
ID Q9FE13;
AC Q9FE13;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296128; CAC13013.1; -.
DR EMBL; AJ296113; CAC12998.1; -.
DR EMBL; AJ296116; CAC13001.1; -.
DR EMBL; AJ296117; CAC13002.1; -.
DR EMBL; AJ296118; CAC13003.1; -.
DR EMBL; AJ296119; CAC13004.1; -.
DR EMBL; AJ296120; CAC13005.1; -.
DR EMBL; AJ296121; CAC13006.1; -.
DR EMBL; AJ296123; CAC13008.1; -.
DR EMBL; AJ296125; CAC13010.1; -.
DR EMBL; AJ296126; CAC13011.1; -.
DR EMBL; AJ296127; CAC13012.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFT 15
Db      2 PFT 4

RESULT 41
Q9FSA0          PRELIMINARY;      PRT;      15 AA.
ID Q9FSA0;
AC Q9FSA0;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene haussknechtii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49733;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296137; CAC13018.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFT 15
Db      2 PFT 4

RESULT 42
Q9FS99          PRELIMINARY;      PRT;      15 AA.
ID Q9FS99;
AC Q9FS99;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene integrifolia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39889;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296135; CAC13019.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFT 15
Db      2 PFT 4
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RESULT 43
Q9FE15          PRELIMINARY;      PRT;      15 AA.
AC Q9FE15;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene sedoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39790;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296112; CAC13035.1; -.
DR EMBL; AJ296104; CAC13029.1; -.
DR EMBL; AJ296106; CAC13029.1; -.
DR EMBL; AJ296107; CAC13030.1; -.
DR EMBL; AJ296108; CAC13031.1; -.
DR EMBL; AJ296109; CAC13032.1; -.
DR EMBL; AJ296110; CAC13033.1; -.
DR EMBL; AJ296111; CAC13034.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 44
Q9FE14          PRELIMINARY;      PRT;      15 AA.
AC Q9FE14;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296134; CAC13026.1; -.
DR EMBL; AJ296129; CAC13022.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 45
Q9FS80          PRELIMINARY;      PRT;      15 AA.
AC Q9FS80;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene zawadskii (Zawadskii's campion).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39923;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296141; CAC13039.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 46
Q9FSB0          PRELIMINARY;      PRT;      15 AA.
AC Q9FSB0;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296124; CAC13009.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1616 MW; C96B0931E2CF0AF6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 47
Q9FE15          PRELIMINARY;      PRT;      15 AA.
AC Q9FE15;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene sedoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39790;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296112; CAC13035.1; -.
DR EMBL; AJ296104; CAC13029.1; -.
DR EMBL; AJ296106; CAC13029.1; -.
DR EMBL; AJ296107; CAC13030.1; -.
DR EMBL; AJ296108; CAC13031.1; -.
DR EMBL; AJ296109; CAC13032.1; -.
DR EMBL; AJ296110; CAC13033.1; -.
DR EMBL; AJ296111; CAC13034.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match          16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

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Q9PRM3
ID Q9PRM3 PRELIMINARY; PRT; 15 AA.
AC Q9PRM3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 17 kDa major immunophilin (Fragment).
OS Gallus Gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE.
RX MEDLINE=94072550; PubMed=7504525;
RA Yem A.W., Reardon I.M., Leone J.W., Heinrikson R.L., Deibel M.R.Jr.;
RT "An active FK506-binding domain of 17,000 daltons is isolated
RL following limited proteolysis of chicken thymus hsp56.";
RL Biochemistry 32:12571-12576(1993)
SQ SEQUENCE 15 AA; 1606 MW; 6269732398D1B71C CRC64;

Query Match 16.7%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db |||
7 TES 9

RESULT 48
Q9RAJ0 PRELIMINARY; PRT; 16 AA.
ID Q9RAJ0;
AC Q9RAJ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE LIMONATE dehydrogenase (Fragment).
OS Arthrobacter globiformis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=1665;
RN [1]_TaxID=1665;
RP SEQUENCE.
RX MEDLINE=96045380; PubMed=7546548;
RA Suhayda C.G., Omura M., Hasegawa S.;
RT "Limonate dehydrogenase from Arthrobacter globiformis: the native
RT enzyme and its N-terminal sequence.";
RL Phytochemistry 40:17-20(1995)
SQ SEQUENCE 16 AA; 1759 MW; 514B2DE906FD5984 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6
Db |||
1 MPF 3

RESULT 49
Q9RAJ4 PRELIMINARY; PRT; 16 AA.
ID Q9RAJ4;
AC Q9RAJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Peptidyl-Asp metalloendopeptidase (Fragment).
OS Pseudomonas fragi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=296;
RN [1]_TaxID=296;

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RP SEQUENCE.
RX MEDLINE=95405303; PubMed=7674963;
RA Hagmann M.L., Geuss U., Fischer S., Kresse G.B.;
RT "Peptidyl-Asp metalloendopeptidase.";
RL Meth. Enzymol. 248:782-787(1995).
SQ SEQUENCE 16 AA; 1868 MW; 0521E93A81CBE07D CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db |||
11 TES 13

RESULT 50
Q44610 PRELIMINARY; PRT; 16 AA.
ID Q44610;
AC Q44610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Shikimate dehydrogenase (Fragment).
GN AROE.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]_TaxID=9;
RP SEQUENCE FROM N.A.
RX MEDLINE=95212914; PubMed=7535281;
RA Roubbakhsh D., Baumann P.;
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera
RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
RT gene.";
RL Gene 155:107-112(1995).
DR EMBL; U10499; AAA79128.1; -.
FT NON TER 1
SQ SEQUENCE 16 AA; 1891 MW; 72A8175598D30DF1 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPK 8
Db |||
9 FPK 11

RESULT 51
Q9RS14 PRELIMINARY; PRT; 16 AA.
ID Q9RS14;
AC Q9RS14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 17 KDa lysine-specific cysteine proteinase (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]_TaxID=837;
RP SEQUENCE.
RX MEDLINE=94103245; PubMed=8276827;
RA Pike R., McGraw W., Potempa J., Travis J.;
RT "Lysine- and arginine-specific proteinases from Porphyromonas
RT gingivalis. Isolation, characterization, and evidence for the existence
RT of complexes with hemagglutinins.";
RL J. Biol. Chem. 269:406-411(1994).
SQ SEQUENCE 16 AA; 1819 MW; D864F9BF367828C6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;

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Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 14 FTE 16
|||
Db 3 FTE 5

RESULT 52

Q8KLP7 Q8KLP7 PRELIMINARY; PRT; 16 AA.
AC Q8KLP7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Adenosine phosphotransferase (Fragment).
GN APT.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RA Wehmeier U.F.;
RT "Analysis of the secDF genes from Streptomyces griseus N2-3-11.";
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ505986; CAD44524.1; -.
KW Transferase.
FT NON TER
SQ SEQUENCE 16 AA; 1838 MW; 5B369FE6365B45F CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 15 TES 17
|||
Db 5 TES 7

RESULT 53

P82597 P82597 PRELIMINARY; PRT; 16 AA.
AC P82597;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thermostable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23) (Fragment).
DE (Fragment).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE.
RC STRAIN=H-257;
RX MEDLINE=20198254; PubMed=10731713;
RA Imamura S., Kitaura S.;
RT "Purification and characterization of a monoacylglycerol lipase from the moderately thermophilic Bacillus sp. H-257.";
RL J. Biochem. 127:419-425(2000).
CC -!- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY OCCURRING WITH 1-MONOLAURYLGLYCEROL.
CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 9 YPV 11
|||
Db 4 YPV 6

RESULT 54

Q9UBQ9 Q9UBQ9 PRELIMINARY; PRT; 16 AA.
AC Q9UBQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Apolipoprotein (A) (Fragment).
GN APOA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93185698; PubMed=7679504;
RA Wade D.P., Clarke J.G., Lindahl G.E., Liu A.C., Zysow B.R., Meer K., Schwartz K., Lawn R.M.;
RT "5' control regions of the apolipoprotein(a) gene and members of the related plasminogen gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1369-1373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93087573; PubMed=1454851;
RA Magaretti N., Acquati F., Magnaghi P., Bruno L., Pontoglio M., Rocchi M., Saccone S., Della Valle G., D'Urso M., LePaslier D., Ottolenghi S., Taramelli R.;
RT "Characterization by yeast artificial chromosome cloning of the linked apolipoprotein(a) and plasminogen genes and identification of the apolipoprotein(a) 5' flanking region.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11584-11588(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91097523; PubMed=2268308;
RA Magaretti N., Bruno L., Pontoglio M., Candiani G., Meroni G., Ottolenghi S., Taramelli R.;
RT "Definition of the transcription initiation site of human plasminogen gene in liver and non hepatic cell lines.";
RL Biochem. Biophys. Res. Commun. 173:1013-1018(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92207924; PubMed=1554698;
RA Ichinose A.;
RT "Multiple members of the plasminogen-apolipoprotein(a) gene family associated with thrombosis.";
RL Biochemistry 31:3113-3118(1992).
DR EMBL; L07899; AAB66587.2; -.
DR EMBL; M90079; AAA35546.1; -.
DR EMBL; M90078; AAA35547.1; -.
DR EMBL; M62890; AAA36454.1; -.
DR EMBL; M86878; AAA51749.1; -.
DR EMBL; M86877; AAB49909.1; -.
KW Lipoprotein.
FT NON TER
SQ SEQUENCE 16 AA; 1912 MW; 66BDPBF28EDB1A69 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 1 HKE 3
|||
Db 3 HKE 5

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RESULT 55
Q95M73
ID Q95M73 PRELIMINARY; PRT; 16 AA.
AC Q95M73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Apolipoprotein (Fragment).
GN A.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21303645; PubMed=11301336;
RA Huby T., Dacht C., Lawn R.M., Wickings J., Chapman M.J., Thillet J.;
RT "Functional analysis of the chimpanzee and human apo(a) promoter
RT sequences. Identification of sequence variations responsible for
RT elevated transcriptional activity in chimpanzee."
RL J. Biol. Chem. 276:22209-22214(2001).
DR EMBL; AY028467; AAK38764.1; -.
KW Lipoprotein.
FT NON_TER
SQ SEQUENCE 16 AA; 1912 MW; 66BDFBF28EDB1A69 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
DB 3 HKE 5

RESULT 56
Q9TRK9
ID Q9TRK9 PRELIMINARY; PRT; 16 AA.
AC Q9TRK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Casein kinase II-24 kDa polypeptide (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=93054738; PubMed=1331100;
RA Ou W.J., Thomas D.Y., Bell A.W., Bergeron J.J.;
RT "Casein kinase II phosphorylation of signal sequence receptor alpha
RT and the associated membrane chaperone calnexin."
RL J. Biol. Chem. 267:23789-23796(1992).
FT NON_TER
SQ SEQUENCE 16 AA; 2053 MW; F31011034124F59B CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
DB 6 EPF 8

RESULT 57
Q8HU42
ID Q8HU42 PRELIMINARY; PRT; 16 AA.
AC Q8HU42;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FebA (Fragment).
OS Passiflora elegans.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Passifloraceae; Passiflora.
OX NCBI_TaxID=159423;
RN [1]
RP SEQUENCE FROM N.A.
RA Muschner V.C., Lorenz A.P., Scherer N.M., Souza-Chies T.T.,
RA Cervi A.C., Salzano F.M., Bonatto S.L., Freitas L.B.;
RT "Comparative Phylogenetic Analysis of Nuclear and Plastid Sequences in
RT Passiflora (Passifloraceae).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032806; AAK69782.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1676 MW; 4A810A81DD549D80 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 12 PFT 14

RESULT 58
Q8HU29
ID Q8HU29 PRELIMINARY; PRT; 16 AA.
AC Q8HU29;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FebA (Fragment).
OS Passiflora haematostigma.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Passifloraceae; Passiflora.
OX NCBI_TaxID=159429;
RN [1]
RP SEQUENCE FROM N.A.
RA Muschner V.C., Lorenz A.P., Scherer N.M., Souza-Chies T.T.,
RA Cervi A.C., Salzano F.M., Bonatto S.L., Freitas L.B.;
RT "Comparative Phylogenetic Analysis of Nuclear and Plastid Sequences in
RT Passiflora (Passifloraceae).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032819; AAK69795.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1676 MW; 4A810A81DD549D80 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 12 PFT 14

RESULT 59
P83511
ID P83511 PRELIMINARY; PRT; 16 AA.
AC P83511;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lectin (DRL) (fragment).

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OS Delonix regia (Royal poinciana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Caesalpinioideae; Caesalpinieae;
OC Delonix.
OX NCBI_TaxID=72433;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Seed;
RX PubMed=12168698;
RA Pando S.C., Macedo M.L.R., Freire M.G.M., Toyama M.H., Novello J.C.,
RA Marangoni S.;
RA "Biochemical characterization of a lectin from Delonix regia seeds.";
RL J. Protein Chem. 21:279-285(2002).
RC -!- FUNCTION: GLUCOSE-SPECIFIC LECTIN.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: OPTIMAL PH IS 8.0-9.0. ACTIVE UP TO 60 DEGREES
CC CELSIUS.
CC -!- MISCELLANEOUS: REQUIRES MANGANESE BUT NOT CALCIUM IONS FOR CELL-
CC AGGLUTINATING ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
DR InterPro: IPR001220; Lectin legB.
DR PROSITE: PS00307; LECTIN LEGUME BETA; PARTIAL.
KW Lectin; Glycoprotein; Manganese.
FT NON TER 16
FT SEQUENCE 16 AA; 1816 MW; D3DA3A36D1C308BE CRC64;

Query Match 16.7%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPK 8
Db |||
5 FPK 7

RESULT 60
ID Q8CIS2 PRELIMINARY; PRT; 16 AA.
AC Q8CIS2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Plasmid cp33-3 (Fragment).
DE Plasmid cp33-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RX PubMed=12149246;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Parmer R.J., Miles L.A.;
RA "Localization of Regulatory Elements Mediating Constitutive and
RT Cytokine-stimulated Plasminogen Gene Expression.";
RL J. Biol. Chem. 277:38579-38588(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RA Garcia Bannach F., Fowler B.J., Gutierrez A., Bugge T.H., Degen J.L.,
RA Parmer R.J., Miles L.A.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY134430; AAN15805.1; -.
FT NON TER 16
FT SEQUENCE 16 AA; 1922 MW; 647558FC6EDB15CC CRC64;

Query Match 16.7%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
Db |||

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Db 3 HKE 5

RESULT 61
ID Q9R9C3 PRELIMINARY; PRT; 17 AA.
AC Q9R9C3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Plasmid cp32-3, possible partition proteins (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OS Plasmid cp32-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Exp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022480; AAC35442.1; -.
DR InterPro: IPR004180; DUF226.
DR Pfam; PF02890; DUF226; 1.
KW Plasmid.
FT NON TER 1
FT SEQUENCE 17 AA; 2069 MW; 7FDE0D04EF50172D CRC64;

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYP 10
Db |||
1 KYP 3

RESULT 62
ID Q9Y3F6 PRELIMINARY; PRT; 17 AA.
AC Q9Y3F6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE EST00098 protein (Fragment).
GN EST00098.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99299247; PubMed=10369878;
RA Gilley J., Fried M.;
RT "Extensive gene order differences within regions of conserved synteny
RT between the Fugu and human genomes: implications for chromosomal
RT evolution and the cloning of disease genes.";
RL Hum. Mol. Genet. 8:1313-1320(1999).
DR EMBL; Y17449; CAB44366.1; -.
FT NON TER 17
FT SEQUENCE 17 AA; 1695 MW; 1EA4692B032AF8D0 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVE 12
Db |||
2 PVE 4

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RESULT 63
Q9UC43
ID Q9UC43 PRELIMINARY; PRT; 17 AA.
AC Q9UC43;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Interferon-alpha-induced protein (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=96132854; PubMed=8557639;
RA Rich S.A.; Bose M.; Tempst P.; Rudofsky U.H.;
RT "Purification, microsequencing, and immunolocalization of p36, a new
RT interferon-alpha-induced protein that is associated with human lupus
RT inclusions."
RL J. Biol. Chem. 271:1118-1126(1996).
SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACEC CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
DB 15 KYP 17

RESULT 64
Q9TRH5
ID Q9TRH5 PRELIMINARY; PRT; 17 AA.
AC Q9TRH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Alpha-S1-casein homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93231344; PubMed=1299613;
RA Neuteboom B.; Giuffrida M.G.; Conti A.;
RT "Isolation of a new ligand-carrying casein fragment from bovine
RT mammary gland microsomes."
RL FEBS Lett. 305:189-191(1992).
SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
DB 4 PFP 6

RESULT 65
Q9SM49
ID Q9SM49 PRELIMINARY; PRT; 17 AA.
AC Q9SM49;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Acetyl-CoA-carboxylase alpha (EC 6.4.1.2) (Fragment).
GN ACC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao J., Molenaar A., Wheeler T.T., Seyfert H.M.;
RT "STAT5-binding is mandatory for lactational stimulation of the bovine
RT promoter PIII of the Acetyl-Coenzyme A-Carboxylase alpha-encoding gene
RT in the mammary gland but not in other tissues."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mao J.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Rostock, Rostock, Germany.
DR EMBL; AJ312201; CAC59690.1; -.
KW Ligase.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2082 MW; 0B379CCF0A078E55 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
DB 9 KEM 11

RESULT 66
Q36741
ID Q36741 PRELIMINARY; PRT; 17 AA.
AC Q36741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Glutaryl CoA dehydrogenase (Fragment).
GN GCDH.
OS Homo sapiens (Human).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95315953; PubMed=7795610;
RA Greenberg C.R.; Reimer D.; Singal R.; Triggs-Raine B.; Chudley A.E.;
RA Dilling L.A.; Philipps S.; Haworth J.C.; Seargeant L.F.; Goodman S.I.;
RT "A G-to-T transversion at the +5 position of intron 1 in the glutaryl
RT CoA dehydrogenase gene is associated with the island lake variant of
RT glutaric acidemia type I."
RL Hum. Mol. Genet. 4:493-495(1995).
DR EMBL; S77773; AAB34724.2; -.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1896 MW; 4D77B628C59A9E32 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
DB 7 TES 9

RESULT 67
Q9S8Y2
ID Q9S8Y2 PRELIMINARY; PRT; 17 AA.
AC Q9S8Y2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
OS Lupinus arboreus (tree lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3872;
RN [1]
RP SEQUENCE.
RX MEDLINE=92344803; PubMed=1368361;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RL Phytochemistry 31:1519-1527(1992).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1877 MW; DB7925924D5F46AF CRC64;

Query Match 16.7%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPF 6
Db 3 MPF 5

RESULT 68
Q9QVS7 PRELIMINARY; PRT; 17 AA.
AC Q9QVS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lactate dehydrogenase-A (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95201434; PubMed=7534515;
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,
RA FAVOR J.;
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the
RT mouse.";
RL Mamm. Genome 5:777-780(1994).
SQ SEQUENCE 17 AA; 1982 MW; B941E0A3F2477D45 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
Db 11 HKE 13

RESULT 69
Q9IHG7 PRELIMINARY; PRT; 17 AA.
AC Q9IHG7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6013TAJ94; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;

DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
OS Lupinus arboreus (tree lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3872;
RN [1]
RP SEQUENCE.
RX MEDLINE=92344803; PubMed=1368361;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RL Phytochemistry 31:1519-1527(1992).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1877 MW; DB7925924D5F46AF CRC64;

Query Match 16.7%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPF 6
Db 3 MPF 5

RESULT 68
Q9QVS7 PRELIMINARY; PRT; 17 AA.
AC Q9QVS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lactate dehydrogenase-A (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95201434; PubMed=7534515;
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,
RA FAVOR J.;
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the
RT mouse.";
RL Mamm. Genome 5:777-780(1994).
SQ SEQUENCE 17 AA; 1982 MW; B941E0A3F2477D45 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3
Db 11 HKE 13

RESULT 69
Q9IHG7 PRELIMINARY; PRT; 17 AA.
AC Q9IHG7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6013TAJ94; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;

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RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233188; AAF35092.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1840 MW; 004DEB222D713051 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16
Db 8 FTE 10

RESULT 70
Q9IH9 PRELIMINARY; PRT; 17 AA.
AC Q9IH9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6427ING95; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233176; AAF35080.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1836 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16
Db 8 FTE 10

RESULT 71
Q9IH4 PRELIMINARY; PRT; 17 AA.
AC Q9IH4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6433PAK95; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233191; AAF35095.1; -.
FT NON_TER 1

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FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 72
Q9IH17 PRELIMINARY; PRT; 17 AA.
AC Q9IH17;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]_TaxID=12080;
RP SEQUENCE FROM N.A.
RC STRAIN=3038USA82DI58;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233168; AAF35072.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 73
Q9IH4 PRELIMINARY; PRT; 17 AA.
AC Q9IH4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]_TaxID=12080;
RP SEQUENCE FROM N.A.
RC STRAIN=7TAJ391;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233181; AAF35085.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 74
Q9IH9 PRELIMINARY; PRT; 17 AA.
AC Q9IH9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]_TaxID=12080;
RP SEQUENCE FROM N.A.
RC STRAIN=2677USA81D48;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233166; AAF35070.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 75
Q9IH4 PRELIMINARY; PRT; 17 AA.
AC Q9IH4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]_TaxID=12080;
RP SEQUENCE FROM N.A.
RC STRAIN=422RUS91;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
RT poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233171; AAF35075.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10
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Search completed: November 25, 2003, 19:34:00
Job time : 34.8023 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMPPKYPVPPFTESQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03.*

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23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	AA072267 Colostrinin derive
2	18	100.0	18	22	AA072520 Colostrinin peptid
3	18	100.0	18	22	AA072552 Colostrinin peptid
4	18	100.0	18	22	AA059330 Ewe colostrinin pe
5	18	100.0	18	23	AA020249 Colostrinin consti
6	18	100.0	18	23	AA051056 Colostrinin consti
7	18	100.0	18	23	AA014598 Neural cell regula
8	11	61.1	14	15	AA058339 Hypotensive polype
9	10	55.6	11	17	AA003290 CNS-inhibiting pep

10	10	55.6	13	17	AA003291 CNS-inhibiting pep
11	7	38.9	7	23	AE032211 Sheep colostrinin
12	6	33.3	6	17	AA003289 CNS-inhibiting pep
13	6	33.3	6	23	AE032212 Sheep colostrinin
14	6	33.3	15	15	AA050330 Hypotensive polype
15	5	27.8	10	22	AE07187 Colostrinin peptid
16	5	27.8	10	22	AE07197 Modified colostrin
17	5	27.8	14	22	AA090055 Human SNP associat
18	5	27.8	15	22	AA072250 Colostrinin derive
19	5	27.8	15	22	AA072504 Colostrinin peptid
20	5	27.8	15	22	AA072536 Colostrinin peptid
21	5	27.8	15	22	AA059322 Ewe colostrinin pe
22	5	27.8	15	23	AE020232 Colostrinin consti
23	5	27.8	15	23	AA051040 Colostrinin consti
24	5	27.8	15	23	AA014581 Neural cell regula
25	5	27.8	16	22	AA059352 Ewe colostrinin pe
26	4	22.2	5	19	AA065794 Polypolyli inhibit
27	4	22.2	6	20	AA06327 Cellulase EGIII-li
28	4	22.2	6	21	AA014886 EGIII-like cellula
29	4	22.2	6	23	AA077071 Endoglucanase EGII
30	4	22.2	6	23	AA077438 EGIII-like cellula
31	4	22.2	6	23	AA087807 Endoglucanase III
32	4	22.2	7	16	AA021388 Plasmidogen activa
33	4	22.2	7	21	AA096209 Arabidopsis AHAS s
34	4	22.2	8	16	AA061422 PF4-related octape
35	4	22.2	8	17	AA005539 Peptide fragment #
36	4	22.2	8	19	AA058608 Platelet factor 4
37	4	22.2	9	21	AA045558 Human B99-1 HLA B*
38	4	22.2	9	21	AA045559 Human B99-1 HLA B*
39	4	22.2	9	21	AA073039 Hepatitis B virus
40	4	22.2	9	22	AA024524 Human MHC class I
41	4	22.2	9	22	AA024745 Human MHC class I
42	4	22.2	9	22	AA024826 Human MHC molecule
43	4	22.2	9	22	AA024925 Human MHC class I
44	4	22.2	9	23	AA094282 Human novel protei
45	4	22.2	9	23	AA094868 Human novel protei
46	4	22.2	9	23	AA095255 Human novel protei
47	4	22.2	9	24	AB020159 MHC binding peptid
48	4	22.2	10	21	AA094204 Human cytotoxic T
49	4	22.2	10	22	AA068075 Antitumour cancer
50	4	22.2	10	22	AA075678 HLA class I bindin
51	4	22.2	10	22	AA049971 Human melanoma ass
52	4	22.2	10	22	AA024575 Human MHC class I
53	4	22.2	10	22	AA024783 Human MHC class I
54	4	22.2	10	22	AA024905 Human MHC molecule
55	4	22.2	10	22	AA024911 Human MHC molecule
56	4	22.2	10	22	AA024914 Human MHC molecule
57	4	22.2	10	22	AA025003 Human MHC class I
58	4	22.2	10	22	AA025222 Human MHC molecule
59	4	22.2	10	23	AA017822 Sponge okadaic aci
60	4	22.2	10	23	AA094390 Human novel protei
61	4	22.2	10	23	AA094412 Human novel protei
62	4	22.2	10	23	AA095356 Human novel protei
63	4	22.2	10	23	AA095384 Human novel protei
64	4	22.2	10	24	AB047212 Staphylococcus aur
65	4	22.2	10	24	AB047239 Staphylococcus aur
66	4	22.2	10	24	AB047292 Staphylococcus aur
67	4	22.2	10	24	AB047319 Staphylococcus aur
68	4	22.2	11	14	AA041812 M13TMD1 mutated fr
69	4	22.2	11	15	AA052835 Streptolysin O pep
70	4	22.2	12	21	AA023183 Hep47-binding hydr
71	4	22.2	12	22	AA057781 Bovine DNaseI pept
72	4	22.2	12	23	AB082324 Epitopic peptide b
73	4	22.2	12	23	AB067387 Human ADP1 tryptic
74	4	22.2	13	15	AA063797 Bacillus thuringie
75	4	22.2	13	17	AA091253 European corn bore
76	4	22.2	13	18	AA019525 B. thuringiensis p
77	4	22.2	13	19	AA080325 Bacillus thuringie
78	4	22.2	13	19	AA046715 N-terminal amino a
79	4	22.2	13	23	AA022620 Human M1ST protein
80	4	22.2	13	23	AA022621 Human M1ST protein
81	4	22.2	14	16	AA058799 Human phospholipas
82	4	22.2	14	20	AA041952 Rheumatoid arthrit

83 4 22.2 14 22 AAB98010 Human peptide #128
 84 4 22.2 14 22 AAU28525 DPI tryptic digest
 85 4 22.2 14 22 AAU26171 Depression-Asocia
 86 4 22.2 14 23 ABG96070 Cysteine-containin
 87 4 22.2 14 24 ABP57207 Breast cancer asso
 88 4 22.2 15 16 AAR70027 Hydroxylamin pepti
 89 4 22.2 15 16 AAR79630 Endocarditis speci
 90 4 22.2 15 16 AAR79631 Endocarditis speci
 91 4 22.2 15 21 AAY93322 Antigenic peptide
 92 4 22.2 15 21 AAY93323 Antigenic peptide
 93 4 22.2 15 21 AAY76361 Fragment of human
 94 4 22.2 15 22 ABP24630 HIV DR super motif
 95 4 22.2 15 22 AAB72253 Colostrinin derive
 96 4 22.2 15 22 AAB72507 Colostrinin peptid
 97 4 22.2 15 22 AAB72539 Colostrinin peptid
 98 4 22.2 15 22 AAB59313 Ewe colostrinin pe
 99 4 22.2 15 23 ABP58951 Human macroprotein
 100 4 22.2 15 23 AAO26556 Human macroprotein

ALIGNMENTS

RESULT 1
 AAB72267
 ID AAB72267 standard; peptide; 18 AA.
 XX AC
 XX AAB72267;
 XX DT 14-MAY-2001 (first entry)
 XX DE
 DE Colostrinin derived cytokine inducing peptide SEQ ID 22.
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX OS Synthetic.
 XX FN WO200111937-A2.
 XX PD 22-FEB-2001.
 XX PF 17-AUG-2000; 2000WO-US22818.
 XX PR 17-AUG-1999; 99US-0149311.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PA (REGG-) REGEN THERAPEUTICS PLC.
 XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX DR WPI; 2001-202804/20.
 XX PT Inducing a cytokine and modulating an immune response, useful for
 FT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX PS Claim 1; Page 34; 50pp; English.
 XX CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKEMPPPKYPVEPFTESQ 18
 DB 1 HKEMPPPKYPVEPFTESQ 18
 RESULT 2
 AAB72520
 ID AAB72520 standard; Peptide; 18 AA.
 XX AC AAB72520;
 XX DT 09-MAY-2001 (first entry)
 XX DE Colostrinin peptide #21.
 KW Dermatological; oxidative stress regulator; colostrinin.
 OS Unidentified.
 XX FN WO200112650-A2.
 XX PD 22-FEB-2001.
 XX PF 17-AUG-2000; 2000WO-US22665.
 XX PR 17-AUG-1999; 99US-0149310.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Stanton GJ, Hughes TK, Boldogh I;
 XX DR WPI; 2001-218342/22.
 XX PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX PS Claim 6; Page 26; 48pp; English.
 XX CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HKEMPPPKYPVEPFTESQ 18
 DB 1 HKEMPPPKYPVEPFTESQ 18
 RESULT 3
 AAB72552
 ID AAB72552 standard; Peptide; 18 AA.
 XX AC AAB72552;
 XX DT 09-MAY-2001 (first entry)
 XX

```

DE Colostrinin peptide #21.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX Unidentified.
OS
XX WO200112651-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
XX
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 18 AA;
XX
XX Query Match 100.0%; Score 18; DB 22; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-13;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HKMPFPKYPVEPFTESQ 18
XX |||||
XX Db 1 HKMPFPKYPVEPFTESQ 18
XX
XX RESULT 4
XX AAB59330
XX ID AAB59330 standard; Peptide; 18 AA.
XX
XX AC AAB59330;
XX
XX DT 21-MAR-2001 (first entry)
XX
XX DE Ewe colostrinin peptide fragment C-5.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX WO2000075173-A2.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
XX
XX 02-JUN-1999; 99GB-0012852.
XX
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from
XX
XX Colostrinin for treating e.g. disorders of the central nervous system
XX and immune system, viral and bacterial infections, and diseases
XX characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 18 AA;
XX
XX Query Match 100.0%; Score 18; DB 22; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-13;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HKMPFPKYPVEPFTESQ 18
XX |||||
XX Db 1 HKMPFPKYPVEPFTESQ 18
XX
XX RESULT 5
XX AAE20249
XX ID AAE20249 standard; peptide; 18 AA.
XX
XX AC AAE20249;
XX
XX DT 18-JUN-2002 (first entry)
XX
XX DE Colostrinin constituent peptide #21.
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX transplantation; implantation; dermatological; vulnetary.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Modified-site 18
XX FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
XX PD 21-FEB-2002.
XX
XX PF 17-AUG-2000; 2000WO-US22776.
XX
XX PR 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
XX patient comprises a blood cell regulator selected from colostrinin, its
XX constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
XX regulator selected from colostrinin, its constituent peptide and/or
XX analogue. The invention is used for modulating the oxidative stress
XX level in a cell e.g. mammalian or human cell present in a cell culture,
XX tissue, organ, or organism; or for treating oxidative damage to the skin
XX of a patient e.g. animal or human; to modulate oxidative stress during/

```


CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13; Length 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKEMPPFKYPVEPFTESQ 18
 |||||
 Db 1 HKEMPPFKYPVEPFTESQ 18

RESULT 6
 AAM51056
 ID AAM51056 standard; Peptide; 18 AA.

AC AAM51056;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide (casein amino acids 121-138).

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified-site 18 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. It is
 CC classified as having a beta-casein homologue precursor, and
 CC corresponds to casein amino acids 121-138. Methods are claimed
 CC for: inducing a cytokine in a cell by contact with an immunological
 CC regulator, where the cell is present in a cell culture, a tissue,
 CC an organ or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide. Cytokines
 CC induced by this peptide in human leucocyte cultures include
 CC interferon-gamma, tumour necrosis factor-alpha and interleukin-10.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKEMPPFKYPVEPFTESQ 18
 |||||
 Db 1 HKEMPPFKYPVEPFTESQ 18

RESULT 7

AAO14598

ID AAO14598 standard; peptide; 18 AA.

XX AAO14598;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 21.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX Unidentified.

FH Key Location/Qualifiers

FT Modified-site 18 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrin peptide used in
 CC the method of the invention.

SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.5e-13;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKEMPPPKYPVEPFTSQ 18

DB 1 HKEMPPPKYPVEPFTSQ 18

RESULT 8

AAR58339
 ID AAR58339 standard; peptide; 14 AA.

XX AC AAR58339;

DT 22-SEP-1994 (first entry)

XX DE Hypotensive polypeptide.

XX KW Hypotensive; antioxidative; calcium absorption; salt; food;
 KW pharmaceuticals; physiologically active agents.

OS Lactobacillus helveticus.

XX JP06041191-A.

PD 15-FEB-1994.

PF 03-MAR-1993; 93JP-0043047.

XX 04-MAR-1992; 92JP-0047340.

XX (CALV) CALPIS SHOKUIN KOGYO KK.

DR WPI; 1994-089332/11.

XX New polypeptide - used in physiologically active agents having
 PT e.g. hypotensive antioxidative and calcium absorption promoting
 PT activity

PS Claim 1-2; Page 10; 10pp; Japanese.

XX Sequences (AAR58319-341) are used in conjunction with
 CC physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.

SQ Sequence 14 AA;

Query Match 61.1%; Score 11; DB 15; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.3e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKEMPPPKYPV 11

DB 1 HKEMPPPKYPV 11

RESULT 9

AAW03290
 ID AAW03290 standard; peptide; 11 AA.

XX AC AAW03290;

DT 23-MAR-1997 (first entry)

XX

DE CNS-inhibiting peptide from casein.
 XX casein; central nervous system; CNS inhibiting; antitussive;
 KW analgesic; sedative.
 XX Synthetic.
 XX JP08269090-A.
 XX 15-OCT-1996.
 XX 28-MAR-1995; 95JP-0094516.
 XX 28-MAR-1995; 95JP-0094516.
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX WPI; 1996-515013/51.
 XX New peptide(s) obt'd. by digestion of casein - useful as drugs
 PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
 PT activities
 XX Claim 1; Page 2; 11pp; Japanese.
 XX Acid casein was prepared from raw milk by acid precipitation, and
 CC beta casein was formed by the product by the method of Hipp et al.
 CC This material was digested with porcine pepsin. The digested protein
 CC was neutralised with NaOH, then heated to inactivate the enzyme. The
 CC product was further digested with bovine pancreatin, trypsin and porcine
 CC kidney-derived LAP and then subjected to reverse phase chromatography
 CC to provide the present peptide.
 CC The peptide is useful as a drug having CNS inhibiting, antitussive,
 CC analgesic and sedative activities
 XX SQ Sequence 11 AA;

Query Match 55.6%; Score 10; DB 17; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVEPFTSQ 18

DB 1 YPVEPFTSQ 10

RESULT 10

AAW03291
 ID AAW03291 standard; peptide; 13 AA.

XX AC AAW03291;

XX 23-MAR-1997 (first entry)

XX CNS-inhibiting peptide from casein.

XX casein; central nervous system; CNS inhibiting; antitussive;
 KW analgesic; sedative.
 XX Synthetic.
 XX JP08269090-A.
 XX 15-OCT-1996.
 XX 28-MAR-1995; 95JP-0094516.
 XX 28-MAR-1995; 95JP-0094516.
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX WPI; 1996-515013/51.

PT New peptide(s) obtd. by digestion of casein - useful as drugs
PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX activities
XX
XX Claim 1; Page 2; 11pp; Japanese.
XX
XX Acid casein was prepared from raw milk by acid precipitation, and
XX beta casein was formed by the product by the method of Hipp et al.
XX This material was digested with porcine pepsin. The digested protein
XX was neutralised with NaOH, then heated to inactivate the enzyme. The
XX product was further digested with bovine pancreatin, trypsin and porcine
XX kidney-derived LAP and then subjected to reverse phase chromatography
XX to provide the present peptide.
XX The peptide is useful as a drug having CNS inhibiting, antitussive,
XX analgesic and sedative activities
XX
XX Sequence 13 AA;
XX
XX Query Match 55.6%; Score 10; DB 17; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.0001;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 9 YPVPPFTTESQ 18
XX | | | | | | | | | |
XX Db 1 YPVPPFTTESQ 10
XX
XX RESULT 11
XX ABG32211
XX ID ABG32211 standard; peptide; 7 AA.
XX AC
XX ABG32211;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Sheep colostrin derived peptide #5.
XX
XX KW Sheep; colostrin; colostrum; cytokine inducer; antigen; dementia;
XX central nervous system disorder; neurological disorder; neurosis;
XX mental disorder; psychosis; neurodegenerative disorder;
XX Alzheimer's disease; motor neuron disease; immune system disorder;
XX acquired immunological deficiency; bacterial infection; viral infection;
XX amyloid plaque; dietary supplement; cachexia; weight loss;
XX senile dementia; Parkinson's disease; emotional disturbance; depression;
XX drug addiction; drug withdrawal.
XX
XX OS Ovis aries.
XX
XX FN WO200246211-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 05-DEC-2001; 2001WO-GB05376.
XX
XX PR 06-DEC-2000; 2000GB-0029777.
XX
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX
XX PI Georgiades JA;
XX
XX DR WPI; 2002-619016/66.
XX
XX PT Novel peptides isolated from colostrin polypeptide, useful for
XX treating viral and bacterial infections, disorders of immune system and
XX central nervous system e.g., Alzheimer's disease, dementia, and as food
XX additive -
XX
XX PS Claim 1; Page 8; 16pp; English.
XX
XX CC The invention relates to a peptide derived from colostrin (a colostrum
XX protein known to be a cytokine inducer) substantially entirely consists
XX of the peptide sequences appearing as ABG32207-ABG32223. Also included
XX are a composition comprising two or more of the peptides in combination

CC with a carrier, a dietary supplement comprising an orally ingestible
CC combination of the peptide in combination with a carrier and an antibody
CC which binds to the peptide, and which is obtainable by using peptide as
CC an antigen. The peptide is useful as a medicament for treating chronic
CC disorders of central nervous system e.g., neurological disorders and/or
CC mental disorders such as psychosis and/or neurosis, dementia,
CC neurodegenerative disorders such as Alzheimer's disease, motor
CC neuron disease, chronic disorders of immune system, diseases
CC with bacterial and viral etiology, acquired immunological deficiencies,
CC chronic bacterial, viral infections. The peptide is also useful for
CC treating diseases characterised by presence of amyloid plaque. The
CC peptide is also useful as a dietary supplement for babies, small
CC children, adults who have been subjected to chemotherapy and/or
CC adults who have suffered from cachexia or weight loss due to chronic
CC disease. The peptide is also useful for treating senile dementia,
CC Parkinson's disease, emotional disturbances and depression. The peptides
CC may also be used as an auxiliary withdrawal treatment for drug addicts,
CC after a period of detoxification, and in persons dependent on stimulants.
CC The present sequence is a colostrin derived peptide of the invention.
XX
XX SQ Sequence 7 AA;
XX
XX Query Match 38.9%; Score 7; DB 23; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 EMPFPKY 9
XX | | | | | | | |
XX Db 1 EMPFPKY 7
XX
XX RESULT 12
XX AAW03289
XX ID AAW03289 standard; peptide; 6 AA.
XX AC AAW03289;
XX
XX DT 23-MAR-1997 (first entry)
XX
XX DB CNS-inhibiting peptide from casein.
XX
XX KW casein; central nervous system; CNS inhibiting; antitussive;
XX analgesic; sedative.
XX
XX OS Synthetic.
XX
XX FN JP08269090-A.
XX
XX PD 15-OCT-1996.
XX
XX PF 28-MAR-1995; 95JP-0094516.
XX
XX PR 28-MAR-1995; 95JP-0094516.
XX
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
XX DR WPI; 1996-515013/51.
XX
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX activities
XX
XX PS Claim 1; Page 2; 11pp; Japanese.
XX
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX beta casein was formed by the product by the method of Hipp et al.
XX This material was digested with porcine pepsin. The digested protein
XX was neutralised with NaOH, then heated to inactivate the enzyme. The
XX product was further digested with bovine pancreatin, trypsin and porcine
XX kidney-derived LAP and then subjected to reverse phase chromatography
XX to provide the present peptide.
XX The peptide is useful as a drug having CNS inhibiting, antitussive,
XX analgesic and sedative activities

XX SQ Sequence 6 AA; 0; Gaps 0; Indels 0; Mismatches 0; Length 6;
 Query Match 33.3%; Score 6; DB 17; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVEPF 14
 Db 1 YPVEPF 6
 |||||

RESULT 13
 ABG32212
 ID ABG32212 standard; peptide; 6 AA.
 XX AC ABG32212;
 XX AC
 DT 05-NOV-2002 (first entry)
 XX DT
 DE Sheep colostrin derived peptide #6.
 XX Sheep; colostrin; colostrum; cytokine inducer; antigen; dementia;
 KW central nervous system disorder; neurological disorder; neurosis;
 KW mental disorder; psychosis; neurodegenerative disorder;
 KW Alzheimer's disease; motor neuron disease; immune system disorder;
 KW acquired immunological deficiency; bacterial infection; viral infection;
 KW amyloid plaque; dietary supplement; cachexia; weight loss;
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;
 KW drug addiction; drug withdrawal.
 XX KW
 OS Ovis aries.
 XX OS
 XX WO200246211-A2.
 PN WO200246211-A2.
 XX WO200246211-A2.
 PD 13-JUN-2002.
 XX PD
 XX 05-DEC-2001; 2001WO-GB05376.
 PF 05-DEC-2001; 2001WO-GB05376.
 XX PF
 XX 06-DEC-2000; 2000GB-0029777.
 PR 06-DEC-2000; 2000GB-0029777.
 XX PR
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX PA
 PI Georgiades JA;
 XX PI
 XX WPI; 2002-619016/66.
 DR WPI; 2002-619016/66.
 XX DR
 PT Novel peptides isolated from colostrin polypeptide, useful for
 PT treating viral and bacterial infections, disorders of immune system and
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food
 PT additive -
 XX PT
 PS Claim 1; Page 8; 16pp; English.
 XX PS
 CC The invention relates to a peptide derived from colostrin (a colostrum
 CC protein known to be a cytokine inducer) substantially entirely consists
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included
 CC are a composition comprising two or more of the peptides in combination
 CC with a carrier, a dietary supplement comprising an orally ingestible
 CC combination of the peptide in combination with a carrier and an antibody
 CC which binds to the peptide, and which is obtainable by using peptide as
 CC an antigen. The peptide is useful as a medicament for treating chronic
 CC disorders of central nervous system e.g., neurological disorders and/or
 CC mental disorders such as psychosis and/or neurosis, dementia,
 CC neurodegenerative disorders such as Alzheimer's disease, motor
 CC neuron disease, chronic disorders of immune system, diseases
 CC with bacterial and viral etiology, acquired immunological deficiencies,
 CC chronic bacterial, viral infections. The peptide is also useful for
 CC treating diseases characterised by presence of amyloid plaque. The
 CC peptide is also useful as a dietary supplement for babies, small
 CC children, adults who have been subjected to chemotherapy and/or
 CC adults who have suffered from cachexia or weight loss due to chronic
 CC disease. The peptide is also useful for treating senile dementia,

CC Parkinson's disease, emotional disturbances and depression. The peptides
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,
 CC after a period of detoxification, and in persons dependent on stimulants.
 CC The present sequence is a colostrin derived peptide of the invention.
 XX CC
 SQ Sequence 6 AA;

Query Match 33.3%; Score 6; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEPFT 15
 Db 1 PVEPFT 6
 |||||

RESULT 14
 AAR58330
 ID AAR58330 standard; peptide; 15 AA.
 XX AC AAR58330;
 XX AC
 DT 22-SEP-1994 (first entry)
 XX DT
 DE Hypotensive polypeptide.
 XX DE
 KW Hypotensive; antioxidative; calcium absorption; salt; food;
 KW pharmaceuticals; physiologically active agents.
 XX KW
 OS Lactobacillus helveticus.
 XX OS
 XX JP06041191-A.
 FN JP06041191-A.
 XX FN
 XX 15-FEB-1994.
 PD 15-FEB-1994.
 XX PD
 XX 03-MAR-1993; 93JP-0043047.
 PF 03-MAR-1993; 93JP-0043047.
 XX PF
 XX 04-MAR-1992; 92JP-0047340.
 PR 04-MAR-1992; 92JP-0047340.
 XX PR
 XX (CALV) CALPIS SHOKUHIN KOGYO KK.
 PA (CALV) CALPIS SHOKUHIN KOGYO KK.
 XX PA
 XX WPI; 1994-089332/11.
 DR WPI; 1994-089332/11.
 XX DR
 XX New polypeptide - used in physiologically active agents having
 XX e.g. hypotensive antioxidative and calcium absorption promoting
 XX activity
 PT activity
 XX PT
 PS Claim 1-2; Page 8; 10pp; Japanese.
 XX PS
 CC Sequences (AAR58319-341) are used in conjunction with
 CC physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.
 XX CC
 SQ Sequence 15 AA;

Query Match 33.3%; Score 6; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFTESQ 18
 Db 6 PFTESQ 11
 |||||

RESULT 15
 AAE07187
 ID AAE07187 standard; peptide; 10 AA.
 XX AC AAE07187;
 XX AC
 XX 06-NOV-2001 (first entry)
 DT 06-NOV-2001 (first entry)

```

XX DE Colostrinin peptide 3.
XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral.
XX OS Unidentified.
XX FH Key
XX FT Modified-site 1
XX PN /note= "N-terminal acetyl; this residue forms a cyclic
XX PD linkage with Pro found at the C-terminal end"
XX PF WO200155199-A1.
XX PR 02-AUG-2001.
XX PR 26-JAN-2001; 2001WO-GB00329.
XX PR 26-JAN-2000; 2000GB-0001825.
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;
XX DR WPI; 2001-488775/53.
XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
XX PT the immune system and the central nervous system comprises ten
XX PT amino-terminal amino acid sequence derived from peptides present in
XX PT colostrinin -
XX PS Claim 1; Page 15; 40pp; English.
XX CC The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child.
XX CC The present sequence is colostrinin peptide 3 related to the invention.
XX SQ Sequence 10 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 32;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 10 PVEPFF 14
XX Db 4 PVEPFF 8
XX RESULT 16
XX AAE07197
XX ID AAE07197 standard; peptide; 10 AA.
XX AC AAE07197;
XX XX
XX DT 06-NOV-2001 (first entry)
XX DE Modified colostrinin cyclic peptide #3.

```

```

XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral; cyclic.
XX OS Synthetic.
XX FH Key
XX FT Modified-site 1
XX PN /note= "N-terminal acetyl; this residue forms a cyclic
XX PD linkage with Pro found at the C-terminal end"
XX PF WO200155199-A1.
XX PR 02-AUG-2001.
XX PR 26-JAN-2001; 2001WO-GB00329.
XX PR 26-JAN-2000; 2000GB-0001825.
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;
XX DR WPI; 2001-488775/53.
XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
XX PT the immune system and the central nervous system comprises ten
XX PT amino-terminal amino acid sequence derived from peptides present in
XX PT colostrinin -
XX PS Example 2; Page 8; 40pp; English.
XX CC The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child.
XX CC The present sequence is modified colostrinin cyclic peptide #3 related to
XX CC the invention.
XX SQ Sequence 10 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 32;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 10 PVEPFF 14
XX Db 5 PVEPFF 9
XX RESULT 17
XX AAG98055
XX ID AAG98055 standard; peptide; 14 AA.
XX AC AAG98055;

```

XX 19-SEP-2001 (first entry)
XX Human SNP associated peptide SEQ ID NO. 697.
XX
XX Human; single nucleotide polymorphism; SNP; angiotensinogen;
KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
KW adenosine triphosphate-dependent RNA helicase;
KW major histocompatibility complex Class I histocompatibility antigen; MHC;
KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX WO200148245-A2.
XX
XX 05-JUL-2001.
XX
XX 27-DEC-2000; 2000WO-US35346.
XX
XX 27-DEC-1999; 99US-0472688.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimketa RA, Leach M;
XX
XX WPI; 2001-418297/44.
XX
XX Polymorphic nucleic acids encoding e.g. angiotensinogen, dehydrogenase,
PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT diseases and infections -
XX
XX Disclosure; Page 444; 484pp; English.
XX
XX The invention relates to nucleic acids (AAH79386-AAH80036) encoding
CC polymorphic variants of proteins (AAG98010-AAG98238) related to
CC angiotensinogen, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC proteins have potential immunosuppressive, immunostimulatory,
CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC antileukemic, neuroprotective and antimicrobial activity and may be
CC useful in gene/protein therapy, vaccines, modulation of the expression
CC and activity of proteins related to angiotensinogen, 4-hydroxybutyrate,
CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC major histocompatibility complex (MHC) Class I histocompatibility antigen
CC and/or phosphoglycerate kinase. Disorders that may be prevented
CC diagnosed and/or treated by the above methods include multifactorial
CC diseases with a genetic component, such as autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers
CC of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC the nervous system, an infection of pathogenic organisms. They may also
CC be used to alter phenotypic traits such as longevity, appearance,
CC strength, speed and endurance.
XX
SQ Sequence 14 AA;
Query Match 27.8%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 PFTES 17
Db 9 PFTES 13
RESULT 18
AAB72250
ID AAB72250 standard; peptide; 15 AA.

XX AAB72250;
XX
XX 14-MAY-2001 (first entry)
XX
XX Colostrin derived cytokine inducing peptide SEQ ID 5.
XX
XX Colostrin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
XX WO200111937-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22818.
XX
XX 17-AUG-1999; 99US-0149311.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
XX WPI; 2001-202804/20.
XX
XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrin as an immunological
PT regulator -
XX
XX Claim 1; Page 34; 50pp; English.
XX
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.
XX
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVEPF 14
Db 8 PVEPF 12
RESULT 19
AAB72504
ID AAB72504 standard; Peptide; 15 AA.
XX
XX AAB72504;
XX
XX 09-MAY-2001 (first entry)
XX
XX Colostrin peptide #5.
XX
XX Dermatological; oxidative stress regulator; colostrin.
XX
XX Unidentified.

```

PN WO200112650-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22665.
XX
XX 17-AUG-1999; 99US-0149310.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2001-218342/22.
XX
XX Modulating oxidative stress level in a cell, involves contacting the
XX cell with an oxidative stress regulator selected from colostrinin, its
XX constituent peptide, analog or their combinations -
XX
XX Claim 6; Page 25; 48pp; English.
XX
XX The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostrinin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PVEPFF 14
Db 8 PVEPFF 12
RESULT 20
ID AAB72536 standard; Peptide; 15 AA.
XX
XX AAB72536;
XX
XX 09-MAY-2001 (first entry)
XX
XX Colostrinin peptide #5.
XX
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
XX colostrum.
XX
XX Unidentified.
XX
XX WO200112651-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
XX
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PVEPFF 14
Db 8 PVEPFF 12
RESULT 21
ID AAB59322 standard; Peptide; 15 AA.
XX
XX AAB59322;
XX
XX 21-MAR-2001 (first entry)
XX
XX Ewe colostrinin peptide fragment B-7.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX WO2000075173-A2.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
XX
XX 02-JUN-1999; 99GB-0012852.
XX
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from
XX colostrinin for treating e.g. disorders of the central nervous system
XX and immune system, viral and bacterial infections, and diseases
XX characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PVEPFF 14
Db 8 PVEPFF 12

```

RESULT 22
AAE20232
ID AAE20232 standard; peptide; 15 AA.
XX
XX
AC AAE20232;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #5.
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulneryary.
XX
XX Unidentified.
OS
XX
XX
FH Key Location/Qualifiers
FT Modified-site 15
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 25; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.
XX
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVEPF 14
Db 8 PVEPF 12
RESULT 23
AAMS1040

ID AAMS1040 standard; Peptide; 15 AA.
XX
XX AAMS1040;
XX
XX 30-MAY-2002 (first entry)
XX
XX Colostrinin constituent peptide.
XX
XX Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 15
FH /note= "optional C-terminal amidation"
XX
XX WO200213849-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22775.
XX
XX 17-AUG-2000; 2000WO-US22775.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
XX WPI; 2002-269150/31.
XX
XX Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue -
XX
XX Claim 1; Page 34; 54pp; English.
XX
XX The present sequence is that of a colostrinin constituent peptide
CC that is preferred for use as an immunological regulator and as a
CC blood cell regulator in claimed methods of the invention. It is
CC classified as having a beta-casein homologue precursor. Methods
CC are claimed for: inducing a cytokine in a cell by contact with an
CC immunological regulator, where the cell is present in a cell
CC culture, a tissue, an organ or an organism, and the cell is
CC mammalian, including human; modulating an immune response in a cell
CC by contact with the immunological regulator under conditions
CC effective to induce a cytokine; modulating an immune response in a
CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator
CC is administered topically or as part of a dietary supplement, and
CC where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation
CC by contacting blood cells with a blood cell regulator, where the
CC blood cells are present in a cell culture or an organism, are
CC mammalian or human, and where the blood cells are increased in
CC number or differentiated; and a method for modulating blood cell
CC proliferation in a patient. A claimed cytokine-inducing composition
CC comprises a pharmaceutical carrier and an active agent such as the
CC present peptide. Cytokines induced by this peptide in human
CC leucocyte cultures include interferon-gamma, tumour necrosis
CC factor-alpha, interleukin-6 and interleukin-10.
XX
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVEPF 14
Db 8 PVEPF 12

RESULT 24
AAO14581
ID AAO14581 standard; peptide; 15 AA.
XX AC AAO14581;
XX DT 27-MAY-2002 (first entry)
XX DE Neural cell regulatory colostrinin peptide 5.
XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
XX KW neural cell treatment.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Modified-site 15 /note= "Optional C-terminal amide"
XX PN WO200213851-A1.
XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22777.
XX PR 17-AUG-2000; 2000WO-US22777.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Boldogh I, Stanton JG, Hughes TK;
XX DR WPI; 2002-269152/31.
XX PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog -
XX PS Claim 7; Page 21; 37pp; English.
XX CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVEPFF 14
Db 8 PVEPFF 12
RESULT 25
AAB59352
ID AAB59352 standard; Peptide; 16 AA.
XX AC AAB59352;
XX DT 21-MAR-2001 (first entry)
XX DE Ewe colostrinin peptide fragment derived sequence #12.
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
OS Ovis sp.
PN WO200075173-A2.
PD 14-DEC-2000.
XX 02-JUN-2000; 2000WO-GB02128.
XX 02-JUN-1999; 99GB-0012852.
PR (REGG-) REGEN THERAPEUTICS PLC.
PA Georgiades JA;
XX PI WPI; 2001-071058/08.
XX DR Peptides having an N-terminal amino acid sequence isolated from
XX PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX PS Claim 8; Page 27; 63pp; English.
XX CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX SQ Sequence 16 AA;
Query Match 27.8%; Score 5; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVEPFF 14
Db 9 PVEPFF 13
RESULT 26
AAW65794
ID AAW65794 standard; peptide; 5 AA.
XX AC AAW65794;
XX DT 19-OCT-1998 (first entry)
XX DE Polyprolyl inhibitor of cyclophilin.
XX KW polyprolyl; cyclophilin; inhibitor; neurotrophic compound; PPI;
XX KW ptiptidy-prolyl isomerase; rotamase; immunophilin protein; degeneration;
XX KW neuronal damage.
XX OS Synthetic.
XX PN WO9825950-A1.
XX PD 18-JUN-1998.
XX PF 08-DEC-1997; 97WO-US23102.
XX PR 09-DEC-1996; 96US-0761302.
XX PA (GUIL-) GUILFORD PHARM INC.
XX PI Hamilton GS, Steiner JP, Wei L;
XX

DR WPI; 1998-348444/30.
 XX
 PT Effecting neuronal activity in mammals - by administering tetra-
 PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,
 PT useful in treatment of neuronal damage or degeneration disorders
 XX
 PS Claim 11; Page 41; 70pp; English.
 XX
 CC The invention relates to a method of effecting a neuronal activity. It
 CC comprises administering a neurotrophic compound with an affinity for a
 CC cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl
 CC isomerase (rotamase) activity. The neurotrophic compound achieves the
 CC stimulation of damaged neurons, promotion of neuronal regeneration or
 CC prevention of neurodegeneration, and treatment of neurological disorder.
 CC The neurotrophic compounds are potent peptidyl-proline isomerase
 CC (rotamase) inhibitors. They are of use in disorders which include
 CC peripheral neuropathy caused by physical injury or disease state, i.e.
 CC physical injury to the brain or spinal cord, stroke, or neurological
 CC disorder leading to neurodegeneration, notably Alzheimer's and
 CC Parkinson's diseases, or amyotrophic lateral sclerosis. The neurotrophic
 CC compounds avoid the side effects of immunosuppressant drugs, including
 CC nephrotoxicity, impaired glomerular filtration, interstitial fibrosis,
 CC involuntary tremors, headaches, and hypertension. They are also free from
 CC the difficulties in delivery and bioavailability of large molecular
 CC weight proteins. The present sequence represents a specifically claimed
 CC neurotrophic compound.
 XX
 SQ Sequence 5 AA;
 Query Match 22.2%; Score 4; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PPKK 8
 Db |||||
 2 PPKK 5
 RESULT 27
 AAY06327
 ID AAY06327 standard; Peptide; 6 AA.
 AC
 XX AAY06327;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Cellulase EGIII-like enzyme conserved motif.
 XX
 KW Cellulase; endoglucanase; EGIII; textile; feed additive; baking;
 KW food processing; grain wet milling; pulp; paper.
 XX
 OS Synthetic.
 XX
 XX WO9931255-A2.
 PN
 XX 24-JUN-1999.
 PD
 XX 14-DEC-1998; 98WO-US26552.
 PF
 XX 16-DEC-1997; 97US-0991720.
 PR
 XX (GEMV) GENENCOR INT INC.
 PA
 XX Bower BS, Fowler T, Phillips JI;
 PI
 XX WPI; 1999-395187/33.
 DR
 XX EGIII like cellulase
 PT
 XX Claim 1c; Page 34; 47pp; English.
 PS
 CC The invention relates to novel enzymes which share certain
 CC conserved sequences (see AAY06325-29), including the present

CC sequence, with EGIII cellulase from *Trichoderma reesei* (see
 CC AAY06330). These novel EGIII-like enzymes contain one or more of
 CC the conserved motifs. PCR primers (see AAX59180-91) based on the
 CC conserved motifs can be used to detect novel EGIII-like enzymes
 CC (see AAY06331-70) in fungal and bacterial sources. The invention
 CC also provides a vector comprising DNA encoding an EGIII-like
 CC enzyme, host cells and a method of producing a cellulase by
 CC culturing the host cell. The EGIII-like cellulases can be used in
 CC the treatment of a cellulose-containing textile, as a feed
 CC additive, in the treatment of wood pulp, in the reduction of
 CC biomass to glucose, in the stone washing of indigo dyed denim, or
 CC as a laundry detergent component (all claimed).
 XX
 SQ Sequence 6 AA;
 Query Match 22.2%; Score 4; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 EPPT 15
 Db |||||
 3 EPPT 6
 RESULT 28
 AAB14886
 ID AAB14886 standard; peptide; 6 AA.
 AC
 XX AAB14886;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE EGIII-like cellulase amino acid string #3.
 XX
 KW Endoglucanase III; EGIII; cellulase; mutant; *Trichoderma reesei*;
 KW enzyme stability; textile treatment; wood pulp treatment; feed additive;
 KW detergent.
 XX
 OS *Acetomonium brachyphenium*.
 OS *Chaetomium brasiliense*.
 OS *Chaetomium vitellium*.
 OS *Emericella desertoru*.
 OS *Fusarium equiseti*.
 OS *Gliocladium roseum*.
 OS *Humicola grisea*.
 OS *Myceliophthora thermophila*.
 OS *Penicillium notatum*.
 OS *Phanerochaete chrysosporium*.
 OS *Trichoderma reesei*.
 XX
 PN WO200037614-A2.
 XX
 XX 29-JUN-2000.
 PD
 XX 12-NOV-1999; 99WO-US26704.
 PF
 XX 18-DEC-1998; 98US-0216295.
 PR
 XX (GEMV) GENENCOR INT INC.
 PA
 XX Mitchinson C, Wendt DJ;
 PI
 XX WPI; 2000-482483/42.
 DR
 XX Novel endoglucanase III or endoglucanase III-like cellulase useful for
 PT treating textiles and wood pulp comprises a substitution or deletion at
 PT specified positions in the wild form of endoglucanase III
 XX
 PS Disclosure; Page 8; 52pp; English.
 XX
 CC The present sequence is an amino acid string found in all cellulases
 CC related to endoglucanase III (EGIII) from *Trichoderma reesei*. The
 CC sequence was used to design primers to amplify EGIII-like genes from

CC genomic DNA libraries constructed from various microorganisms. The
 CC isolated genes were found to share significant homology with EGIII from
 CC Trichoderma reesei. Certain substitution and deletion mutations have
 CC been incorporated into EGIII and EGIII-like cellulases to produce
 CC variant enzymes with improved stability, e.g. increased resistance to
 CC temperature stress. The mutants may be used in textile and wood pulp
 CC treatment, as a feed additive, and for reducing biomass to glucose.
 CC They are also useful for stonewashing or indigo dyed denim and as an
 CC agent in laundry and dish detergents.

SQ Sequence 6 AA;
 Query Match 22.2%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
 Db 3 EPFT 6
 |||||
 |||||

RESULT 29
 AAU77071
 ID AAU77071 standard; peptide; 6 AA.
 AC AAU77071;
 XX
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Endoglucanase EGIII-like cellulase BOX3 motif #1.
 XX
 KW EGIII; cellulase; BOX3; endoglucanase III; detergent;
 KW cellulose treatment; stonewashing; indigo dyed denim; feed additive;
 KW wood pulp treatment; biomass reduction; laundry; dish detergent;
 KW milling; depilling; softening; surface fibre removal; anti-greying.
 XX
 OS Acetomonium chrysogenum.
 OS Chaetomium brasiliense.
 OS Chaetomium vitellium.
 OS Emericella desertoru.
 OS Fusarium equiseti.
 OS Gliocladium roseum.
 OS Humicola grisea var thermoida.
 OS Myceliophthora thermophila.
 OS Penicillium notatum.
 OS Phanerochaete chrysosporium.
 XX
 FN WO200212466-A2.
 XX
 XX 14-FEB-2002.
 PD
 XX
 FF 31-JUL-2001; 2001WO-US23991.
 XX
 XX 04-AUG-2000; 2000US-0633085.
 PR
 XX (GEMV) GENENCOR INT INC.
 PA
 XX
 FI Day AG, Gualfetti P, Mitchinson C, Shaw A;
 XX
 XX WPI; 2002-241752/29.
 DR
 XX
 PT Novel variant of endoglucanase III or endoglucanase III-like cellulase
 PT for treating cellulose containing textile, has performance sensitive
 PT residues replaced to residue having modified stability -
 XX
 XX Disclosure; Page 6; 47pp; English.
 PS
 XX The invention relates to a variant of endoglucanase III (EGIII) or
 CC EGIII-like cellulase comprising a substitution or deletion at a position
 CC corresponding to one or more of residues W7, G31, A35, T145, Y147, Q162
 CC and/or Y168 in EGIII from Trichoderma reesei. Also included are a
 CC DNA encoding the variant, a vector comprising the DNA, a host cell
 CC transformed with the vector and a detergent composition comprising a

CC surfactant and the variant. The variant is useful in the treatment of a
 CC cellulose containing textile, stonewashing or indigo dyed denim or as a
 CC feed additive or in the treatment of wood pulp, in reduction of biomass
 CC to glucose. The detergent composition is useful as the main component of
 CC a laundry or dish detergent and is further useful as pre-wash
 CC composition, pre-soak composition or for cleaning during the regular wash
 CC or clean cycle. The variant increases value of animal feed, improves the
 CC drainability of food pulp, enhances food products and reduces fibre in
 CC grain during grain wet (or dry) milling process. Further cellulase
 CC improves the feel e.g. smoothness and/or appearance e.g. removing pills
 CC and fibrils which tend to reduce the sharpness in appearance of a
 CC fabric, of cellulose containing fabric, and imparts desirable effects
 CC such as depilling, softening, anti-pilling, surface fiber removal,
 CC anti-greying and cleaning. The present sequence is a BOX motif found
 CC in the EGIII-like cellulases, used to construct degenerate primers
 CC for isolation of the genes encoding the EGIII-like cellulases.

SQ Sequence 6 AA;
 Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
 Db 3 EPFT 6
 |||||
 |||||

RESULT 30
 AAU77438
 ID AAU77438 standard; peptide; 6 AA.
 XX
 AC AAU77438;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE EGIII-like cellulase consensus peptide #3.
 XX
 KW Endoglucanase III-like cellulase; EGIII-like; fungus;
 KW cellulose containing textile.
 XX
 OS Synthetic.
 OS WO200212464-A2.
 FN
 XX
 PD 14-FEB-2002.
 XX
 XX 31-JUL-2001; 2001WO-US23989.
 PF
 XX
 PR 04-AUG-2000; 2000US-0632426.
 XX
 XX (GEMV) GENENCOR INT INC.
 PA
 XX
 FI Mitchinson C, Ropp TH, Swanson BA;
 XX
 XX WPI; 2002-241750/29.
 DR
 XX
 XX Novel endoglucanase III (EGIII)-like cellulase variant comprising
 XX substitution/deletion at positions corresponding to specific residues
 XX in EGIII from Trichoderma reesei, useful for treating cellulose
 XX containing textile -
 PT
 PS Disclosure; Page 5; 41pp; English.
 XX
 XX The present invention relates to novel endoglucanase III (EGIII)-like
 CC cellulase variants which comprise a substitution or deletion at a
 CC position corresponding to one or more of residues W79, M154 and/or
 CC M18 in mature EGIII from the fungus, Trichoderma reesei. The variants
 CC are useful in the treatment of a cellulose containing textile. By
 CC substituting other amino acids for the native methionines at
 CC positions 79, 118 and 154 (sites where oxidation of the enzyme takes
 CC place) in EGIII from T. reesei, oxidatively more stable enzymes are
 CC obtained. The present sequence represents an EGIII-like cellulase

CC consensus peptide used to construct degenerate primers for the
 CC isolation of EGIII-like cellulases from different organisms.
 XX
 SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPFT 15
 DB 3 EPFT 6

RESULT 31
 AAU87807
 ID AAU87807 standard; Peptide; 6 AA.
 AC
 XX
 XX AAU87807;
 DT 05-JUN-2002 (first entry)
 XX
 DE Endoglucanase III (EGIII)-like cellulase peptide #3.

XX Endoglucanase III cellulase; EGIII; textile; stonewash;
 KW indigo dyed denim; wood pulp; feed additive; grain wet milling;
 KW grain dry milling; detergent; pre-wash composition;
 KW pre-soak composition; paper processing; surfactant mediated stress;
 KW thermal mediated stress.
 XX

OS Synthetic.

XX WO200212462-A2.

PN 14-FEB-2002.

XX 31-JUL-2001; 2001WO-US23946.

XX 04-AUG-2000; 2000US-0632570.

XX (GEMV) GENENCOR INT INC.

XX Mitchinson C, Gualfetti P, Phillips JI;

XX WPI; 2002-241748/29.

XX Variant endoglucanase-III, useful in treatment of cellulose containing
 PT textile and wood pulp, in treatment of biomass to glucose and as a feed
 PT additive, is a variant of EGIII from *Trichoderma reesei* -
 XX

PS Disclosure; Page 6; 44pp; English.

XX The invention describes a variant endoglucanase (EG)-III or EGIII-like
 CC cellulase (I), comprising a substitution or deletion at a position
 CC corresponding to residues P201, G370 and/or V210 in EGIII from
 CC *Trichoderma reesei*. (I) is useful in the treatment of a cellulose
 CC containing textile such as stonewashing or indigo dyed denim, in the
 CC treatment of wood pulp, in the reduction of biomass to glucose and as a
 CC feed additive. (I) is also useful in the treatment of starch during grain
 CC wet milling or dry milling to facilitate the production of glucose, high
 CC fructose corn syrup and/or alcohol. A detergent composition containing
 CC (I) is useful as pre-wash compositions, pre-soak compositions, and for
 CC cleaning during the regular wash or rinse cycle. (I) is useful in the
 CC processing of pulp and paper. (I) confers improved performance, including
 CC stability in the presence of thermal and/or surfactant mediated stress.
 CC This sequence represents a peptide encoded by a degenerate primer that
 CC can be used as a probe to identify EGIII-like cellulases in fungal
 CC genomic DNA.
 XX

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 EPFT 15
 DB 3 EPFT 6

RESULT 32
 AAW21388
 ID AAW21388 standard; peptide; 7 AA.
 XX
 XX AAW21388;
 DT 29-JUL-1997 (first entry)
 XX

XX Plasminogen activator inhibitor 1 derived signal oligopeptide #16.
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; prolactin;
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
 KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX Homo sapiens.

XX WO9519568-A1.

XX 20-JUL-1995.

XX 12-JAN-1995; 95WO-US00575.

XX 14-JAN-1994; 94US-0182248.

XX (RATH/) RATH M.

XX Rath M;

XX WPI; 1995-263953/34.

XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as
 PT regions of max. hydrophilicity, used in modulating communication
 PT between protein(s)
 XX
 PS Claim 5; Page 54; 88pp; English.

XX The sequences given in AAW21201-560 represent hydrophilic signal oligo-
 CC peptides. These signal oligopeptides are localised on the surface
 CC of the protein and are represented by the hydrophilicity maxima of
 CC the protein. These peptides are enriched in charged amino acids
 CC arranged with neutral spacer amino acids. The specific signal
 CC character of these oligopeptides is determined by a characteristic
 CC combination of conformation and charge within the signal sequence.
 CC These oligopeptides may be used as vaccines in the treatment of
 CC human disease, as competitive inhibitors to prevent or reduce the
 CC metabolic action or interaction of a selected protein by blocking
 CC its specific signal sequences, or as therapeutic agents to function
 CC as feedback regulators to reduce synthesis rate of a selected protein.
 CC These peptides may be modified by omitting one or more amino acids at
 CC the N- and/or C-terminal, by substituting one or more amino acids
 CC without consideration of charge and polarity, by substituting one or
 CC more amino acids with amino acid residues with similar charge and/or
 CC polarity, by omitting one or more amino acids or a combination of these.

XX Sequence 7 AA;

Query Match 22.2%; Score 4; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPPF 7
|
|
|
|
Db 2 MPPF 5

RESULT 33
AA96209
ID AAY96209 standard; Peptide; 7 AA.

XX AC AAY96209;
XX DT 11-AUG-2000 (first entry)
XX DE Arabidopsis AHAS small subunit F3 gene fragment N-terminal sequence.
XX KW Herbicide-resistance; acetohydroxy-acid synthase; AHAS;
KW acetolactate synthase; imidazolinone; sulfonyleurea;
KW triazopyrimidine sulfonamide; sulfamoylurea; enzyme;
KW pyrimidyl-oxy-benzoic acid; sulfonylecarboxamide; transgenic plant;
KW branched-chain amino acid synthesis.

XX OS Arabidopsis.

XX DN W0200026390-A2.

XX PD 11-MAY-2000.

XX PF 28-OCT-1999; 99WO-US25452.

XX PR 29-OCT-1998; 98US-0106239.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Kakefuda G, Costello C, Sun M, Hu W;

XX DR WPI; 2000-365633/31.

XX PT New polynucleotide encoding eukaryotic acetohydroxy-acid synthetase
small subunit protein for producing transgenic herbicide resistant
plants and identifying mutations affecting enzymatic activity of the
synthetase -

XX PS Disclosure; Page 25; 57pp; English.

XX CC Arabidopsis acetohydroxy-acid synthase (AHAS) small subunit is needed
for branched-chain amino acid synthesis and so is essential for life.
XX CC AHAS is also known as acetolactate synthase. Inhibition of this enzyme
in plants would lead to plant death and therefore inhibitors would be
XX CC potential herbicides. Certain herbicides are known to inhibit AHAS:
XX CC imidazolinones, sulfonyleureas, triazopyrimidine sulfonamides,
XX CC pyrimidyl-oxy-benzoic acids, sulfamoylureas and sulfonylecarboxamides.
XX CC Mutant AHAS may be resistant to these herbicides and may be used to
XX CC create herbicide resistant transgenic plants e.g. dicot and monocot crop
XX CC plants. A thrombin cleavage site was incorporated into an AHAS small
XX CC subunit gene. The AHAS small subunit gene fragments were cloned into
XX CC plasmid expression vectors, and were expressed as glutathione
XX CC transferase/ AHAS small subunit fusion proteins. The glutathione
XX CC transferase was then cleaved via the thrombin cleavage site. Cleavage
XX CC however modifies the N-terminal sequence of the AHAS small subunit gene
XX CC fragments, in that the glycine and serine residues of the cleavage site
XX CC are maintained on the AHAS protein. The present sequence details the
XX CC N-terminal sequence of one such AHAS small subunit gene fragment,
XX CC F3, which is a near full length AHAS small subunit gene, with the
XX CC modification due to cleavage.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
|
|
|
|
Db 3 VEPF 6

RESULT 34

AA61422
ID AAR61422 standard; peptide; 8 AA.

XX AC AAR61422;

XX DT 25-MAR-2003 (updated)

XX DT 25-AUG-1995 (first entry)

XX DE PF4-related octapeptide.

XX KW antiinflammatory; platelet factor 4; PF-4 autoimmune disease;
KW graft-versus-host; reperfusion injury; atherosclerosis; asthma.

XX OS Synthetic.

XX PN W09500543-A1.

XX PD 05-JAN-1995.

XX PF 17-JUN-1994; 94WO-US06888.

XX PR 18-JUN-1993; 93US-0080371.

XX PA (COUN/) COUNTS D F.

XX PA (DUFF/) DUFF R G.

XX PI Counts DF, Duff RG;

XX DR WPI; 1995-052005/07.

XX PT New peptide(s) and derivs. based on platelet factor 4 - used for
inhibiting an immune response, including an inflammatory response
in e.g. autoimmune diseases.

XX PS Disclosure; Page 44; 99pp; English.

XX CC New peptides are disclosed which include any peptide, peptide
XX CC derivative or peptide analogue which comprises either (i) at least a
XX CC 4 amino acid portion of PF-4 (see AAR61401) or a functionally equivalent
XX CC sequence, or (ii) at least a 6 amino acid sequence which is at least
XX CC 66% homologous to a portion of the PF-4 sequence, or a functionally
XX CC equivalent sequence. Pref. the peptide contains the sequence
XX CC Thr-Ser-Gln and/or Val-Arg-Pro, and more preferably Thr-Thr-Ser-Gln
XX CC and/or Val-Arg-Pro-Arg. The most preferred peptide is
XX CC Thr-Thr-Ser-Gln-Val-Arg-Pro-Arg (see AAR61393), designated CT-112.
XX CC The peptide may be derivatised at the N- and/or C-terminal, or may be
XX CC cyclised, substituted, truncated or contain D-amino acid residues.
XX CC The present sequence is an analogue CT-112 containing Glu substitution.
XX CC The peptides exhibit antiinflammatory activity and may be used to treat
XX CC autoimmune diseases (such as insulin-dependent diabetes, ulcerative
XX CC colitis, rheumatoid arthritis, scleroderma, mixed connective tissue
XX CC disease and SLE), reperfusion tissue damage, inflammatory lung disease,
XX CC graft-versus-host disease, atherosclerosis and asthma.
XX CC When tested for antiinflammatory activity by a single 6 mg/kg
XX CC subcutaneous dose using the mouse ear acute inflammation model,
XX CC peptide CT-112 gave an inhibition value of 64.9%. In comparison,
XX CC the present sequence gave a value of 43.2%.
XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|
|
|
|

Db 1 TESQ 4

RESULT 35
AAW05539
ID AAW05539 standard; peptide; 8 AA.
AC AAW05539;
XX
XX 17-JUN-1997 (first entry)
XX
XX Peptide fragment #1 of aminopeptidase of the invention.
XX
XX Aminopeptidase; aspergillus oryzae; enzyme; protein hydrolysate; gluten;
KW protease; N-terminus.
KW
XX Aspergillus oryzae.
XX
XX WO9628542-A1.
XX
XX 19-SEP-1996.
XX
XX 15-MAR-1996; 96WO-DK00104.
XX
XX 16-MAR-1995; 95DK-0000262.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Dambmann C, Halkier T, Kauppinen S, Ostergaard PR;
PI Si JQ, Spendler T;
XX
XX WPI; 1996-464617/46.
XX
XX Enzyme with aminopeptidase activity - used in bread or
PT dough-improving compens., and to reduce the bitter taste of proteins
PT or protein hydrolysates for foodstuffs, partic. cheese or cocoa
XX
XX Claim 7; Page 56; 75pp; English.
XX
XX AAW05538-W05543 represent fragments of the Aspergillus oryzae
CC aminopeptidase (see AAW05589) of the invention. Aminopeptidases are
CC capable of removing one or more amino terminal residues from
CC polypeptides. The enzyme is used in a preparation to reduce the bitter
CC taste of proteins or protein hydrolysates for foodstuffs, particularly
CC cheese or cocoa, so improving their flavour. It is also useful in a bread
CC or dough-improving composition, and in the preparation of baked products
CC from a flour dough or frozen dough. The enzyme is also useful to improve
CC dough stickiness, crumb structure or crust colour of a baked product. The
CC enzyme preparation can also be used to clean contact lenses and in
CC brewing. The enzyme does not degrade the network of the gluten normally
CC seen when proteases are used in the preparation of baked products. Thus,
CC the dough characteristics and crumb structure are unaffected.
XX
XX Sequence 8 AA;
SQ

Query Match 22.2%; Score 4; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
| | | |
Db 4 VEPF 7

RESULT 36
AAW58608
ID AAW58608 standard; peptide; 8 AA.
XX
XX AAW58608;
AC
XX 25-MAR-2003 (updated)
DT 08-SEP-1998 (first entry)
XX

DE Platelet factor 4 derived peptide SEQ ID NO:30.
XX
XX Platelet factor 4; PF4; anti-inflammatory; inhibition; inflammation;
KW autoimmune disease; graft versus host disease; reperfusion injury;
KW atherosclerosis; asthma.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX US5776892-A.
PN
XX 07-JUL-1998.
XX
XX 16-JUN-1994; 94US-0259550.
PF
XX 16-JUN-1994; 94US-0259550.
PR 21-DEC-1990; 90US-0631823.
XX
PR 24-MAR-1993; 93US-0037486.
XX
PR 18-JUN-1993; 93US-0080371.
XX
XX (CURA-) CURATIVE HEALTH SERVICES INC.
PA
XX Counts DF, Duff RG;
PI
XX WPI; 1998-398086/34.
XX
XX New antiinflammatory peptide(s) based on platelet factor 4 sequences
PT - used for treating e.g. autoimmune diseases, graft versus host
PT disease, reperfusion injury, atherosclerosis or asthma
XX
XX Claim 2; Column 75; 55pp; English.
XX
XX The present sequence represents a peptide which is related to platelet
CC factor 4 (PF4) and can be used to inhibit an inflammatory response.
CC Peptides, peptide analogues and peptide derivatives of PF4 can be used
CC for treating e.g. autoimmune diseases such as insulin dependent
CC diabetes, Goodpasture's syndrome, pemphigus and pemphigoid, primary
CC biliary cirrhosis, ulcerative colitis, rheumatoid arthritis,
CC scleroderma, mixed connective tissue disease and lupus erythematosus,
CC graft versus host disease, septic shock, reperfusion injury (including
CC injury subsequent to myocardial or cerebral infarction),
CC atherosclerosis, asthma and inflammatory lung disease. The peptides
CC give a new and effective method of inhibiting the inflammatory response
CC by acting on cytokines rather than the prior art arachidonic acid.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 8 AA;
SQ

Query Match 22.2%; Score 4; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
| | | | |
Db 1 TESQ 4

RESULT 37
AAB45558
ID AAB45558 standard; Protein; 9 AA.
XX
XX AAB45558;
AC
XX
XX 02-MAR-2001 (first entry)
DT
XX Human B99-1 HLA B*4403 immunogenic peptide SEQ ID NO 95.
DE
XX Tumor-associated antigen; B99; immunogenic; humoral immune response;
KW cellular immune response; immunotherapy; cancer; kidney; lung; colon;
KW pancreas; breast; stomach; vaccine; diagnosis; treatment.
XX
XX Homo sapiens.
OS

XX	Claim 11; Page 65; 130pp; English.				
XX					
XX	Sequences AA72398-Y73086 represent hepatitis B virus (HBV)-derived MHC				
CC	class I (CTL) epitopes which are claimed for use in the present				
CC	invention. The invention relates to a novel expression vector comprising				
CC	a promoter operably linked to a fusion gene encoding a major				
CC	histocompatibility complex (MHC) targetting sequence, and two or more				
CC	heterologous peptide epitopes. The MHC targetting sequence may be a				
CC	class I targetting sequence, which directs an MHC class I epitope to				
CC	a cytosolic pathway or to the endoplasmic reticulum, or an MHC class				
CC	II targetting sequence, which directs extracellular antigens to				
CC	enter the endocytic pathway to be processed into antigen peptides				
CC	for presentation on MHC class II molecules. The heterologous				
CC	epitopes may comprise either helper T lymphocyte (HTL) epitopes,				
CC	or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL				
CC	epitope such as a pan DR epitope (PADRE). The vectors are useful				
CC	for stimulating an immune response in vivo, as well as for use in				
CC	assaying the human immunogenicity of a human T cell peptide epitope in				
CC	vivo in a non-human mammal. They provide a nucleic acid vaccine for				
CC	enhancing immunity against infectious pathogens, such as viruses (e.g.,				
CC	HIV, hepatitis B (HBV and hepatitis C (HCV)) bacteria, protozoa (e.g.,				
CC	Plasmodium falciparum, the cause of malaria) and also tumour cells and				
CC	autoimmune diseases. Universal MHC class II epitopes are advantageously				
CC	combined with other MHC class I and class II epitopes to increase the				
CC	number of cells that are activated in response to a given antigen and				
CC	provide a broader population coverage of MHC-reactive alleles.				
XX					
XX	Sequence 9 AA;				
XX					
XX	Query Match 22.2%; Score 4; DB 21; Length 9;				
XX	Best Local Similarity 100.0%; Pred. No. 9.3e+05;				
XX	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX					
Qy	14 FTES 17				
DB					
DB	2 FTES 5				
XX					
XX	RESULT 40				
XX	AA24524				
ID	AA24524 standard; Peptide; 9 AA.				
XX	AA24524;				
XX					
DT	04-DEC-2001 (first entry)				
XX					
DE	Human MHC class I molecule HLA-A1 binding 83P5G4 peptide #1.				
XX					
KW	83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;				
KW	tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;				
KW	cytosolic; gene therapy; antibody therapy; ribozyme; blood; cervix;				
KW	single chain monoclonal antibody; urine; uterus; rectum; stomach; human;				
XX	chromosome iq31-q32.				
XX					
XX	Homo sapiens.				
XX					
PN	WO200159115-A2.				
XX					
XX	16-AUG-2001.				
PD					
XX	09-FEB-2001; 2001WO-US04426.				
XX					
PF	09-FEB-2000; 2000US-0181261.				
XX					
PR	(UROC-) UROGENESYS INC.				
XX					
PA	Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;				
XX	Mitchell SC, Jakobovits A;				
PI					
XX	WPI; 2001-514669/56.				
XX					
XX	An isolated 83P5G4-related protein useful as a diagnostic and/or				
PT					

therapeutic agent in multiple cancers such as prostate, bladder and bone cancer -

Example 15; Page 74; 112pp; English.

The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||||
DB 2 TESQ 5

RESULT 41
AAM24745
ID AAM24745 standard; Peptide; 9 AA.
XX
AC AAM24745;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-A3 binding 83P5G4 peptide #22.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytosolic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PW WO200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181361.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DBH, Challita-eid PM, Paris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
PT An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX
PS Example 15; Page 79; 112pp; English.

The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
 ||||
 Db 2 TESQ 5

RESULT 42
 AAM24826
 ID AAM24826 standard; Peptide; 9 AA.

XX AC AAM24826;

DT 04-DEC-2001 (first entry)

XX DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #3.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 XX cytosatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.

XX OS Homo sapiens.

XX PN WO200159115-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX PR 09-FEB-2000; 2000US-0181261.

XX PA (UROG-) UROGENESYS INC.

XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX PL Mitchell SC, Jakobovits A;

XX DR WPI; 2001-514669/56.

XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or
 PT therapeutic agent in multiple cancers such as prostate, bladder and
 PT bone cancer -

XX PS Example 15; Page 81; 112pp; English.

XX CC The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
 ||||
 Db 2 TESQ 5

RESULT 43
 AAM24925
 ID AAM24925 standard; Peptide; 9 AA.

XX AC AAM24925;

DT 04-DEC-2001 (first entry)

XX DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #2.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 XX cytosatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.

XX OS Homo sapiens.

XX PN WO200159115-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX PR 09-FEB-2000; 2000US-0181261.

XX PA (UROG-) UROGENESYS INC.

XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX PL Mitchell SC, Jakobovits A;

XX DR WPI; 2001-514669/56.

XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or
 PT therapeutic agent in multiple cancers such as prostate, bladder and
 PT bone cancer -

XX PS Example 15; Page 84; 112pp; English.

XX CC The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TESQ 18
| | | |
Db 4 TESQ 7
| | | |
RESULT 44
AAU94282
ID AAU94282 standard; Peptide; 9 AA.
AC AAU94282;
XX
XX 02-JUL-2002 (first entry)
XX Human novel protein CaTrF2E11 HLA binding peptide #115.
XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX
OS Homo sapiens.
XX
XX WO200214361-A2.
FN
XX
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US25782.
PF
XX 17-AUG-2000; 2000US-226329P.
PR
XX (AGEN-) AGENSYS INC.
PA
PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX WPI; 2002-269179/31.
DR
XX
XX Monitoring 83P2H3 gene products for monitoring the presence of cancer
PT in a subject, comprises determining the status of 83P2H3 gene products
PT in a tissue sample from the subject and comparing it to a normal sample
PI
XX
XX Example 11; Page 172; 270pp; English.
XX
XX The invention relates to monitoring 83P2H3 (a calcium transport
CC protein whose gene is located on chromosome 7q34) gene products in a
CC biological sample from a patient who has or is suspected of having
CC cancer (especially prostate cancer), comprises: (a) determining the
CC status of 83P2H3 gene products expressed by cells in a tissue sample from
CC an individual and (b) comparing the status to the status of 83P2H3 gene
CC products in a normal sample. Also included are modulators of 83P2H3
CC function or status, generating antibodies/immune response against
CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding
CC peptides derived from the protein, delivering a cytotoxic agent to
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
CC antibody, a recombinant protein comprising an antigen-binding region of
CC the antibody, a non-human transgenic animal that produces the recombinant
CC protein, a hybridoma that produces the recombinant protein, a single-
CC chain monoclonal antibody that comprises the variable domains of the
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for

CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CaTrF2E11.
XX
XX SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KYPV 11
| | | |
Db 6 KYPV 9
| | | |
RESULT 45
AAU94868
ID AAU94868 standard; Peptide; 9 AA.
AC AAU94868;
XX
XX 02-JUL-2002 (first entry)
XX Human novel protein CaTrF2E11 HLA binding peptide #401.
XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX
OS Homo sapiens.
XX
XX WO200214361-A2.
FN
XX
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US25782.
PF
XX 17-AUG-2000; 2000US-226329P.
PR
XX (AGEN-) AGENSYS INC.
PA
PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX WPI; 2002-269179/31.
DR
XX
XX Monitoring 83P2H3 gene products for monitoring the presence of cancer
PT in a subject, comprises determining the status of 83P2H3 gene products
PT in a tissue sample from the subject and comparing it to a normal sample
PI
XX
XX Example 11; Page 193; 270pp; English.
XX
XX The invention relates to monitoring 83P2H3 (a calcium transport
CC protein whose gene is located on chromosome 7q34) gene products in a
CC biological sample from a patient who has or is suspected of having
CC cancer (especially prostate cancer), comprises: (a) determining the
CC status of 83P2H3 gene products expressed by cells in a tissue sample from
CC an individual and (b) comparing the status to the status of 83P2H3 gene
CC products in a normal sample. Also included are modulators of 83P2H3
CC function or status, generating antibodies/immune response against
CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding
CC peptides derived from the protein, delivering a cytotoxic agent to
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
CC antibody, a recombinant protein comprising an antigen-binding region of
CC the antibody, a non-human transgenic animal that produces the recombinant
CC protein, a hybridoma that produces the recombinant protein, a single-
CC chain monoclonal antibody that comprises the variable domains of the
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for

CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11

Db 1 KYPV 4

RESULT 46

AAU95255

ID AAU95255 standard; Peptide; 9 AA.

AC AAU95255;

DT 02-JUL-2002 (first entry)

DE Human novel protein CaTrF2E11 HLA binding peptide #588.

XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US25782.

XX 17-AUG-2000; 2000US-226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Bid PM, Faris M, Safran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;

XX WPI; 2002-269179/31.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer
 PT in a subject, comprises determining the status of 83P2H3 gene products
 PT in a tissue sample from the subject and comparing it to a normal sample

XX

PS Example 11; Page 208; 270pp; English.

XX The invention relates to monitoring 83P2H3 (a calcium transport
 CC protein whose gene is located on chromosome 7q34) gene products in a
 CC biological sample from a patient who has or is suspected of having
 CC cancer (especially prostate cancer), comprises: (a) determining the
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from
 CC an individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3 gene
 CC function or status, generating antibodies/immune response against
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding
 CC peptides derived from the protein, delivering a cytotoxic agent to
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11

Db 4 KYPV 7

RESULT 47

ABJ20159

ID ABJ20159 standard; Peptide; 9 AA.

AC ABJ20159;

XX 10-APR-2003 (first entry)

XX MHC binding peptide SEQ ID No 324.

XX Antirheumatic; antiallergic; antiarthritic; neurotropic; neuroprotective;
 KW antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.

XX Synthetic.

XX WO200294981-A2.

XX 28-NOV-2002.

XX 16-MAY-2002; 2002WO-IL00393.

XX 16-MAY-2001; 2001US-290958P.
 PR 29-MAY-2001; 2001US-0865548.
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 XX Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
 XX WPI; 2003-210043/20.
 XX Identifying peptides that are capable of binding to major
 PT histocompatibility complex (MHC) molecules of a particular haplotype by
 PT analyzing peptides bound to the soluble and secreted form of the MHC
 PT molecules of the particular haplotype -
 XX Claim 58; Page 226; 238pp; English.
 XX The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention.
 XX Sequence 9 AA;
 SQ Query Match 22.2%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 EPFT 15
 DB |||||
 5 EPFT 8
 RESULT 48
 AAY94204
 ID AAY94204 standard; peptide; 10 AA.
 XX AC
 XX AAY94204;
 XX 28-JUL-2000 (first entry)
 XX Human cytotoxic T lymphocyte-recognised gata-1 peptide hug 378-87.
 XX Hug 378-87; peptide; epitope; gata-1 gene; leukaemia; immunotherapy;
 KW transcription factor.
 XX Homo sapiens.
 XX WO200026249-A1.
 XX 11-MAY-2000.
 XX 02-NOV-1999; 99WO-GB03572.
 XX 02-NOV-1998; 98GB-0023897.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Stauss HJ, Gao L;
 XX WPI; 2000-376123/32.
 XX Novel peptides comprising WT-1 and GATA-1 epitopes, their fragments or
 PT variants, useful as vaccines for cancer immunotherapy -
 XX

PS Claim 3; Page 74; 93pp; English.
 XX The present sequence is peptide epitope hug 378-87, produced by gata-1
 CC expressing cells and found at residues 378-387 of the gata-1 protein,
 CC which is recognised by cytotoxic T lymphocytes. Gata-1 is aberrantly
 CC expressed in leukaemias. The peptide can be used as a vaccine to
 CC stimulate the elimination, by cytotoxic T lymphocytes, of cancer cells
 CC aberrantly expressing gata-1. In addition, the nucleic acid encoding the
 CC peptide may also be used in the same manner. Alternatively, the peptide
 CC may be used in vitro to produce activated cytotoxic T lymphocytes.
 XX Sequence 10 AA;
 SQ Query Match 22.2%; Score 4; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MPFP 7
 DB |||||
 3 MPFP 6
 RESULT 49
 AAG68075
 ID AAG68075 standard; peptide; 10 AA.
 XX AC
 XX AAG68075;
 XX 17-DEC-2001 (first entry)
 XX Antitumour cancer cell recognition peptide PI9-9.
 XX Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.
 XX Homo sapiens.
 XX JP2001245675-A.
 XX 11-SEP-2001.
 XX 25-DEC-2000; 2000JP-0393047.
 XX 28-DEC-1999; 99JP-0374322.
 XX (ITOY/) ITO Y.
 XX WPI; 2001-610076/70.
 XX New peptides for recognizing cancer cells with tumor specific cytotoxic
 PT T lymphocytes and for treating cancer -
 XX Example 1; Page 10; 14pp; Japanese.
 XX The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides
 CC of sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity
 CC with the above mentioned sequences; and (4) peptides with one or more
 CC deleted, substituted, added or inserted amino acid(s) of the above
 CC mentioned sequences, particularly those having recognising property due
 CC to HLA-A2402 binding CTL, especially having at least 5 amino acids,
 CC used for medicine, particularly anticancer agents, derived from
 CC antitumour antigenic peptides of lck, src family, SART-1, SART-3 or
 CC cyclophilin B genes. The antitumour peptides have cytostatic activities.
 CC The peptides are used for the treatment of cancer. The peptides cause
 CC activation of CTL in cancer patients. The present sequence represents
 CC a peptide used in an example from the present invention.
 XX Sequence 10 AA;
 SQ

Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMPF 6
|||
DB 5 EMPF 8

RESULT 50
AAB75678
ID AAB75678 standard; Peptide; 10 AA.
XX AC AAB75678;
XX 10-APR-2001 (first entry)
XX DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:81.
XX Human; cancer associated antigen precursor; cancer associated antigen;
KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
KW vaccine; cancer.
XX OS Homo sapiens.
XX WO200100874-A2.
XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-US17207.
XX 30-JUN-1999; 99US-0346498.
XX (LUDW-) LUDWIG INST CANCER RES.
XX PI Sahin U, Tureci O, Pfreundschuh M;
XX WPI; 2001-112465/12.
XX Diagnosing a disorder characterized by expression of a human cancer
PT associated antigen precursor; comprises detecting interaction of an
PT agent with a nucleic acid molecule encoding the antigen precursor -
XX

PS Example 10; Page 63; 126pp; English.

XX The present invention describes a method for diagnosing a disorder
CC characterised by expression of a human cancer associated antigen (CAA)
CC precursor (I) coded by a NA Group 1 nucleic acid molecule (N1)
CC comprising contacting the biological sample with an agent (A) that
CC specifically binds to N1, (I) or its fragment, complexed with an human
CC leukocyte antigen (HLA) molecule and determining the interaction between
CC the agent and N1 or (I). (I) has cytostatic activity and can be used in
CC gene therapy and vaccine production. The method can be used for treating
CC a subject with a condition characterised by expression of (I) in cells
CC of a subject. AAB75607 and AAB75608 represent proteins from human cancer
CC associated antigen precursors, and AAB75609 to AAB75802 represent HLA
CC class I binding motifs in human cancer associated antigen precursors
CC given in the exemplification of the present invention.
XX

SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
|||
DB 5 PVEP 8

RESULT 51
AAB49971
ID AAB49971 standard; peptide; 10 AA.

XX AAB49971;
XX 08-MAR-2001 (first entry)
XX Human melanoma associated antigen MAGE-12 peptide.
XX Human; melanoma associated antigen; vaccine; cancer; immunogen.
XX OS Homo sapiens.
XX WO2000071573-A2.
XX 30-NOV-2000.
XX 17-MAY-2000; 2000WO-EP04465.
XX 21-MAY-1999; 99IT-MI01121.
XX (GENE-) GENERA SPA.
XX Traversari C, Tanzarella S, Bordignon C;
XX WPI; 2001-032020/04.
XX Novel peptides that bind to allele HLA-B (asterisk)3701, useful for
PT preparing anti-tumour medicament, and as a cancer vaccine -
XX Claim 1; Page 23; 33pp; English.
XX The present invention provides novel peptides based on the melanoma
CC associated antigens MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5 and MAGE-12.
CC These peptides can be used in vaccines to treat cancer, particularly
CC melanoma.
XX SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPFT 15
|||
DB 2 EPFT 5

RESULT 52
AAM24575
ID AAM24575 standard; Peptide; 10 AA.

XX AC AAM24575;
XX 04-DEC-2001 (first entry)
XX Human MHC class I molecule HLA-A1 binding 83P5G4 peptide #52.
XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.

XX OS Homo sapiens.
XX WO200159115-A2.
XX 16-AUG-2001.
XX 09-FEB-2001; 2001WO-US04426.
XX 09-FEB-2000; 2000US-0181261.
XX (UROG-) UROGENESYS INC.
XX PA

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
 PI Mitchell SC, Jakobovits A;
 XX WPI; 2001-514669/56.
 XX
 XX An isolated 83P5G4-related protein useful as a diagnostic and/or
 PT therapeutic agent in multiple cancers such as prostate, bladder and
 PT bone cancer -
 XX
 XX Example 15; Page 75; 112pp; English.
 XX
 XX The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 22.2%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TESQ 18
 Db 2 TESQ 5
 |||||
 RESULT 53
 AAM24783
 ID AAM24783 standard; Peptide; 10 AA.
 XX
 AC AAM24783;
 XX
 XX 04-DEC-2001 (first entry)
 DT
 XX
 DE Human MHC class I molecule HLA-A3 binding 83P5G4 peptide #60.
 XX
 XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200159115-A2.
 PN
 XX
 XX 16-AUG-2001.
 PD
 XX
 XX 09-FEB-2001; 2001WO-US04426.
 PF
 XX
 XX 09-FEB-2000; 2000US-0181261.
 PR
 XX
 XX (UROG-) UROGENESYS INC.
 PA
 XX
 XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
 PI Mitchell SC, Jakobovits A;
 XX WPI; 2001-514669/56.
 XX
 XX An isolated 83P5G4-related protein useful as a diagnostic and/or

PT therapeutic agent in multiple cancers such as prostate, bladder and
 PT bone cancer -
 XX
 XX Example 15; Page 80; 112pp; English.
 XX
 XX The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 22.2%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TESQ 18
 Db 5 TESQ 8
 |||||
 RESULT 54
 AAM24905
 ID AAM24905 standard; Peptide; 10 AA.
 XX
 AC AAM24905;
 XX
 XX 04-DEC-2001 (first entry)
 DT
 XX
 DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #82.
 XX
 XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200159115-A2.
 PN
 XX
 XX 16-AUG-2001.
 PD
 XX
 XX 09-FEB-2001; 2001WO-US04426.
 PF
 XX
 XX 09-FEB-2000; 2000US-0181261.
 PR
 XX
 XX (UROG-) UROGENESYS INC.
 PA
 XX
 XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
 PI Mitchell SC, Jakobovits A;
 XX WPI; 2001-514669/56.
 XX
 XX An isolated 83P5G4-related protein useful as a diagnostic and/or
 PT therapeutic agent in multiple cancers such as prostate, bladder and
 PT bone cancer -
 XX
 XX Example 15; Page 83; 112pp; English.
 XX
 XX The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific

CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
 ||||
 Db 3 TESQ 6

RESULT 55
 AAM24911
 ID AAM24911 standard; Peptide; 10 AA.

XX AAM24911;

DT 04-DEC-2001 (first entry)

XX Human MHC molecule HLA-A11 binding 83P5G4 peptide #88.

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytotactic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.

XX Homo sapiens.

XX WO200159115-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04426.

XX 09-FEB-2000; 2000US-0181261.

XX (UROG-) UROGENESYS INC.

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX Mitchell SC, Jakobovits A;

XX WPI; 2001-514669/56.

XX Example 15; Page 84; 112pp; English.
 CC The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
 ||||
 Db 2 TESQ 5

RESULT 56
 AAM24914
 ID AAM24914 standard; Peptide; 10 AA.

XX AAM24914;

XX 04-DEC-2001 (first entry)

XX Human MHC molecule HLA-A11 binding 83P5G4 peptide #91.

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytotactic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.

XX Homo sapiens.

XX WO200159115-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04426.

XX 09-FEB-2000; 2000US-0181261.

XX (UROG-) UROGENESYS INC.

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX Mitchell SC, Jakobovits A;

XX WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or
 therapeutic agent in multiple cancers such as prostate, bladder and
 bone cancer -

XX Example 15; Page 84; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 CC many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 CC peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells.

XX

```

SQ Sequence 10 AA;
Query Match      22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 4 TESQ 7

RESULT 57
AAM25003
ID AAM25003 standard; Peptide; 10 AA.
XX
AC AAM25003;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #80.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN WO200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
PT An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX
PS Example 15; Page 86; 112pp; English.
XX
CC The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
SQ Sequence 10 AA;
Query Match      22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 4 TESQ 7

RESULT 58
AAM25222
ID AAM25222 standard; Peptide; 10 AA.
XX
AC AAM25222;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC molecule HLA-B35 binding 83P5G4 peptide #99.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN WO200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
PT An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX
PS Example 15; Page 92; 112pp; English.
XX
CC The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
SQ Sequence 10 AA;
Query Match      22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 5 TESQ 8

RESULT 59
AAO17822
ID AAO17822 standard; peptide; 10 AA.

```


XX Homo sapiens.
XX AAU95356
XX WO200214361-A2.
XX AC
XX AAU95356;
XX PD 21-FEB-2002.
XX DT 02-JUL-2002 (first entry)
XX DE Human novel protein CaTrF2E11 HLA binding peptide #639.
XX XX
XX KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
XX KW calcium transport protein; cancer; prostate cancer; cytostatic;
XX KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200214361-A2.
XX XX
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US25782.
XX PR 17-AUG-2000; 2000US-226329P.
XX PS (AGEN-) AGENSYS INC.
XX XX
XX PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
XX PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX XX
XX DR WPI; 2002-269179/31.
XX XX
XX PT Monitoring 83P2H3 gene products for monitoring the presence of cancer
XX PT in a subject, comprises determining the status of 83P2H3 gene products
XX PT in a tissue sample from the subject and comparing it to a normal sample
XX PT -
XX XX
XX PS Example 11; Page 177; 270pp; English.
XX XX
XX CC The invention relates to monitoring 83P2H3 (a calcium transport
XX CC protein whose gene is located on chromosome 7q34) gene products in a
XX CC biological sample from a patient who has or is suspected of having
XX CC cancer (especially prostate cancer), comprises: (a) determining the
XX CC status of 83P2H3 gene products expressed by cells in a tissue sample from
XX CC an individual and (b) comparing the status to the status of 83P2H3 gene
XX CC products in a normal sample. Also included are modulators of 83P2H3
XX CC function or status, generating antibodies/immune response against
XX CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
XX CC 12q24.1) using identified HLA (human leukocyte antigen) binding
XX CC peptides derived from the protein, delivering a cytotoxic agent to
XX CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
XX CC antibody, a recombinant protein comprising an antigen-binding region of
XX CC the antibody, a non-human transgenic animal that produces the recombinant
XX CC protein, a hybridoma that produces the recombinant protein, a single-
XX CC chain monoclonal antibody that comprises the variable domains of the
XX CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
XX CC polynucleotide that encodes the monoclonal antibody and inducing an
XX CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
XX CC protein that comprises a T cell or B cell epitope, and contacting the
XX CC epitope with an immune system T cell or B cell, respectively. The method
XX CC is useful for monitoring 83P2H3 gene products in a biological sample for
XX CC monitoring the presence of cancer in an individual. The modulator is
XX CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
XX CC treating cancer and the vector is useful for treating a patient with a
XX CC cancer that expresses 83P2H3. The immunological methods are useful for
XX CC generating an immune response against 83P2H3, and for detecting the
XX CC presence of 83P2H3-related protein or polynucleotide in a biological
XX CC sample from a patient who has or who is suspected of having cancer. The
XX CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
XX CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
XX CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
XX CC isolating 83P2H3 homologues/related molecules, and for generating anti-
XX CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
XX CC is an HLA binding peptide motif from 83P2H3 or its related protein
XX CC CaTrF2E11.
XX XX
XX SQ Sequence 10 AA;
XX XX
XX Query Match 22.2%; Score 4; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 4.2e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX Qy 8 KYPV 11
XX |||||
XX Db 7 KYPV 10

CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
 CC neutrophils, monocytes and endothelial cells or involving acute or
 CC chronic inflammation reactions. The diseases or disorders include
 CC cardiovascular diseases, disease of the central nervous system,
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
 CC diseases, respiratory diseases and HIV infection.
 XX
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPK 8
 |||||
 Db 5 PPK 8

RESULT 65
 ABR47239
 ID ABR47239 standard; Peptide; 10 AA.
 XX
 AC ABR47239;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #2428.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP08004.
 XX
 PR 11-JUL-2001; 2001WO-EP08004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 WPI; 2003-247783/25.
 XX
 DR The present invention relates to peptides (ABR44811-ABR47162 and
 XX ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
 PT from Staphylococcus aureus. The peptide fragments are useful in the
 PT prophylaxis or treatment of diseases or disorders involving the
 PT kidney diseases -
 XX
 PS Example 1; Page 55; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and
 CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
 CC from Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the
 CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
 CC neutrophils, monocytes and endothelial cells or involving acute or
 CC chronic inflammation reactions. The diseases or disorders include
 CC cardiovascular diseases, disease of the central nervous system,
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
 CC diseases, respiratory diseases and HIV infection.
 XX
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPFT 15
 |||||
 Db 4 EPFT 7

RESULT 66
 ABR47292
 ID ABR47292 standard; Peptide; 10 AA.
 XX
 AC ABR47292;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #2481.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP08004.
 XX
 PR 11-JUL-2001; 2001WO-EP08004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 WPI; 2003-247783/25.
 XX
 DR Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases -
 XX
 PS Example 1; Page 56; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and
 CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
 CC from Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the
 CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
 CC neutrophils, monocytes and endothelial cells or involving acute or
 CC chronic inflammation reactions. The diseases or disorders include
 CC cardiovascular diseases, disease of the central nervous system,
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
 CC diseases, respiratory diseases and HIV infection.
 XX
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPFP 7
 |||||
 Db 4 MPFP 7

```

RESULT 67
ABR47319
ID ABR47319 standard; Peptide; 10 AA.
XX AC
XX ABR47319;
XX 10-JUN-2003 (first entry)
DT DT
XX DE
XX DE Staphylococcus aureus CHIPS-related peptide #2508.
XX KW
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
XX KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
XX KW inflammation; cardiovascular disease; central nervous system disease;
XX KW gastrointestinal disease; skin disease; genitourinary disease;
XX KW joint disease; respiratory disease; HIV infection; antiinflammatory;
XX KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
XX KW gynecological; immunosuppressive; anti-HIV.
XX OS
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PN
XX PN WO200306048-A1.
XX PD
XX PD 23-JAN-2003.
XX PF
XX PF 11-JUL-2001; 2001WO-EP08004.
XX PR
XX PR 11-JUL-2001; 2001WO-EP08004.
XX PA
XX PA (JARI-) JARI PHARM BV.
XX PI
XX PI Van Kessel CPM, Gosselaar-de Haas CUC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX DR
XX DR WPI; 2003-247783/25.
XX PT
XX PT Combination of peptides derived from chemotaxis inhibiting protein from
XX PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX PT prophylaxis and treatment of inflammation, cardiovascular, skin and
XX PT kidney diseases -
XX XX
XX XX Example 1; Page 56; 89pp; English.
XX CC
XX CC The present invention relates to peptides (ABR44811-ABR47162 and
XX CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
XX CC from Staphylococcus aureus. The peptide fragments are useful in the
XX CC prophylaxis or treatment of diseases or disorders involving the
XX CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
XX CC neutrophils, monocytes and endothelial cells or involving acute or
XX CC chronic inflammation reactions. The diseases or disorders include
XX CC cardiovascular diseases, disease of the central nervous system,
XX CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
XX CC diseases, respiratory diseases and HIV infection.
XX SQ
XX SQ Sequence 10 AA;
XX Query Match 22.2%; Score 4; DB 24; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 4.2e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY
XX QY 11 VEPF 14
XX DB
XX DB 3 VEPF 6
XX RESULT 68
AAR41812
ID AAR41812 standard; Protein; 11 AA.
XX AC
XX AC AAR41812;
XX OS
30-MAR-1994 (first entry)
XX DE
XX DE MI3TMD1 mutated fragment.
XX KW
XX KW Transformation; fungus; blood coagulation; prevention; platelet;
XX KW aggregation; thrombolytic activity; thrombolysis; human thrombomodulin;
XX KW site-directed mutagenesis; promotion; protein C; activation;
XX KW thrombin.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT
XX FT Misc-difference 6 /note= "Asp replaced by Glu"
XX PN
XX PN JP05213998-A.
XX XX
XX XX 24-AUG-1993.
XX XX
XX XX 02-AUG-1991; 91JP-0282369.
XX XX
XX XX 03-AUG-1990; 90JP-0204978.
XX XX
XX XX 30-JUL-1991; 91JP-0189984.
XX PA
XX PA (ASAH ) ASAH CHEM IND CO LTD.
XX DR
XX DR WPI; 1993-299652/38.
XX DR
XX DR N-PSDB; AAQ48847.
XX PT
XX PT Novel polypeptide obtd. by culturing transformed fungus - having
XX PT blood coagulation preventing, platelet aggregation preventing and
XX PT thrombolytic activities
XX XX
XX XX Disclosure; Fig 6; 65pp; Japanese.
XX CC
XX CC MI3TMD1 was mutated using mutagenic oligonucleotide Tm2, resulting
XX CC in the replacement of Asp for Glu.
XX CC Novel polypeptides, obtd. by culturing transformed fungus, have
XX CC blood coagulation preventing, platelet aggregation preventing
XX CC and thrombolytic activities.
XX CC In an example, plasmid MI3mp19TMD3 (constructed from pSV2TMJ2
XX CC (ATCC 67238) contg. a human thrombomodulin sequence) was subjected
XX CC to site directed mutagenesis to prepare pSV2TMD7. Plasmid pSV2TMD7
XX CC was transfected to COS-1 cells. The activity of promoting protein C
XX CC activation by thrombin of the peptide produced by the transformed
XX CC COS-1 cell was measured. The amt. of the peptide was determined.
XX SQ
XX SQ Sequence 11 AA;
XX Query Match 22.2%; Score 4; DB 14; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY
XX QY 10 PVEP 13
XX DB
XX DB 4 PVEP 7
XX RESULT 69
AAR52835
ID AAR52835 standard; peptide; 11 AA.
XX AC
XX AC AAR52835;
XX XX
XX XX 25-MAR-2003 (updated)
XX DT
XX DT 20-JAN-1995 (first entry)
XX XX
XX XX Streptolysin O peptide antigen.
XX DE
XX DE Streptolysin O; peptide antigen; streptococcal infection; diagnosis;
XX KW rheumatoid arthritis; glomerulonephritis.
XX XX
XX XX Synthetic.

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XX EP600326-A2.
 XX
 PD 08-JUN-1994.
 XX
 XX 20-NOV-1993; 93EP-0118697.
 XX
 XX 28-NOV-1992; 92DE-4240056.
 XX
 PA (BOFF) BOEHRINGER MANNHEIM GMBH.
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Burns G, Engel W, Seigel C;
 XX
 XX WPI; 1994-177677/22.
 DR
 XX New streptolysin O-peptide antigen - for detecting specific
 PT antibodies and is immunogens e.g. in vaccines, for diagnosis of,
 PT and protection against, streptococcal infections
 XX
 PS Claim 1; Page 10; 11pp; German.
 XX
 CC Synthetic peptides having this sequence or at least a 4 (pref. less
 CC than 7) amino acid fragment of it are streptolysin O peptide
 CC antigens. The antigens are useful in immunoassays to determine
 CC specific antibodies, e.g. to differentiate between rheumatism and
 CC rheumatoid arthritis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX Sequence 11 AA;
 SQ
 Query Match 22.2%; Score 4; DB 15; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEMP 5
 Db |||||
 6 KEMP 9
 RESULT 70
 AAB23183
 ID AAB23183 standard; peptide; 12 AA.
 XX
 AC AAB23183;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Hsp47-binding hydrophobic phage display dodecapeptide, SEQ ID NO:5.
 XX
 KW Hsp47-binding hydrophobic dodecapeptide; phage display library;
 KW Hsp47 external domain; carcinoma; cancer; targeting molecule;
 KW therapy; diagnosis; detection; imaging; drug delivery; invasion;
 KW migration; metastasis; modulation; tumour; skin; basal cells; colon;
 KW large intestine; lung; breast; bladder; oral cancer;
 KW head and neck cancer; larynx; nasopharynx; adrenal cortex;
 KW apocrine gland; kidney; liver; pancreas; prostate.
 XX
 OS Synthetic.
 XX
 PN WO200054805-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06588.
 XX
 XX 15-MAR-1999; 99US-0124481.
 PR
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA
 XX Sauk JJ;
 PI
 XX

DR WPI; 2000-655997/63.
 XX
 PT Treating, diagnosing or modulating a carcinoma cell, which expresses
 PT Heat shock protein 47 on its surface, involves administering an agent
 PT comprising targeting moiety which binds to Hsp47 external domain
 XX
 PS Claim 6; Page 8; 87pp; English.
 XX
 CC The invention relates to methods of treating and diagnosing carcinomas
 CC in which heat shock protein 47 (Hsp47) is expressed on the surface
 CC of the carcinoma cells, involving administering an agent comprising a
 CC targeting moiety which specifically binds to the external domain of
 CC Hsp47. The invention also relates to peptides (AAB23181-B23203) which
 CC specifically bind to external domains of such surface-localised Hsp47
 CC molecules and have sequences encompassed by the generic sequences
 CC XHYHYXXXHYXXXHyHy or HYXXXHYXXXHYXXX where X, independently, can be
 CC any amino acid and Hy, independently, can be any hydrophobic amino acid.
 CC The invention also encompasses methods of screening for agents which
 CC bind Hsp47 external domains. Hsp47-binding agents can be used to
 CC treat Hsp47-expressing carcinomas, and for modulating the activity of a
 CC tumour cell with respect to invasion, migration, motility or metastasis,
 CC or to its interaction with the extracellular matrix. The targeting
 CC moiety (such as an Hsp47-binding peptide, a toxin or an antibody) may be
 CC coupled with a therapeutic moiety (such as a cytotoxic agent or a
 CC therapeutic gene) for cancer treatment, or with a detectable moiety for
 CC imaging. Carcinomas which may be treated or diagnosed according to
 CC methods of the invention include those of the skin, basal cells, large
 CC intestine, lung, colon, breast, bladder, oral, head and neck, larynx,
 CC nasopharynx, adrenal cortex, apocrine glands, kidney, liver, pancreas, or
 CC prostate. Targeting carcinoma cells with Hsp47-binding agents results in
 CC efficient delivery of therapeutic agents, reduced doses, reduced side
 CC effects and sensitive detection or imaging of carcinoma cells. Sequences
 CC AAB23181-B23191 represent predominantly hydrophobic phage display library
 CC dodecapeptides identified as being able to bind Hsp47 in an
 CC exemplification of the invention.
 XX
 SQ Sequence 12 AA;
 Query Match 22.2%; Score 4; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KYPV 11
 Db |||||
 7 KYPV 10
 RESULT 71
 AAB57781
 ID AAB57781 standard; Peptide; 12 AA.
 XX
 AC AAB57781;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Bovine DNaseI peptide #5.
 XX
 KW Retrotransposon; genetic defect; cystic fibrosis.
 XX
 OS Bos taurus.
 XX
 PN US6150160-A.
 XX
 PD 21-NOV-2000.
 XX
 PF 28-APR-1997; 97US-0847844.
 XX
 XX 16-NOV-1995; 95US-0006831.
 PR 15-NOV-1996; 96US-0749805.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA (UYPE-) UNIV PENNSYLVANIA.
 PI
 XX

PI Moran JV, Dombroski BA, Kazazian HH, Boeke JD;
 XX WPI; 2001-060015/07.
 XX
 XX DNAC comprising a promoter P and an L1 cassette sequence having a core
 PT retrotransposon element, useful for random insertion of a heterologous
 PT or homologous DNA sequence into a cell genome and for correcting
 PT genetic defects -
 XX
 XX Disclosure; Fig 7; 87pp; English.
 PS
 XX
 XX The present invention relates to DNA for a promoter and an L1
 CC cassette sequence having a core retrotransposon element. The invention
 CC is useful for random insertion of a heterologous or homologous DNA
 CC sequence into a cell genome, and for correction of a genetic defect
 CC in the cell into which the insertion is made. Genetic defects which
 CC may be corrected includes cystic fibrosis, mutations in the
 CC dystrophin gene, genetic defects associated with blood clotting and
 CC other genetic defects.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 22.2%; Score 4; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 YPVE 12
 DB 5 YPVE 8
 RESULT 72
 ID ABB82324 standard; peptide; 12 AA.
 AC ABB82324;
 XX
 XX 08-JAN-2003 (first entry)
 DT
 DE Epitopic peptide binding to a human antibody against C. trachomatis.
 XX
 XX Epitope; immunostimulant; antibacterial; vaccine; gene therapy.
 KW Chlamydia trachomatis.
 OS Chlamydia trachomatis.
 XX
 XX WO200272622-A2.
 PN
 XX 19-SEP-2002.
 PD
 XX 12-FEB-2002; 2002WO-GB00597.
 PF
 XX 12-FEB-2001; 2001GB-0003387.
 PR
 XX (YABA-) YABA LTD.
 PA
 XX Jones GE;
 PI
 XX WPI; 2002-740797/80.
 DR
 XX New epitopic peptide derived from Chlamydia trachomatis, useful as a
 XX vaccine for the induction of protection against Chlamydia trachomatis
 PT infections -
 PT
 XX Claim 1; Page 33; 37pp; English.
 PS
 XX Sequences ABB82301-340 represent epitopic peptides that bind specifically
 CC to a human antibody against Chlamydia trachomatis. The peptides are
 CC useful in vaccine preparations for the induction of protection against
 CC infection by C. trachomatis. The epitopic sequences or a compound
 CC comprising them can be used in medicine, such as in diagnosing,
 CC prognosing or treating infections caused by C. trachomatis.
 XX
 XX Sequence 12 AA;
 QY

Query Match 22.2%; Score 4; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 YPVE 12
 DB 5 YPVE 8
 RESULT 73
 ID ABB67387 standard; Peptide; 12 AA.
 XX
 XX ABB67387;
 AC
 XX 07-OCT-2002 (first entry)
 DT
 XX Human ADPI tryptic digest peptide #96.
 DE
 XX Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
 KW Alzheimer's disease-associated feature; neuroprotective;
 KW Alzheimer's disease-associated protein isoform; nootropic;
 KW ADPI tryptic digest peptide.
 XX
 XX Homo sapiens.
 OS
 XX WO200246767-A2.
 PN
 XX 13-JUN-2002.
 PD
 XX 29-NOV-2001; 2001WO-GB05289.
 PF
 XX 08-DEC-2000; 2000US-254431P.
 PR
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Herath HMAC, Parekh RB, Rohlf C;
 PI
 XX WPI; 2002-508575/54.
 DR
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprises detecting Alzheimer's disease-associated features or
 PT Alzheimer's disease-associated protein isoforms in brain tissue
 PT from the subject -
 XX
 XX Claim 7; Page 83; 427pp; English.
 PS
 XX The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in
 CC a subject. The method comprises analysing a sample of brain tissue
 CC from a subject by 2D electrophoresis to generate a 2D array of
 CC Alzheimer's disease-associated features (ADFs), whose relative
 CC abundance correlates with the presence, absence, stage or severity of
 CC AD and comparing the abundance of each feature with the abundance of
 CC that chosen feature in brain tissue from persons free from AD. The
 CC invention also describes Alzheimer's disease-associated protein
 CC isoforms (ADPIs) detectable in brain tissue. The methods and
 CC compositions of the invention are useful for the screening, diagnosis
 CC or prognosis of AD in a subject, for determining the stage or severity
 CC of AD in a subject, for identifying a subject at risk of developing AD,
 CC or for monitoring the effect of therapy administered to a subject
 CC having AD. Antibodies capable of binding to ADPIs are useful for
 CC treating or preventing AD, and for determining the efficacy of a given
 CC treatment regime. An agent that modulates the activity of ADPI is
 CC useful in the manufacture of a medicament for the treatment or
 CC prevention of AD in a subject. ABB67292-ABB68038 represent human ADPI
 CC tryptic digest peptides.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 22.2%; Score 4; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
 ||||
 Db 4 TESQ 7

RESULT 74

AAR63797
 ID AAR63797 standard; Peptide; 13 AA.

XX AAR63797;

XX AC

XX DT 25-MAR-2003 (updated)

DT 13-JUL-1995 (first entry)

XX Bacillus thuringiensis anion exchange factor N-terminal peptide.

XX Vegetative insecticidal protein; VIP; Bacillus thuringiensis;

KW pesticide; Diabrotica virgifera virgifera; insecticide.

XX AC

OS Bacillus thuringiensis.

XX AC

XX Key Location/Qualifiers

FT Misc-difference 1

FT /note= "any amino acid"

FT Misc-difference 13

FT /note= "any amino acid"

XX AC

XX WO9421795-A1.

XX AC

PD 29-SEP-1994.

XX AC

PF 23-MAR-1994; 94WO-US03131.

XX AC

PR 25-MAR-1993; 93US-0037057.

XX AC

XX (CIBA) CIBA GEIGY AG.

XX AC

PI Carr B, Desai N, Kostichka N, Kozziel MG, Mullins MA;

PI Nye GJ, Warren GW;

XX AC

XX WPI; 1994-317015/39.

XX AC

XX Novel pesticidal proteins and Bacillus strains - e.g. useful for

PT control of Diabrotica virgifera virgifera

XX AC

PS Claim 35; Page 77; 108pp; English.

XX AC

CC AAR63795-R63802 are auxiliary proteins that enhance the pesticidal
 CC activity of the vegetative insecticidal proteins (VIPs) described
 CC in AAR63792-R63794 and AAR75690. The protein peptide combination can
 CC be used in a variety of systems for controlling plant and non-plant
 CC pests, including insects, fungi, bacteria, nematodes, protozoan
 CC pathogens and animal-parasitic liver flukes. However it is esp.
 CC useful in the control of Diabrotica virgifera virgifera.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX AC

SQ Sequence 13 AA;

Query Match 22.2%; Score 4; DB 15; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPP 14
 ||||
 Db 6 VEPP 9

RESULT 75

AAR91253

ID AAR91253 standard; Peptide; 13 AA.

XX

AC AAR91253;

XX AC

DT 25-MAR-2003 (updated)

DT 14-AUG-1996 (first entry)

XX AC

DE European corn borer-active protein N-terminal peptide.

XX AC

KW Pesticide; insecticide; biological control agent; Lepidoptera;

KW Coleoptera; transgenic plant; maize; insect resistance;

KW European corn borer; Ostrinia nubilalis.

XX AC

OS Bacillus thuringiensis strain AB88 (NRRL B-21225).

XX AC

XX Key Location/Qualifiers

FT Misc-difference 1

FT /note= "unidentified amino acid"

FT Misc-difference 13

FT /note= "unidentified amino acid"

XX AC

PN WO9610083-A1.

XX AC

PD 04-APR-1996.

XX AC

XX 27-SEP-1995; 95WO-EP03826.

XX AC

PR 05-JUN-1995; 95US-0463483.

PR AC

PR 28-SEP-1994; 94US-0314594.

XX AC

PA (CIBA) CIBA GEIGY AG.

XX AC

XX Warren GW, Kozziel MG, Mullins MA, Nye GJ, Carr B, Desai NM;

PI Kostichka K, Duck NB, Estruch JU;

XX AC

DR WPI; 1996-200921/20.

XX AC

PT Bacillus strain producing insecticidal protein during vegetative

PT growth - used in the control of Lepidoptera and Coleoptera pests

XX AC

PS Example 17; Page 75; 242pp; English.

XX AC

CC N-terminal sequences (AAR91252 and AAR91253) were obtd. from anion
 CC exchange fractions 23 and 28, respectively, of a European corn
 CC borer-active 60 kDa protein of Bacillus thuringiensis AB88. This
 CC strain also produces a protein active against black cutworm (see
 CC also AAR91243).

CC (Updated on 25-MAR-2003 to correct PI field.)

XX AC

SQ Sequence 13 AA;

Query Match 22.2%; Score 4; DB 17; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPP 14
 ||||
 Db 6 VEPP 9

Search completed: November 25, 2003, 19:27:09

Job time : 46.9419 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8837 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKMPFPKVPVETESQ 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

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6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
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12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
16:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
17:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
18:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-281-652-22
2	5	27.8	15	15	US-10-281-652-5
3	4	22.2	6	12	US-10-441-626-27
4	4	22.2	7	9	US-09-997-900-11
5	4	22.2	9	10	US-09-780-053-17
6	4	22.2	9	10	US-09-780-053-319
7	4	22.2	9	10	US-09-780-053-238
8	4	22.2	9	10	US-09-780-053-418
9	4	22.2	9	12	US-09-932-165-265
10	4	22.2	9	12	US-09-932-165-851
11	4	22.2	9	12	US-09-932-165-1238
12	4	22.2	9	12	US-10-062-109A-4
13	4	22.2	9	12	US-10-062-109A-44
14	4	22.2	9	12	US-10-005-480A-4
15	4	22.2	9	12	US-10-005-480A-44

16	4	22.2	9	12	US-10-371-069-190	Sequence 190, App
17	4	22.2	9	12	US-10-371-645-190	Sequence 190, App
18	4	22.2	10	10	US-09-780-053-68	Sequence 68, App
19	4	22.2	10	10	US-09-780-053-276	Sequence 276, App
20	4	22.2	10	10	US-09-780-053-398	Sequence 398, App
21	4	22.2	10	10	US-09-780-053-404	Sequence 404, App
22	4	22.2	10	10	US-09-780-053-407	Sequence 407, App
23	4	22.2	10	10	US-09-780-053-496	Sequence 496, App
24	4	22.2	10	10	US-09-780-053-715	Sequence 715, App
25	4	22.2	10	12	US-09-932-165-373	Sequence 373, App
26	4	22.2	10	12	US-09-932-165-395	Sequence 395, App
27	4	22.2	10	12	US-09-932-165-1339	Sequence 1339, App
28	4	22.2	10	12	US-09-932-165-1351	Sequence 1351, App
29	4	22.2	10	12	US-10-062-109A-55	Sequence 55, App
30	4	22.2	10	12	US-10-062-109A-71	Sequence 71, App
31	4	22.2	10	12	US-10-005-480A-55	Sequence 55, App
32	4	22.2	10	12	US-10-005-480A-71	Sequence 71, App
33	4	22.2	11	15	US-10-062-710-173	Sequence 173, App
34	4	22.2	11	15	US-10-094-401-148	Sequence 148, App
35	4	22.2	12	15	US-10-057-789-142	Sequence 142, App
36	4	22.2	12	15	US-10-212-628-142	Sequence 142, App
37	4	22.2	12	15	US-10-216-122-89	Sequence 89, App
38	4	22.2	13	10	US-09-966-955A-31	Sequence 31, App
39	4	22.2	13	10	US-09-966-955A-32	Sequence 32, App
40	4	22.2	13	12	US-10-271-078-26	Sequence 26, App
41	4	22.2	14	11	US-09-791-393-100	Sequence 100, App
42	4	22.2	14	11	US-09-791-389-100	Sequence 100, App
43	4	22.2	14	12	US-10-271-078-33	Sequence 33, App
44	4	22.2	15	11	US-09-892-877-381	Sequence 381, App
45	4	22.2	15	11	US-09-991-799-2	Sequence 2, App
46	4	22.2	15	11	US-09-948-783-381	Sequence 381, App
47	4	22.2	15	14	US-10-001-873-120	Sequence 120, App
48	4	22.2	15	15	US-10-281-652-8	Sequence 8, App
49	4	22.2	15	15	US-10-264-303-11	Sequence 11, App
50	4	22.2	16	12	US-10-175-270-13	Sequence 13, App
51	4	22.2	16	12	US-10-161-791-181	Sequence 181, App
52	4	22.2	16	15	US-10-225-567A-1110	Sequence 1110, App
53	4	22.2	16	15	US-10-225-567A-1727	Sequence 1727, App
54	4	22.2	17	9	US-09-864-761-46168	Sequence 46168, A
55	4	22.2	17	12	US-10-161-791-362	Sequence 362, App
56	4	22.2	18	9	US-09-864-761-48184	Sequence 48184, A
57	4	22.2	18	15	US-10-094-401-196	Sequence 196, App
58	4	22.2	20	9	US-09-841-132-236	Sequence 236, App
59	4	22.2	20	9	US-09-841-132-237	Sequence 237, App
60	4	22.2	20	9	US-09-841-132-238	Sequence 238, App
61	4	22.2	20	9	US-09-841-132-239	Sequence 239, App
62	4	22.2	20	11	US-09-983-802-664	Sequence 664, App
63	3	16.7	3	12	US-10-253-532-126	Sequence 126, App
64	3	16.7	4	10	US-09-982-172-186	Sequence 186, App
65	3	16.7	4	10	US-09-947-387-27	Sequence 27, App
66	3	16.7	4	11	US-09-994-078-2	Sequence 2, App
67	3	16.7	4	12	US-10-237-160-1	Sequence 1, App
68	3	16.7	4	12	US-10-253-532-122	Sequence 122, App
69	3	16.7	4	12	US-10-253-532-125	Sequence 125, App
70	3	16.7	4	12	US-10-087-942-20	Sequence 20, App
71	3	16.7	4	12	US-10-087-942-31	Sequence 31, App
72	3	16.7	4	12	US-10-313-338A-1	Sequence 1, App
73	3	16.7	4	12	US-10-313-790A-1	Sequence 1, App
74	3	16.7	4	12	US-10-138-375-27	Sequence 27, App
75	3	16.7	4	14	US-10-041-030-28	Sequence 28, App
76	3	16.7	4	15	US-10-087-905-20	Sequence 20, App
77	3	16.7	4	15	US-10-087-905-31	Sequence 31, App
78	3	16.7	4	15	US-10-059-261-25	Sequence 25, App
79	3	16.7	4	15	US-10-059-261-133	Sequence 133, App
80	3	16.7	4	15	US-10-006-869-199	Sequence 199, App
81	3	16.7	5	12	US-10-253-532-117	Sequence 117, App
82	3	16.7	5	12	US-10-253-532-121	Sequence 121, App
83	3	16.7	5	12	US-10-253-532-124	Sequence 124, App
84	3	16.7	5	12	US-10-226-629A-9	Sequence 9, App
85	3	16.7	5	12	US-10-294-891-49	Sequence 49, App
86	3	16.7	5	12	US-10-276-601-4	Sequence 4, App
87	3	16.7	5	12	US-10-020-354-112	Sequence 112, App
88	3	16.7	5	12	US-10-145-206-110	Sequence 110, App

89 3 16.7 5 15 US-10-155-407A-12 Sequence 12, Appl
90 3 16.7 5 15 US-10-006-869-200 Sequence 200, App
91 3 16.7 5 15 US-10-006-869-202 Sequence 202, App
92 3 16.7 5 15 US-10-006-869-1566 Sequence 1566, Ap
93 3 16.7 5 15 US-10-006-869-1568 Sequence 1568, Ap
94 3 16.7 5 15 US-10-096-986-13 Sequence 13, Appl
95 3 16.7 5 15 US-10-058-513-16 Sequence 16, Appl
96 3 16.7 5 15 US-10-281-652-15 Sequence 15, Appl
97 3 16.7 5 15 US-10-206-699-199 Sequence 199, App
98 3 16.7 6 9 US-09-062-113-1 Sequence 1, Appl
99 3 16.7 6 10 US-09-529-759-26 Sequence 26, Appl
100 3 16.7 6 10 US-09-529-759-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-22
; Sequence 22, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-22

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKEMPFPKYPVEPFTESQ 18
Db 1 HKEMPFPKYPVEPFTESQ 18

RESULT 2
US-10-281-652-5
; Sequence 5, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-5

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEPFF 14
Db 8 PVEPFF 12

RESULT 3
US-10-441-626-27
; Sequence 27, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1 Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGIII-like cellulase amino acid string
US-10-441-626-27

Query Match 22.2%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
Db 3 EPFT 6

RESULT 4
US-09-997-900-11
; Sequence 11, Application US/09997900
; Patent No. US20020053098A1
; GENERAL INFORMATION:
; APPLICANT: Kakefuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; FILE REFERENCE: 043753/241148 (5849-20A)
; CURRENT APPLICATION NUMBER: US/09/997,900
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 09/426,568
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT

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; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PESTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid P3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
US-09-997-900-11

Query Match          22.2%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
    ||||
Db 3 VEPF 6

RESULT 5
US-09-780-053-17
; Sequence 17, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-17

Query Match          22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 2 TESQ 5

RESULT 6
US-09-780-053-238
; Sequence 238, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09

```

```

; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-238

Query Match          22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 2 TESQ 5

RESULT 7
US-09-780-053-319
; Sequence 319, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-319

Query Match          22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 2 TESQ 5

RESULT 8
US-09-780-053-418
; Sequence 418, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261

```

; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 418
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-418

Query Match 22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
|||
Db 4 TESQ 7

RESULT 9
US-09-932-165-265
; Sequence 265, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-265

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
|||
Db 6 KYPV 9

RESULT 10
US-09-932-165-851
; Sequence 851, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 851
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-851

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
|||
Db 1 KYPV 4

RESULT 11
US-09-932-165-1238
; Sequence 1238, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1238
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1238

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
|||
Db 4 KYPV 7

RESULT 12
US-10-062-109A-4
; Sequence 4, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:

```

; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-4

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VEPF 14
        ||||
Db       4 VEPF 7

```

```

RESULT 13
US-10-062-109A-44
; Sequence 44, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-44

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VEPF 14
        ||||
Db       2 VEPF 5

```

```

RESULT 14
US-10-005-480A-4
; Sequence 4, Application US/10005480A
; Publication No. US20030191073A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-4

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VEPF 14
        ||||
Db       4 VEPF 7

```

```

RESULT 15
US-10-005-480A-44
; Sequence 44, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-44

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VEPF 14
        ||||
Db       2 VEPF 5

```

```

RESULT 16
US-10-371-069-190
; Sequence 190, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.

```

```
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-10-371-069-190

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 FTES 17
DB      2 FTES 5

RESULT 17
US-10-371-645-190
; Sequence 190, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-10-371-645-190

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 FTES 17
DB      2 FTES 5
```

```
RESULT 18
US-09-780-053-68
; Sequence 68, Application US/097800053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-68

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TESQ 18
DB      2 TESQ 5

RESULT 19
US-09-780-053-276
; Sequence 276, Application US/097800053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-276

Query Match      22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TESQ 18
DB      5 TESQ 8
```

RESULT 20
US-09-780-053-398
; Sequence 398, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 398
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-398

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||
Db 3 TESQ 6

RESULT 21
US-09-780-053-404
; Sequence 404, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 404
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-404

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||
Db 2 TESQ 5

RESULT 22
US-09-780-053-407
; Sequence 407, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 407
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-407

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||
Db 4 TESQ 7

RESULT 23
US-09-780-053-496
; Sequence 496, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-496

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
|||
Db 5 TESQ 8

RESULT 24

US-09-780-053-715
; Sequence 715, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P54: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 715
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-715

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
|||
Db 5 TESQ 8

RESULT 25
US-09-932-165-373
; Sequence 373, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 373
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-373

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
|||

Db 6 KYPV 9
RESULT 26
US-09-932-165-395
; Sequence 395, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 395
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-395

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
|||
Db 7 KYPV 10

RESULT 27
US-09-932-165-1339
; Sequence 1339, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1339
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1339

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11
DB 5 KYPV 8

RESULT 28

US-09-932-165-1351
Sequence 1351, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: PARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CatrP2E11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 1351
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1351

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11
DB 1 KYPV 4

RESULT 29

US-10-062-109A-55
Sequence 55, Application US/10062109A
Publication No. US20030165505A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.01
CURRENT APPLICATION NUMBER: US/10/062,109A
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55

TYPE: PRT
ORGANISM: Homo sapiens
US-10-062-109A-55

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPP 14
DB 2 VEPP 5

RESULT 30

US-10-062-109A-71
Sequence 71, Application US/10062109A
Publication No. US20030165505A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.01
CURRENT APPLICATION NUMBER: US/10/062,109A
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-062-109A-71

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPP 14
DB 4 VEPP 7

RESULT 31

US-10-005-480A-55
Sequence 55, Application US/10005480A
Publication No. US20030191073A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.00
CURRENT APPLICATION NUMBER: US/10/005,480A
CURRENT FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765


```

; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-789-142

Query Match          22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 2 VEPF 5

RESULT 36
US-10-212-628-142
; Sequence 142, Application US/10212628
; Publication No. US20030087329A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; FILE REFERENCE: NAD11.022CP1
; CURRENT APPLICATION NUMBER: US/10/212,628
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/057,789
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-212-628-142

Query Match          22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 2 VEPF 5

RESULT 37
US-10-216-122-89
; Sequence 89, Application US/10216122
; Publication No. US20030121063A1
; GENERAL INFORMATION:
; APPLICANT: Kazarian, Haig H.
; APPLICANT: Osterag, Eric
; APPLICANT: DeBerardinis, Ralph
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
; FILE REFERENCE: 053893-5006-03
; CURRENT APPLICATION NUMBER: US/10/216,122
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/653,812
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 08/847,844
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: US 08/749,805

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; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/006,831
; PRIOR FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-216-122-89

Query Match          22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVE 12
Db 5 YPVE 8

RESULT 38
US-09-966-955A-31
; Sequence 31, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:
; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clnk-related Gene, MIST (Mast Cell Immunoreceptor)
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/237030
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: HUMAN
US-09-966-955A-31

Query Match          22.2%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFPK 8
Db 10 PFPK 13

RESULT 39
US-09-966-955A-32
; Sequence 32, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:
; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clnk-related Gene, MIST (Mast Cell Immunoreceptor)
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28

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; PRIOR APPLICATION NUMBER: 60/237030
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: HUMAN
US-09-966-955A-32

Query Match 22.2%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPKK 8
|||
Db 1 PPKK 4

RESULT 40

US-10-271-078-26
; Sequence 26, Application US/10271078
; Publication No. US20030186267A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLLRCF
; FILE REFERENCE: D0157 NP
; CURRENT APPLICATION NUMBER: US/10/271,078
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: U.S. 60/328,478
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-271-078-26

Query Match 22.2%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5
|||
Db 8 KEMP 11

RESULT 41

US-09-791-393-100
; Sequence 100, Application US/09791393
; Publication No. US2003032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens

; ORGANISM: homo sapien
US-09-791-393-100

Query Match 22.2%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMPF 6
|||
Db 2 EMPF 5

RESULT 42

US-09-791-389-100
; Sequence 100, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-100

Query Match 22.2%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMPF 6
|||
Db 2 EMPF 5

RESULT 43

US-10-271-078-33
; Sequence 33, Application US/10271078
; Publication No. US20030186267A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLI
; FILE REFERENCE: D0157 NP
; CURRENT APPLICATION NUMBER: US/10/271,078
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: U.S. 60/328,478
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-271-078-33

Query Match 22.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEMP 5
||||
Db 8 KEMP 11

RESULT 44

US-09-892-877-381
; Sequence 381, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: PZ028P1
; CURRENT APPLICATION NUMBER: US/09/892,877
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 381
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-877-381

Query Match 22.2%; Score 4; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
||||
Db 12 TESQ 15

RESULT 45

US-09-991-799-2
; Sequence 2, Application US/09991799
; Publication No. US20030100012A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Plasma Protease C1 Biopolymer Markers Predictive of Alzheimers D
; FILE REFERENCE: 2132.086
; CURRENT APPLICATION NUMBER: US/09/991,799
; CURRENT FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-799-2

Query Match 22.2%; Score 4; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
||||
Db 2 KYPV 5

RESULT 46

US-09-948-783-381
; Sequence 381, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: PZ028P2
; CURRENT APPLICATION NUMBER: US/09/948,783
; CURRENT FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231,846
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 09/892,877
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/437,658
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/09847
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/085,093
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,094
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,105
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,180
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,927
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,906
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,924
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,928
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,920
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 381
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-948-783-381

Query Match 22.2%; Score 4; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
||||
Db 12 TESQ 15

RESULT 47

US-10-001-879-120
; Sequence 120, Application US/10001879
; Publication No. US20020127237A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 15

;
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-120

Query Match 22.2%; Score 4; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 FPKY 9
|||
Db 8 FPKY 11

RESULT 48
US-10-281-652-8
; Sequence 8, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-8

Query Match 22.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 FPKK 8
|||
Db 3 FPKK 6

RESULT 49
US-10-264-303-11
; Sequence 11, Application US/10264303
; Publication No. US20030124060A1
; GENERAL INFORMATION:
; APPLICANT: Roux, Kenneth
; APPLICANT: Sathe, Shridhar
; APPLICANT: Teuber, Suzanne
; TITLE OF INVENTION: Purified Linear Epitopes from Cashew Nuts, Nucleic Acids Encoding
; TITLE OF INVENTION: Thereof and Associated Methods
; FILE REFERENCE: 28396 and 30728
; CURRENT APPLICATION NUMBER: US/10/264,303
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,793
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/371,774
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Anacardium occidentale

US-10-264-303-11

Query Match 22.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 13 PFTE 16
|||
Db 10 PFTE 13

RESULT 50
US-10-175-270-13
; Sequence 13, Application US/10175270
; Publication No. US20030168548A1
; GENERAL INFORMATION:
; APPLICANT: PETERSON, JOHNNY W.
; APPLICANT: SAINI, SHAMSHER S.
; APPLICANT: WOOD, THOMAS G.
; APPLICANT: CHOPRA, ASHOK K.
; TITLE OF INVENTION: ANTI-INFLAMMATORY AND OTHER THERAPEUTIC PROPHYLACTIC OR DIAGNO
; TITLE OF INVENTION: SYNTHETIC MELITTIN AND NE
; TITLE OF INVENTION: W RELATED PEPTIDES
; FILE REFERENCE: UTSG:213
; CURRENT APPLICATION NUMBER: US/10/175,270
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/458,397
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: PCT/US98/12340
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-175-270-13

Query Match 22.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 14 FTES 17
|||
Db 3 FTES 6

RESULT 51
US-10-161-791-181
; Sequence 181, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-181

Query Match 22.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPK 8
|||
Db 5 PPK 8

RESULT 52
US-10-225-567A-1110
Sequence 1110, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1110
LENGTH: 16
TYPE: PPT
ORGANISM: Homo sapiens
US-10-225-567A-1110

Query Match 22.2%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPK 8
|||
Db 10 PPK 13

RESULT 53
US-10-225-567A-1727
Sequence 1727, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1727
LENGTH: 16
TYPE: PPT
ORGANISM: Homo sapiens
US-10-225-567A-1727

Query Match 22.2%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
|||
Db 9 YPVE 12

RESULT 54
US-09-864-761-46168
Sequence 46168, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45168
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL135787.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EST_HUMAN HIT: AA595480.1, EVALUATE 2.90e-02
US-09-864-761-46168

Query Match 22.2%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5
Db 10 KEMP 13

RESULT 55
US-10-161-791-362
; Sequence 362, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids

; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-362

Query Match 22.2%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
Db 10 PVEP 13

RESULT 56
US-09-864-761-48184
; Sequence 48184, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48184
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022238.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2

OTHER INFORMATION: EST_HUMAN HIT: AL121033.1, EVALUE 3.70e-02
US-09-864-761-48184

Query Match 22.2%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFTE 16
|||
Db 1 PFTE 4

RESULT 57
US-10-094-401-196
; Sequence 196, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Cohen, Edward H.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
; CURRENT APPLICATION NUMBER: US/10/094,401
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/331,352
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/292,975
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: albumin binding peptide
US-10-094-401-196

Query Match 22.2%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMPF 6
|||
Db 10 EMPF 13

RESULT 58
US-09-841-132-236
; Sequence 236, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-236

Query Match 22.2%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
|||
Db 17 YPVE 20

RESULT 59
US-09-841-132-237
; Sequence 237, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-237

Query Match 22.2%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
|||
Db 12 YPVE 15

RESULT 60
US-09-841-132-238
; Sequence 238, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-238

Query Match 22.2%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
|||
Db 7 YPVE 10

RESULT 61
US-09-841-132-239

```

; Sequence 239, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.459C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; US-09-841-132-239

Query Match      22.2%  Score 4;  DB 9;  Length 20;
Best Local Similarity 100.0%;  Pred. No. 6.6e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  9 YPVE 12
    |||||
Db  2 YPVE 5

RESULT 62
US-09-983-802-664
; Sequence 664, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/983.802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919

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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-983-802-664

Query Match      22.2%  Score 4;  DB 11;  Length 20;
Best Local Similarity 100.0%;  Pred. No. 6.6e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  5 PFPK 8
    |||||
Db  16 PFPK 19

RESULT 63
US-10-253-532-126
; Sequence 126, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Gestruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/324,528
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 126
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-126

Query Match      16.7%; Score 3; DB 12; Length 3;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TES 17
DB      1 TES 3

RESULT 64
US-09-982-172-156
; Sequence 156, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-156

Query Match      16.7%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVE 12
DB      1 PVE 3

RESULT 65
US-09-947-387-27
; Sequence 27, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0230005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 27
; LENGTH: 4

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RESULT 71
US-10-087-942-31
; Sequence 31, Application US/10087942
; Publication No. US20030165808A1
; GENERAL INFORMATION:
; APPLICANT: Haaland, Perry D.
; APPLICANT: Sherman, Douglas B.
; APPLICANT: Stewart II, Walter W.
; APPLICANT: Lloyd, Sheila A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR
; FORMULATING CULTURE MEDIA
; FILE REFERENCE: P3250
; CURRENT APPLICATION NUMBER: US/10/087,942
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/359,260
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
; OTHER INFORMATION: peptide
US-10-087-942-31

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
Db 2 YPV 4

RESULT 72
US-10-313-338A-1
; Sequence 1, Application US/1031338A
; Publication No. US20030170226A1
; GENERAL INFORMATION:
; APPLICANT: Klaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF AU
; FILE REFERENCE: 1776-1-7
; CURRENT APPLICATION NUMBER: US/10/313,338A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-338A-1

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
Db 2 PFP 4

RESULT 73
US-10-313-790A-1
; Sequence 1, Application US/10313790A
; Publication No. US20030170227A1
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Mu, David
; APPLICANT: Xiang, Phil
; APPLICANT: Peng, Yue
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; APPLICANT: Klaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF
; FILE REFERENCE: 1776-1-6
; CURRENT APPLICATION NUMBER: US/10/313,790A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-790A-1

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
Db 2 PFP 4

RESULT 74
US-10-138-375-27
; Sequence 27, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prote
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-138-375-27

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3

RESULT 75
US-10-041-030-28
; Sequence 28, Application US/10041030
; Publication No. US20020150934A1
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Mu, David
; APPLICANT: Xiang, Phil
; APPLICANT: Peng, Yue
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; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian
; TITLE OF INVENTION: Pellino Polypeptides and Polynucleotides
; FILE REFERENCE: 018781-006810US
; CURRENT APPLICATION NUMBER: US/10/041,030
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/259,502
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence identity in comparison of pellino 1 and
; OTHER INFORMATION: pellino 2
US-10-041-030-28

Query Match 16.7%; Score 3; DB 14; Length 4;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
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Db 2 FTE 4

Search completed: November 25, 2003, 20:37:00
Job time : 29.8837 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMPPKYPVEPFTBSQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

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Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

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Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4	22.2	7	1	US-08-261-206A-22
5	4	22.2	7	4	US-09-426-568A-11
6	4	22.2	8	1	US-08-259-550A-30
7	4	22.2	8	2	US-08-929-922B-7
8	4	22.2	8	3	US-09-342-394-7
9	4	22.2	8	3	US-09-580-064-7
10	4	22.2	8	4	US-09-718-709-7
11	4	22.2	9	4	US-09-311-784A-190
12	4	22.2	11	1	US-08-158-351-3
13	4	22.2	11	1	US-08-482-576-3
14	4	22.2	12	3	US-08-847-844A-89
15	4	22.2	13	1	US-08-471-033-11
16	4	22.2	13	2	US-08-471-044-11
17	4	22.2	13	2	US-08-463-483A-11
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19	4	22.2	13	2	US-08-470-566B-11
20	4	22.2	13	2	US-08-838-219B-11
21	4	22.2	13	2	US-08-469-334-11
22	4	22.2	13	3	US-09-300-529-11
23	4	22.2	13	3	US-09-233-336A-11
24	4	22.2	13	3	US-09-233-752A-11
25	4	22.2	13	3	US-09-402-036-11
26	4	22.2	13	4	US-09-904-226-11
27	4	22.2	14	6	5171684-21
					Patent No. 5171684

1 US-08-080-073-25
15 US-08-967-101-168
15 2 US-08-687-956A-7
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15 2 US-08-592-541-168
15 2 US-08-591-629-5
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Sequence 181, App
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Sequence 362, App
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Sequence 4, Appli
Sequence 8, Appli
Sequence 664, App
Sequence 236, App
Sequence 237, App
Sequence 238, App
Sequence 239, App
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Sequence 238, App
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Sequence 5, Appli
Sequence 163, App
Sequence 3, Appli
Sequence 19, Appl
Sequence 27, Appl
Sequence 1, Appli
Sequence 27, Appl
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Patent No. 5215966
Patent No. 5215966
Sequence 14, Appl
Sequence 28, Appl
Sequence 67, Appl
Sequence 12, Appl
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Sequence 81, Appl
Sequence 83, Appl
Sequence 86, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 4, Appli
Sequence 73, Appli

ALIGNMENTS

RESULT 1
US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-22

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKEMPPPKYVPEPTESQ 18
Db 1 HKEMPPPKYVPEPTESQ 18
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RESULT 2
US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-5

Query Match 27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEFP 14
Db 8 PVEFP 12
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RESULT 3
US-09-216-295-27
; Sequence 27, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328e1 Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-216-295-27

Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPPT 15
Db 3 EPPT 6
|||||

RESULT 4
US-08-261-206A-22
; Sequence 22, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 22:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-22

Query Match      22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13
    ||||
Db 2 PVEP 5

RESULT 5
US-09-426-568A-11
; Sequence 11, Application US/09426568A
; Patent No. 6348643
; GENERAL INFORMATION:
; APPLICANT: Kakafuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; FILE REFERENCE: 008103/195497
; CURRENT APPLICATION NUMBER: US/09/426,568A
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid F3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
; US-09-426-568A-11

Query Match      22.2%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
    ||||
Db 3 VEPF 6

RESULT 6
US-08-259-550A-30
; Sequence 30, Application US/08259550A
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-22

Query Match      22.2%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 1 TESQ 4

RESULT 7
US-08-929-922B-7
; Sequence 7, Application US/08929922B
; Patent No. 5994113
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: sterigaard, Peter Rahbek
; APPLICANT: Patkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5994113o No. 5994113disk of No. 5994113th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,550A
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7142-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-259-550A-30

Query Match      22.2%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
    ||||
Db 1 TESQ 4

RESULT 7
US-08-929-922B-7
; Sequence 7, Application US/08929922B
; Patent No. 5994113
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: sterigaard, Peter Rahbek
; APPLICANT: Patkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5994113o No. 5994113disk of No. 5994113th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922B
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123

```

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-929-922B-7

Query Match 22.2%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 4 VEPF 7

RESULT 8
US-09-342-394-7
; Sequence 7, Application US/09342394
; Patent No. 6143546
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spandler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Patkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 61435460 NO. 6143546disk of No. 6143546th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/342,394
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922
; FILING DATE: 15-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-09-342-394-7

Query Match 22.2%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 4 VEPF 7

RESULT 9
US-09-580-064-7
; Sequence 7, Application US/09580064
; Patent No. 6200792
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spandler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Patkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6200792o No. 6200792disk of No. 6200792th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/580,064
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/929,922
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-09-580-064-7

Query Match 22.2%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 4 VEPF 7

RESULT 10
US-09-718-709-7
; Sequence 7, Application US/09718709

Patent No. 6413559
GENERAL INFORMATION:
APPLICANT: Kauppinen, Sakari
Si, Joan Qi
Spendler, Tina
Dambmann, Claus
Halkier, Torben
stergaard, Peter Rabbek
Patkar, Shankant Anant
Hansen, Kim
TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6413559 No. 6413559disk of No. 6413559th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/718,709
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/929,922
FILING DATE: 15-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4355,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-718-709-7
Query Match 22.2%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 VEPF 14
Db 4 VEPF 7
RESULT 11
US-09-311-784A-190
Sequence 190, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
Immune Response and Methods of Using the Same

FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 190
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-09-311-784A-190
Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 FTES 17
Db 2 FTES 5
RESULT 12
US-08-158-351-3
Sequence 3, Application US/08158351
Patent No. 5445820
GENERAL INFORMATION:
APPLICANT: SEIDEL, Christoph
APPLICANT: BURNS, Geoffrey
APPLICANT: ENGEL, Wolf-Dieter
TITLE OF INVENTION: STREPTOLYSIN O PEPTIDE ANTIGENS AND
METHODS FOR THE DETERMINATION OF STREPTOLYSIN ANTIBODIES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
STREET: 655 Fifteenth Street N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,351
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 40 056.2
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 1614-3052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-158-351-3
Query Match 22.2%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5
Db 6 KEMP 9

RESULT 13

US-08-482-576-3
; Sequence 3, Application US/08482576
; Patent No. 568659
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, Christoph
; APPLICANT: BURNS, Geofffrey
; APPLICANT: ENGEL, Wolf-Dieter
; TITLE OF INVENTION: STREPTOLYSIN O PEPTIDE ANTIGENS AND
; TITLE OF INVENTION: METHODS FOR THE DETERMINATION OF STREPTOLYSIN
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W., Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,576
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 40 056.2
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1614-3052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-576-3

QY 2 KEMP 5
Db 6 KEMP 9

RESULT 14

US-08-847-844A-89
; Sequence 89, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOERKE, JEFF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS

; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-2302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-847-844A-89

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 5 YPVE 8

RESULT 15

US-08-471-033-11
; Sequence 11, Application US/08471033
; Patent No. 5770696
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,033
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: P-40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLv3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; US-08-471-033-11

```

```

Query Match 22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 11 VEPF 14
Db ||||
6 VEPF 9

```

```

RESULT 16
US-08-471-044-11
; Sequence 11, Application US/08471044
; Patent No. 5840868
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,044
; FILING DATE: 06-JUN-1995

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLv3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; US-08-471-044-11

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Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 11 VEPF 14
Db ||||
6 VEPF 9

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RESULT 17
US-08-463-483A-11
; Sequence 11, Application US/08463483A
; Patent No. 5849870
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,483A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594

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;/ FILING DATE: 09-SEP-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/218,018
;/ FILING DATE: 23-MAR-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/037,057
;/ FILING DATE: 25-MAR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Spruill, W. Murray
;/ REGISTRATION NUMBER: 32,943
;/ REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 919-541-8615
;/ TELEFAX: 919-541-8689
;/ INFORMATION FOR SEQ ID NO: 11:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 13 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ ORGANISM: Bacillus thuringiensis
;/ US-08-463-483A-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 18
US-08-471-046A-11
; Sequence 11, Application US/08471046A
; Patent No. 5866326
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866326artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US/08/471,046A
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: US 08/218,018
;/ FILING DATE: 23-MAR-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/037,057
;/ FILING DATE: 25-MAR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Meigs, J. Timothy
;/ REGISTRATION NUMBER: 38,241
;/ REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SQLV4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 919-541-8587
;/ TELEFAX: 919-541-8689
;/ INFORMATION FOR SEQ ID NO: 11:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 13 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ ORGANISM: Bacillus thuringiensis
;/ US-08-471-046A-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 19
US-08-470-566B-11
; Sequence 11, Application US/08470566B
; Patent No. 5872212
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5872212artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,566B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET INFORMATION: CGC1695/CIP3/DIV4 - SQLv4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-08-470-5668-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 20
US-08-838-219B-11
; Sequence 11, Application US/08838219B
; Patent No. 5877012
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 5877012el Class of Proteins for the
; TITLE OF INVENTION: Control of Plant Pests
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,219B
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3

; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-08-838-219B-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 21
US-08-469-334-11
; Sequence 11, Application US/08469334
; Patent No. 5990383
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5990383el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,334
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,483
; FILING DATE:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
US-08-469-334-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 22
US-09-300-529-11
; Sequence 11, Application US/09300529
; Patent No. 6066783
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: Genes Encoding Insecticidal Proteins
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 606783artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,529
; FILING DATE: TEA
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,334
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19506L

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
US-09-300-529-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 23
US-09-233-336A-11
; Sequence 11, Application US/09233336A
; Patent No. 6107279
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 6107279el Class of Proteins for the
; TITLE OF INVENTION: Control of Plant Pests
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,336A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/838,219
; APPLICATION NUMBER: 08/838,219
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582

; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
US-09-233-336A-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 24
US-09-233-752A-11
; Sequence 11, Application US/09233752A
; Patent No. 6137033
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Marcha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 6137033el Class of Proteins for the
; TITLE OF INVENTION: Control of Plant Pests
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,752A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,219
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
US-09-233-752A-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 25
US-09-402-036-11
; Sequence 11, Application US/09402036
; Patent No. 6291156
; GENERAL INFORMATION:
; APPLICANT: Estruch, Juan J.
; APPLICANT: Yu, Cao-Guo
; APPLICANT: Warren, Gregory W.
; APPLICANT: Desai, Nalini
; APPLICANT: Koziel, Michael
; APPLICANT: Nye, Gordon
; TITLE OF INVENTION: Plant Pest Control
; FILE REFERENCE: S-21284C
; CURRENT APPLICATION NUMBER: US/09/402,036
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: PCT/EP98/01952
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 08/838,219
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,263
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,265
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/463,483
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/314,594
; PRIOR FILING DATE: 1994-09-09
; PRIOR APPLICATION NUMBER: 08/218,018
; PRIOR FILING DATE: 1994-03-24
; PRIOR APPLICATION NUMBER: 08/037,057
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(13)
; OTHER INFORMATION: Xaa represents any amino acid
US-09-402-036-11

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 26
US-09-904-226-11
; Sequence 11, Application US/09904226

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; Patent No. 6429360
; GENERAL INFORMATION:
; APPLICANT: Estruch, Juan J.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Desai, Nalini
; APPLICANT: Koziel, Michael
; APPLICANT: Nye, Gordon
; TITLE OF INVENTION: Plant Pest Control
; FILE REFERENCE: S-21284D
; CURRENT APPLICATION NUMBER: US/09/904,226
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP98/01952
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 08/838,219
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,263
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,265
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/453,483
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/314,594
; PRIOR FILING DATE: 1994-09-09
; PRIOR APPLICATION NUMBER: 08/218,018
; PRIOR FILING DATE: 1994-03-24
; PRIOR APPLICATION NUMBER: 08/037,057
; PRIOR FILING DATE: 1993-03-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE: <221> SITR<222> (1)..(13)<223> Xaa represents any amino acid
US-09-904-226-11

Query Match      22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VEPF 14
Db      6 VEPF 9

RESULT 27
5171684-21
; Patent No. 5171684
; APPLICANT: YEN, KWANG-MU;BLATT, LAWRENCE M.;KARL, MICHAEL R.
; TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
; MONOOXYGENASE OF PSEUDOMONAS MENDOCINA KR-1
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/590,374
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 177,631
; FILING DATE: 05-APR-1988
; SEQ ID NO:21:
; LENGTH: 14
5171684-21

Query Match      22.2%; Score 4; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
Db      9 YPVE 12

RESULT 28
US-08-080-073-25
```

```
; Sequence 25, Application US/08080073
; Patent No. 5384255
; GENERAL INFORMATION:
; APPLICANT: Ciechanover, Aaron J.
; APPLICANT: Blumenfeld, Nava
; APPLICANT: Gonen, Hedva
; TITLE OF INVENTION: Ubiquitin Carrier Enzyme E2-F1,
; Purification, Production, and Use
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/080,073
; FILING DATE: 21-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1448.0050000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-080-073-25

Query Match      22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PKYP 10
Db      7 PKYP 10

RESULT 29
US-08-967-101-168
; Sequence 168, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
```

```

; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-101-168

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PYTE 16
      |||||
Db      9 PTE 12

RESULT 30
US-08-687-956A-7
; Sequence 7, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; STREET: FLOOR
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PYTE 16
      |||||
Db      9 PTE 12

RESULT 31
US-08-687-956A-8
; Sequence 8, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; STREET: FLOOR
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVEP 13
      |||||
Db      11 PVEP 14

US-08-687-956A-7

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVEP 13
      |||||
Db      11 PVEP 14

US-08-687-956A-8

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVEP 13
      |||||
Db      11 PVEP 14

US-08-687-956A-8
```

RESULT 32
US-08-592-541-168
; Sequence 168, Application US/08592541
; Patent No. 5986054
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-592-541-168

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 33
US-08-591-629-5
; Sequence 5, Application US/08591629
; Patent No. 5993808
; GENERAL INFORMATION:
; APPLICANT: MELCHERS, Leo Sjoerd
; APPLICANT: APOTHEKER-DE GROOT, Marion
; APPLICANT: BOL, John Ferdinand
; APPLICANT: CORNELIJSSEN, Bernardus Johannes Clemens
; APPLICANT: LINTHORST, Hubertus Josephus Maria
; APPLICANT: PONSTEIN, Anne Silene
; APPLICANT: SELA-BUURLAGE, Marianne Beatrix
; TITLE OF INVENTION: Plant chitinases, DNA coding therefor and
; plants containing same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladass & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: NY
; COUNTRY: USA

ZIP: 10023-7604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC 4.86 SX 50 Mhz
; OPERATING SYSTEM: DOS 6.20
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,629
; FILING DATE: 15-FEB-96
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02761
; FILING DATE: 17-AUG-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93202425.0
; FILING DATE: 17-AUG-93
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, CLIFFORD J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-010627-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; DEVELOPMENTAL STAGE: TMV-induced
; TISSUE TYPE: leaf
US-08-591-629-5

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVE 12
Db 4 YPVE 7

RESULT 34
US-09-124-698-168
; Sequence 168, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:

Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	13	PFTF 16							
Db	9	PFTF 12							
RESULT 36									
US-08-496-841C-165									
; Sequence 165, Application US/08496841C									
; Patent No. 6210919									
; GENERAL INFORMATION:									
; APPLICANT: ST. GEORGE-HYSLOP, PETER H									
; ROMMENS, JOHANNA M									
; FRASER, PAUL E									
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED									
; TO ALZHEIMER'S DISEASE									
; NUMBER OF SEQUENCES: 175									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Darby & Darby, PC									
; STREET: 805 Third Avenue									
; CITY: New York									
; STATE: New York									
; COUNTRY: U.S.A.									
; ZIP: 10022									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: Patentin Release #1.0, Version #1.30									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/08/496,841C									
; FILING DATE: 28-Jun-1995									
; CLASSIFICATION: <Unknown>									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Paul F. Fehlner, Ph.D.									
; REGISTRATION NUMBER: 35,135									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: (212) 527-7700									
; TELEFAX: (212) 753-6237									
; INFORMATION FOR SEQ ID NO: 165:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 15 amino acids									
; TYPE: amino acid									
; STRANDEDNESS: single									
; TOPOLOGY: linear									
; MOLECULE TYPE: peptide									
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:									
; US-08-496-841C-165									
Query Match 22.2%; Score 4; DB 3; Length 15;									
Best Local Similarity 100.0%; Pred. No. 2.3e-02;									
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	13	PFTF 16							
Db	9	PFTF 12							
RESULT 37									
US-09-124-523-168									
; Sequence 168, Application US/09124523									
; Patent No. 6395960									
; GENERAL INFORMATION:									
; APPLICANT: ST. GEORGE-HYSLOP, PETER H									
; ROMMENS, JOHANNA M									
; APPLICANT: FRASER, PAUL E									
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED									
; TO ALZHEIMER'S DISEASE									
; NUMBER OF SEQUENCES: 183									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT									
; STREET: High Street Tower - 125 High Street									

```
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-124-523-168

Query Match          22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 PFTE 16
Db      9 PFTE 12

RESULT 38
US-09-636-796A-168
; Sequence 168, Application US/09636796A
; Patent No. 6485911
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; ROMMENS, JOHANNA M
; FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/636,796A
; FILING DATE: 11-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-641-803-8

Query Match          22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 PFTE 16
Db      9 PFTE 12

RESULT 39
US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-09-641-803-8

Query Match          22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PFPK 8
Db      3 PFPK 6

RESULT 40
US-08-602-999A-181
; Sequence 181, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
```

; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-181

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPKK 8
Db 5 PPKK 8
|||||

RESULT 41
US-09-500-124-181
; Sequence 181, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-181

Query Match 22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPKK 8
Db 5 PPKK 8
|||||

RESULT 42
US-08-602-999A-362
; Sequence 362, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-362

Query Match 22.2%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
||||

Db 10 PVEP 13

RESULT 43

US-09-500-124-362
; Sequence 362, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-362

Query Match 22.2%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
||||

Db 10 PVEP 13

RESULT 44

US-08-105-454-4
; Sequence 4, Application US/08105454
; Patent No. 6071715
; GENERAL INFORMATION:
; APPLICANT: Qian, Yue-Wei
; APPLICANT: Lee, Eva Y.-H. P.

; TITLE OF INVENTION: No. 6071715el Proteins Which Bind to
; TITLE OF INVENTION: Retinoblastoma Proteins and Their
; TITLE OF INVENTION: Encoding DNA Sequences
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 2300 One American Center
; CITY: Austin
; STATE: TX
; COUNTRY: USA
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,454
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSK:196/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-105-454-4

Query Match 22.2%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEMP 5
||||

Db 7 KEMP 10
||||

RESULT 45

US-09-407-687-8
; Sequence 8, Application US/09407687
; Patent No. 6548634
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; APPLICANT: Kavanaugh, Michael
; TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor
; TITLE OF INVENTION: Affinity
; FILE REFERENCE: 1517.001
; CURRENT APPLICATION NUMBER: US/09/407,687
; CURRENT FILING DATE: 1999-09-28
; EARLIER APPLICATION NUMBER: 60/102,667
; EARLIER FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-407-687-8

Query Match 22.2%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPP 7
Db 2 MPP 5

RESULT 46
US-09-227-357-664
; Sequence 664, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-664

Query Match 22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFPK 8
Db 16 PFPK 19

RESULT 47
US-09-556-877-236
; Sequence 236, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probet, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-236

Query Match 22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 17 YPVE 20

RESULT 48
US-09-556-877-237
; Sequence 237, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probet, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877

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; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
        |||||
Db      12 YPVE 15

RESULT 49
US-09-556-877-238
; Sequence 238, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-238

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
        |||||
Db      7 YPVE 10

RESULT 50
US-09-556-877-239
; Sequence 239, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-239

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
        |||||
Db      12 YPVE 15

RESULT 51
US-09-620-412C-236
; Sequence 236, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-236

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
        |||||
Db      17 YPVE 20

RESULT 52
US-09-620-412C-237
; Sequence 237, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
        |||||
Db      12 YPVE 15
```

```
RESULT 53
US-09-620-412C-238
; Sequence 238, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-238

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      9 YPVE 12
Db      7 YPVE 10

RESULT 54
US-09-620-412C-239
; Sequence 239, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-239

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      9 YPVE 12
Db      7 YPVE 10

RESULT 55
US-09-598-419-236
; Sequence 236, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
```

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; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-236

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      9 YPVE 12
Db      17 YPVE 20

RESULT 56
US-09-598-419-237
; Sequence 237, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      9 YPVE 12
Db      12 YPVE 15

RESULT 57
US-09-598-419-238
; Sequence 238, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-238
```

Query Match 22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 7 YPVE 10

RESULT 58

US-09-598-419-239
; Sequence 239, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; REFERENCE/DOCKET NUMBER: 210121.469C6
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-239

Query Match 22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 2 YPVE 5

RESULT 59

US-08-224-868-5
; Sequence 5, Application US/08224868
; Patent No. 5698448
; GENERAL INFORMATION:
; APPLICANT: Soldin, Steven J.
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE DRUG BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,868
; FILING DATE: 08-APR-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/200,404
; FILING DATE: 23-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/782,761
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,115

; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/279,176
; FILING DATE: 02-DEC-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/841,792
; FILING DATE: 26-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/521,074
; FILING DATE: 09-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 64688/125/CHRE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-224-868-5
Query Match 16.7%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
Db 2 EPF 4

RESULT 60

US-08-747-137-163
; Sequence 163, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: Yen, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "Pro-Amide"
US-08-747-137-163

Query Match 16.7%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 YPV 11
DB 1 YPV 3
RESULT 61
US-08-415-655-3
Sequence 3, Application US/08415655
Patent No. 6025480
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Lee, Mong-hong
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
TITLE OF INVENTION: SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/47418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-415-655-3

Query Match 16.7%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVE 12
DB 2 PVE 4
RESULT 62
US-09-330-970-19
Sequence 19, Application US/09330970
Patent No. 6146876
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: White, David
TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
TITLE OF INVENTION: Phosphodiesterase
FILE REFERENCE: 5800-28
CURRENT APPLICATION NUMBER: US/09/330,970
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: 09/277,423
EARLIER FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-09-330-970-19

Query Match 16.7%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TES 17
DB 1 TES 3

RESULT 63
US-09-357-952-27
Sequence 27, Application US/09357952
Patent No. 6248904
GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Who
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protea
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735-0030001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
US-09-357-952-27

Query Match 16.7%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

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Db      1 VEP 3
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RESULT 64
US-09-411-531A-1
; Sequence 1, Application US/09411531A
; Patent No. 6251391
; GENERAL INFORMATION:
; APPLICANT: Wilkinson, Randall
; TITLE OF INVENTION: Compositions and methods relating to the
; inhibition of casomorphin and glutomorphin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Graybeal Jackson Haley
; STREET: 777-108th Ave. NE, Suite 2460
; CITY: Bellevue
; STATE: Washington
; COUNTRY: USA
; ZIP: 98004-5117
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411.531A
; FILING DATE: 01-Oct-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 1776-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (425) 455-5575
; TELEFAX: (425) 455-1046
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-411-531A-1
Query Match      16.7%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PPP 7
|||
Db      2 PFP 4

RESULT 65
US-09-521-650-27
; Sequence 27, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
Query Match      16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VEP 13
|||
Db      1 VEP 3

RESULT 66
US-09-168-888-27
; Sequence 27, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules ar
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-27
Query Match      16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VEP 13
|||
Db      1 VEP 3

RESULT 67
US-09-187-859-199
; Sequence 199, Application US/09187859A
; Patent No. 6358920
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; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-187-859-199

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VEP 13
      |||
Db      1 VEP 3

RESULT 68
US-09-411-605A-1
; Sequence 1, Application US/09411605A
; Patent No. 6447772
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of Symptoms Of Au
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/411,605A
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-605A-1

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PFP 7
      |||
Db      2 PFP 4

RESULT 69
US-09-839-542B-199
; Sequence 199, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-839-542B-199

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VEP 13
      |||
Db      1 VEP 3

RESULT 70
5215966-12
; Patent No. 5215966
; APPLICANT: HOLZMANN, GUNTER;RADDATZ, PETER;SCHMITGES,
; CLAUS J.;MINCK, KLAUS OTTO;JONCZYK, ALFRED;SOMEROEK,
; JOHANNES;GANTE, JOACHIM
; TITLE OF INVENTION: PEPTIDE AND RENIN INHIBITORS
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/126,060
; FILING DATE: 27-NOV-1987
; SEQ ID NO:12:
; LENGTH: 4
5215966-12

Query Match          16.7%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PFP 7
      |||
Db      2 PFP 4

RESULT 71
5215966-14
; Patent No. 5215966
; APPLICANT: HOLZMANN, GUNTER;RADDATZ, PETER;SCHMITGES,
; CLAUS J.;MINCK, KLAUS OTTO;JONCZYK, ALFRED;SOMEROEK,
; JOHANNES;GANTE, JOACHIM
; TITLE OF INVENTION: PEPTIDE AND RENIN INHIBITORS
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/126,060
; FILING DATE: 27-NOV-1987
; SEQ ID NO:14:
; LENGTH: 4
5215966-14

Query Match          16.7%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFT 15
      |||
Db      2 PFT 4

RESULT 72
US-07-708-035-14
; Sequence 14, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohmad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; TITLE OF INVENTION: and Nervous Systems
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
|||
Db 1 VEP 3

RESULT 75
US-07-895-300A-12
; Sequence 12, Application US/07895300A
; Patent No. 5279823
; GENERAL INFORMATION:
; APPLICANT: Frenz, John
; APPLICANT: Shire, Steven J.
; APPLICANT: Sliwowski, Mary B.
; TITLE OF INVENTION: PURIFIED FORMS OF DNase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/895,300A
; FILING DATE: 19920608
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hensley, Max D.
; REGISTRATION NUMBER: 27,043
; REFERENCE/DOCKET NUMBER: 747
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-895-300A-12

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
|||
Db 1 FTE 3

Search completed: November 25, 2003, 20:29:59
Job time : 15.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-23
Perfect score: 18
Sequence: 1 SLRLTDEKHLPLPLVQ 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	27.8	18	2	S04229
2	4	22.2	9	2	S66419
3	4	22.2	15	2	S20410
4	4	22.2	16	2	S66613
5	4	22.2	19	2	S60633
6	4	22.2	20	1	LFBSU
7	4	22.2	20	2	S23742
8	4	22.2	20	2	F56046
9	4	22.2	20	2	S56005
10	3	16.7	6	2	B33932
11	3	16.7	7	2	PQ0663
12	3	16.7	8	2	T14906
13	3	16.7	8	2	S10783
14	3	16.7	9	2	PT0080
15	3	16.7	10	2	C26997
16	3	16.7	10	2	T36893
17	3	16.7	10	2	S18396
18	3	16.7	10	2	C35389
19	3	16.7	10	2	C39745
20	3	16.7	10	2	A61007
21	3	16.7	10	2	A56633
22	3	16.7	10	2	C39111
23	3	16.7	10	2	B45482
24	3	16.7	10	2	C39398
25	3	16.7	10	2	A47364
26	3	16.7	10	2	A61354
27	3	16.7	10	2	PX0060
28	3	16.7	10	2	T13838
29	3	16.7	10	2	T14219

30	16.7	10	2	C54226	light-harvesting p
31	16.7	10	2	PA0116	ferredoxin-NADP re
32	16.7	10	2	PS0220	ferredoxin-NADP re
33	16.7	11	2	S42449	ant1 protein - pha
34	16.7	11	2	D58502	27K bile and galb
35	16.7	11	2	I33098	173K exoantigen -
36	16.7	11	2	I52304	gene rSSTR4 protei
37	16.7	11	2	T17081	cytochrome-c oxida
38	16.7	11	2	P00034	dextranucrase (EC
39	16.7	12	2	S29764	alpha-macroglobuli
40	16.7	12	2	S65136	kallikrein K2 - hu
41	16.7	12	2	P00663	dyctrophin-associa
42	16.7	12	2	B60228	Fe mu (IgM) recept
43	16.7	12	4	JX0315	aminotransferase c
44	16.7	12	4	S49073	frame shifted cyta
45	16.7	13	2	PQ0491	self-incompatibili
46	16.7	13	2	A60856	inhibin alpha chai
47	16.7	13	2	S15755	actin 7 - soybean
48	16.7	13	2	JZVHP1	crabrolin - Europe
49	16.7	13	2	P00125	serine proteinase
50	16.7	13	2	PC4055	hypothetical 13 pr
51	16.7	13	2	D56661	S-locus specific g
52	16.7	13	2	S09019	hemolytic protein
53	16.7	13	2	I84603	deoxynucleotidyltr
54	16.7	13	2	A61458	Ig kappa chain V-I
55	16.7	13	2	S57571	T cell receptor al
56	16.7	13	2	PH0138	T-cell receptor be
57	16.7	14	2	JN0390	histamine-releasin
58	16.7	14	2	S19803	ubiquitin - potato
59	16.7	14	2	B29743	translation initia
60	16.7	14	2	C33098	223K exoantigen -
61	16.7	14	2	D61308	hemocyanin chain 5
62	16.7	14	2	PT0259	Ig heavy chain CRD
63	16.7	14	2	S57572	T cell receptor V-
64	16.7	14	2	PC4382	dehydrin 4.5K poly
65	16.7	15	2	A26997	unspecific monoocy
66	16.7	15	2	B56661	S-locus specific g
67	16.7	15	2	PQ0681	photosystem I 19.0
68	16.7	15	2	PQ0545	capsid protein VP1
69	16.7	15	2	B39109	hypothetical 1.5K
70	16.7	15	2	A35232	gentisate 1,2-diox
71	16.7	15	2	S61284	phosphoprotein, 80
72	16.7	15	2	S62820	protein disulfide-
73	16.7	15	2	PA0051	protein QF200016 -
74	16.7	15	2	PA0060	protein QF200037 -
75	16.7	15	2	PA0106	protein QF200076 -
76	16.7	15	2	PA0063	ubiquitin - fungus
77	16.7	15	2	PS0221	gastrin-releasing
78	16.7	15	2	PH1788	T cell receptor al
79	16.7	15	2	A56049	urinary tract ston
80	16.7	15	4	I38336	hypothetical TEL/M
81	16.7	16	2	I57530	gene c-fms protein
82	16.7	16	2	A61268	cytochrome P450-th
83	16.7	16	2	S29631	beta-glucosidase (
84	16.7	16	2	E58503	superoxide dismuta
85	16.7	16	2	T09741	photosystem I chai
86	16.7	16	2	H49039	T-cell receptor be
87	16.7	16	2	G24687	T-cell receptor be
88	16.7	16	2	JH0517	insulin-like growt
89	16.7	16	2	I46275	hemoglobin beta-x
90	16.7	16	2	PH1637	Ig H chain V-D-J r
91	16.7	16	2	B40291	cytochrome P450mtf
92	16.7	16	2	F54226	light-harvesting p
93	16.7	17	2	S66198	alcohol dehydrogen
94	16.7	17	2	JP0046	ribosomal protein
95	16.7	17	2	S15754	actin 6 - soybean
96	16.7	17	2	B44873	caldesmon - rabbit
97	16.7	17	2	I54269	vitamin D binding
98	16.7	17	2	A59069	excretory gland al
99	16.7	17	2	S60171	sex-lethal protein
100	16.7	17	2	A42920	fatty acid ethyl e

ALIGNMENTS

RESULT 1

S04229
M4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)
N:Alternate names: glycosylasparaginase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C:Accession: S04229
R:Tollersrud, O.K.; Aronson Jr., N.N.
Biochem. J. 260, 101-108, 1989
A:Title: Purification and characterization of rat liver glycosylasparaginase.
A:Reference number: S04228; MUID:89374025; PMID:2775174
A:Accession: S04229
A:Molecule type: protein
A:Residues: 1-18 <TOL>
C:Superfamily: M4-(beta-N-acetylglucosaminyl)-L-asparaginase
C:Keywords: hydrolase

Query Match 27.8%; Score 5; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17
|||
Db 3 PLPLV 7

RESULT 2

S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S66419
R:Kuwabara, T.
FEBS Lett. 371, 195-198, 1995

A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinacia oleracea
A:Reference number: S66419; MUID:95402209; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KOW>

Query Match 22.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
|||
Db 6 DVEK 9

RESULT 3

S20410
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)

N:Alternate names: LHCI protein kinase
C:Species: chloroplast Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: S20410
R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.
FEBS Lett. 298, 33-35, 1992

A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome b6/f complex
A:Reference number: S20410; MUID:92183823; PMID:1544419
A:Accession: S20410
A:Molecule type: protein
A:Residues: 1-15 <GAL>
C:Genetics:

A:Genome: chloroplast
C:Function:
A:Description: is responsible for the regulation of energy distribution between photosystem II and photosystem I
A:Note: does not exhibit redox-controlled activation
C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
|||
Db 6 DVEK 9

RESULT 4

S66613
protein p12E - Friend murine leukemia virus (fragments)

C:Species: Friend murine leukemia virus
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66613
R:Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.
Eur. J. Biochem. 232, 373-380, 1995
A:Title: Localization of the palmitoylation site in the transmembrane protein p12E of Friend murine leukemia virus
A:Reference number: S66613; MUID:96035869; PMID:7556184
A:Accession: S66613
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9;10-16 <HEN>

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
|||
Db 4 SLTL 7

RESULT 5

S60633
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion
C:Species: mitochondrion Artemia sp. (brine shrimp)
A:Variety: strain La Mata
C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
C:Accession: S60633
R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
J. Mol. Evol. 38, 156-168, 1994

A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and asexual populations
A:Reference number: S60624; MUID:94223692; PMID:8169960
A:Accession: S60633
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-19 <PER>

A:Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
A:Experimental source: strain La Mata
A:Note: the source is designated as Artemia parthenogenetica
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Genetics:

A:Gene: ATP8
A:Genome: mitochondrion
A:Genetic code: SGC4

C:Superfamily: H+-transporting ATP synthase protein 8
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 22.2%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LFLP 15
|||
Db 5 LFLP 8

RESULT 6

LFBSTU
tet leader peptide - Bacillus cereus plasmid pBC16

C:Species: Bacillus cereus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S09233
 R;Palva, A.; Vidgren, G.; Simonsen, M.; Rintala, H.; Laamanen, P.
 Nucleic Acids Res. 18, 1635, 1990
 A;Title: Nucleotide sequence of the tetracycline resistance gene of pBC16 from *Bacillus*
 A;Reference number: S09233; MUID:90221899; PMID:2109312
 A;Accession: S09233
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-20 <PAL>
 A;Cross-references: EMBL:X51366; NID:g39459; PIDN:CAA35750.1; PID:g39460
 C;Genetics:
 A;Genome: plasmid
 C;Superfamily: tet leader peptide

Query Match 22.2%; Score 4; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 ||||
 Db 17 SLTL 20

RESULT 7
 S23742
 tet leader peptide - *Staphylococcus hyicus*
 C;Species: *Staphylococcus hyicus*
 C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
 C;Accession: S23742
 R;Schwarz, S.; Cardoso, M.; Wegener, H.C.
 Antimicrob. Agents Chemother. 36, 580-588, 1992
 A;Title: Nucleotide sequence and phylogeny of the tet(L) tetracycline resistance determi
 A;Reference number: S23742; MUID:92321725; PMID:1622166
 A;Accession: S23742
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-20 <SCH>
 A;Cross-references: EMBL:X60828; NID:g43682; PIDN:CAA43219.1; PID:g43683
 A;Note: the authors translated the codon GGA for residue 14 as Ala
 C;Superfamily: tet leader peptide

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 ||||
 Db 17 SLTL 20

RESULT 8
 F56046
 urinary tract stone matrix protein 8, 14K - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
 C;Accession: F56046
 R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
 submitted to the Protein Sequence Database, February 1995
 A;Description: Isolation, characterization and sequence of stone proteins.
 A;Reference number: A56046
 A;Accession: F56046
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <BIN>

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLTD 6
 ||||
 Db 12 TLTD 15

RESULT 9
 S56005
 lysosomal protein 22K - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C;Accession: S56005
 R;Kuwana, T.; Mullock, B.M.; Luzio, J.P.
 Biochem. J. 308, 937-946, 1995
 A;Title: Identification of a lysosomal protein causing lipid transfer, using a fluor
 A;Reference number: S56005; MUID:97104296; PMID:8948454
 A;Accession: S56005
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <KUW>

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 ||||
 Db 17 SLTL 20

RESULT 10
 B33932
 Ig mu chain D region (D23) - mouse
 C;Species: *Mus musculus* (house mouse)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
 C;Accession: B33932
 R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
 A;Title: Two murine natural polyclonal autoantibodies are encoded by nonmutated ge
 A;Reference number: A33932; MUID:89282823; PMID:2499887
 A;Accession: B33932
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-6 <BAC>
 A;Cross-references: GB:M27107
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EKL 10
 ||||
 Db 1 EKL 3

RESULT 11
 PQ0663
 membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
 C;Species: porcine epidemic diarrhea virus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
 C;Accession: PQ0663
 R;Bridge, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
 J. Gen. Virol. 74, 1795-1804, 1993
 A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epid
 issable gastroenteritis virus.
 A;Reference number: JQ2191; MUID:93389433; PMID:8397280
 A;Accession: PQ0663
 A;Molecule type: mRNA
 A;Residues: 1-7 <BRI>
 A;Cross-references: GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:g584083
 C;Comment: This virus is coronavirus related to human coronavirus 229E.
 C;Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12
|||
Db 4 LHL 6

RESULT 12

Ti4906
hypothetical protein - parsley
C:Species: Petroselinum crispum (parsley)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14906
R:Feildbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Weishaar, B.
Plant Cell 6, 1607-1621, 1994
A:Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.
A:Reference number: Z18259; MUID:95128172; PMID:7827494
A:Accession: T14906
A>Status: preliminary;
A:Cross-references: EMBL:S75395; NID:g913201; PID:e194245
A:Molecule type: DNA
A:Residues: 1-8 <FEU>
A:Keywords: translated from GB/EMBL/DBSJ

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 4 TLT 6

RESULT 13

S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin.
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 2 PLP 4

RESULT 14

PT0080
60K Ca binding protein - edible frog (fragment)
C:Species: Rana esculenta (edible frog)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PT0080
R:Treveso, S.; Zorzato, P.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 444-450, 1991
A:Title: Frog brain expresses a 60 kDa Ca²⁺ binding protein similar to mammalian calretinin.
A:Reference number: PT0080; MUID:91207333; PMID:2018493
A:Accession: PT0080
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <TRE>

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
|||
Db 2 PLV 4

RESULT 15

C26997
unspecific monooxygenase (EC 1.14.14.1) isozyme E, phenobarbital-inducible, hepatic
N:Alternate names: cytochrome P450
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-Mar-1999
C:Accession: C26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16- α -hydroxylase.
A:Reference number: A26997; MUID:8800604; PMID:3651420
A:Accession: C26997
A:Molecule type: protein
A:Residues: 1-10 <GRA>
A:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
|||
Db 7 LTL 9

RESULT 16

I36893
apolipoprotein A-I - green monkey (fragment)
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C:Accession: I36893
R:Scorci-Thomas, M.; Kearns, M.W.
J. Biol. Chem. 266, 18045-18050, 1991
A:Title: Transcriptional regulation of the apolipoprotein A-I gene.
A:Reference number: A57766; MUID:92011532; PMID:1917942
A:Accession: I36893
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <RES>
A:Cross-references: GB:M69224; NID:g176486; PIDN:AAA35357.1; PID:g553152
C:Superfamily: apolipoprotein A-I

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
|||
Db 6 LTL 8

RESULT 17

S18396
probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter Hansenii (f)
C:Species: Acetobacter Hansenii
C>Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C:Accession: S18396
R:Levy, H.R.; Cook, C.
Arch. Biochem. Biophys. 291, 161-167, 1991
A:Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase.
A:Reference number: S18396; MUID:92027789; PMID:1929428
A:Accession: S18396
A:Molecule type: protein
A:Residues: 1-10 <LEV>
A:Experimental source: ATCC 23769
C:Function:
A:Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phosph

A:Pathway: pentose phosphate pathway
C:Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HLP 13
Db 2 HLP 4

RESULT 18

A56339
urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
C:Species: Morganella morganii
C>Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993
C:Accession: C35389
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A>Title: Morganella morganii urease: purification, characterization, and isolation of gene
A:Reference number: A35389; MUID:90264298; PMID:2345135
A:Accession: C35389
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HUA>
C:Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9
Db 8 VEK 10

RESULT 19

C39745
sphingomyelinase - Rhodococcus sp. (fragment)
C:Species: Rhodococcus sp.
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: C39745
R;Ito, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A>Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidases. Evidence using these activator proteins.
A:Reference number: A39745; MUID:91210321; PMID:1850427
A:Accession: C39745
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <ITO>

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15
Db 3 PLP 5

RESULT 20

A61007
hementin (EC 3.4.-.-) - Amazon leech (fragment)
C:Species: Haementeria ghilianii (Amazon leech)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A61007
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 359-369, 1990
A>Title: Purification and characterization of hementin, a fibrinogenolytic protease from
A:Reference number: A61007; MUID:90256973; PMID:2187898
A:Accession: A61007

A:Molecule type: protein
A:Residues: 1-10 <SWA>
C:Keywords: anticoagulant; hydrolase; saliva

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
Db 2 TLT 4

RESULT 21

A56333
neomyosuppressin - flesh fly (Sarcophaga bullata)
N;Alternate names: Neb-MS
C:Species: Sarcophaga bullata
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C:Accession: A56333
R;Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; Bueds, H.; De Loof, A.
Comp. Biochem. Physiol. C 102, 239-245, 1992
A>Title: Isolation, primary structure and synthesis of neomyosuppressin, a myoinhibitor
A:Reference number: A56333; MUID:93047886; PMID:1358537
A:Accession: A56333
A:Molecule type: protein
A:Residues: 1-10 <FON>

A:Experimental source: head
A>Note: sequence extracted from NCBI backbone (NCBIP:119072)
C:Keywords: amidated carboxyl end; neuropeptide
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TDV 7
Db 1 TDV 3

RESULT 22

C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C:Species: Eptatretus stoutii (Pacific hagfish)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: C39111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A>Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity
A:Reference number: A39111; MUID:91156684; PMID:2000382
A:Accession: C39111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <VAR>

C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17
Db 7 PLV 9

RESULT 23

B45482
platelet activating factor acetylhydrolase - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 05-May-1995
C:Accession: B45482
R;Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.

J. Biol. Chem. 268, 3857-3865, 1993
 A:Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Purified from platelets.
 A:Reference number: A45482; MUID:93179380; PMID:8440681
 A:Accession: B45482
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <STA>

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
 ||||
 Db 2 PLV 4

RESULT 24

C39398
 Fc mu (IgM) receptor surface complex gamma chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 20-Mar-1998
 C:Accession: C39398
 R:Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
 A:Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 genes.
 A:Reference number: A39398; MUID:91219496; PMID:2023945
 A:Accession: C39398
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <CAM>

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 ||||
 Db 4 LPL 6

RESULT 25

A47364
 placental lactogen-I precursor - mouse (fragment)
 C:Species: Mus sp. (mouse)
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
 C:Accession: A47364
 R:Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
 Mol. Endocrinol. 7, 181-188, 1993
 A:Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene promoter.
 A:Reference number: A47364; MUID:93225959; PMID:8469232
 A:Accession: A47364
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 <RES>
 A:Cross-references: GB:S58124; NID:g299449

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
 ||||
 Db 3 LTL 5

RESULT 26

A61354
 carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)
 N:Alternate names: endoplasmic reticulum protein ERP61; glucose regulated protein GRP58;
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C:Accession: A61354

R:Murthy, M.S.R.; Pande, S.V.
 Mol. Cell. Biochem. 122, 133-138, 1993
 A:Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the p115.
 A:Reference number: A61354; MUID:94049728; PMID:8232244
 A:Accession: A61354
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <MUR>
 C:Keywords: acyltransferase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
 ||||
 Db 6 LTD 8

RESULT 27

PX0060
 lysosome-associated membrane glycoprotein 2 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-1995
 C:Accession: PX0060
 R:Akasaka, K.; Yamaguchi, Y.; Furuno, K.; Tsuji, H.
 J. Biochem. 110, 922-927, 1991
 A:Title: Purification, some properties, and tissue distribution of a major lysosomal enzyme.
 A:Reference number: PX0060; MUID:92176167; PMID:1794981
 A:Accession: PX0060
 A:Molecule type: protein
 A:Residues: 1-10 <AKA>
 A:Experimental source: liver
 C:Keywords: glycoprotein; membrane protein

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
 ||||
 Db 5 LTD 7

RESULT 28

T13838
 cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
 C:Species: mitochondrion Bipes biporus
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
 C:Accession: T13838
 R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997
 A:Title: Two novel gene orders and the role of light-strand replication in rearrangement of cytochrome c oxidase subunit I in the Bipes biporus mitochondrion.
 A:Reference number: Z17789; MUID:97153826; PMID:9000757
 A:Accession: T13838
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 <MAC>
 A:Cross-references: EMBL:U71335; NID:gl753232; PID:gl753235; PIDN:AAB48271.1
 C:Genetics:
 A:Genome: mitochondrion
 A>Note: COL
 C:Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
 ||||
 Db 2 SLT 4

RESULT 29

TL4219
cytochrome-c oxidase (EC 1.9.3.1) chain I - Xenosaurus grandis mitochondrion (fragment)
C;Species: Mitochondrion Xenosaurus grandis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: TL4219
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: Z17789; MUID: 97153826; PMID: 9000757
A;Accession: TL4219
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71333; NID: g5739536; PIDN: AAC62821.1; PID: g1753275
C;Genetics:
A;Genome: mitochondrion
A;Note: C01
C;Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
DB 2 TLT 4

RESULT 30

C54226
light-harvesting protein B-830 alpha-3 chain - Chromatium purpuratum (fragment)
C;Species: Chromatium purpuratum
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: C54226
R;Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.
Biochemistry 33, 2178-2184, 1994
A;Title: Purification and characterization of the peripheral antenna of the purple-sulfur
A;Reference number: A54226; MUID: 94162224; PMID: 8117674
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <KER>
C;Keywords: antenna complex; light-harvesting polypeptide

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LVQ 18
DB 7 LVQ 9

RESULT 31

PA0116
ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 03-Jun-2002
C;Accession: PA0116
R;Kamo, M.; Tsugita, A.
submitted to JIPID, March 1995
A;Reference number: PA0114
A;Accession: PA0116
A;Molecule type: protein
A;Residues: 1-10 <KAM>
A;Experimental source: leaf
C;Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
DB 1 VEK 3

RESULT 32

PS0220
ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C;Accession: PS0220
R;Uchiyama, Y.; Tsugita, A.
submitted to JIPID, August 1991
A;Reference number: PS0205
A;Accession: PS0220
A;Molecule type: protein
A;Residues: 1-10 <UCH>
C;Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
DB 1 VEK 3

RESULT 33

S42449
ant1 protein - phage P7
C;Species: phage P7
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C;Accession: S42449
R;Citron, M.; Schuster, H.
Cell 62, 591-598, 1990
A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A;Reference number: S42448; MUID: 90335968; PMID: 1696181
A;Accession: S42449
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <CIT>
A;Cross-references: EMBL:M35139; NID: g215705; PIDN: AAA32437.1; PID: g215707

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
DB 4 PLV 6

RESULT 34

D58502
27K bile and gallbladder stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: D58502
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: D58502
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BIN>
A;Experimental source: human bile and gallbladder stones

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTD 6
|||
Db 4 LTD 6

RESULT 35

133098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: I33098

R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098

A:Accession: I33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
|||
Db 6 LPL 8

RESULT 36

I52304
gene rSSTR4 protein - rat (fragment)
C:Species: Rattus sp. (rat)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
C:Accession: I52304
R:Xu, Y.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 206, 935-941, 1995
A>Title: Characterization of the proximal promoter region of the rat somatostatin receptor
A:Reference number: I52304; MUID:95134278; PMID:7832807
A:Accession: I52304
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S75475; NID:9914315
C:Genetics:
A:Gene: rSSTR4

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
|||
Db 7 LPL 9

RESULT 37

Ti7081
cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynocephalus raddei mitochondrion (fragment)
C:Species: mitochondrion Phrynocephalus raddei
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C:Accession: Ti7081

R:Nacey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997

A>Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A:Reference number: Z18674; MUID:97315309; PMID:9169559
A:Accession: Ti7081

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <MAC>

A:Cross-references: EMBL:U82691; NID:G3603148; PID:G3603151; PIDN:AA62302.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
|||
Db 3 TLT 5

RESULT 38

PU0034
dextransucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)
C:Species: Streptococcus bovis

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Sep-1996
C:Accession: PU0034

R:Uezono, Y.; Tsumori, H.; Mukasa, H.
submitted to JIPID, October 1993

A>Description: Purification and properties of glucosyltransferase synthesizing 1,6-a

A:Reference number: PU0034

A:Accession: PU0034

A:Molecule type: protein

A:Residues: 1-11 <UE2>

A:Experimental source: ATCC 9809

C;Keywords: Glycosyltransferase; hexosyltransferase

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
|||
Db 7 TLT 9

RESULT 39

S29764
alpha-macroglobulin proteinase inhibitor - bullfrog (fragment)
C:Species: Rana catesbeiana (bullfrog)

C>Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 07-May-1999

C:Accession: S29764

R:Rubenstein, D.S.; Thøgersen, I.B.; Pizzo, S.V.; Enghild, J.J.

Biochem. J. 290, 85-95, 1993

A>Title: Identification of monomeric alpha-macroglobulin proteinase inhibitors in bi

teins: inhibitor from the American bullfrog Rana catesbeiana.

A:Reference number: S29764; MUID:93176138; PMID:7679897

A:Accession: S29764

A:Molecule type: protein

A:Residues: 1-12 <RUB>

A:Experimental source: plasma

C:Function:

A>Description: inhibits the proteinases of different catalytic class

C:Superfamily: alpha-2-macroglobulin

C;Keywords: monomer; proteinase inhibitor

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HLP 13
|||
Db 3 HLP 5

RESULT 40

S65136

kallikrein K2 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S65136

R:Depertes, D.; Chapdelaine, P.; Tremblay, R.R.; Brunet, C.; Berton, J.; Hebert, J.

Biochim. Biophys. Acta 1245, 311-316, 1995

A;Title: Isolation of prostatic kallikrein hK2, also known as hGK-1, in human seminal pl
 A;Reference number: S65136; MUID:96125726; PMID:8541306
 A;Accession: S65136
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <DEP>

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12
 |||
 Db 7 LHL 9

RESULT 41

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C;Accession: PN0663

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0663

A;Molecule type: protein

A;Residues: 1-12 <YOS>

A;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
 |||
 Db 3 PLP 5

RESULT 42

B60228

Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)

N;Alternate names: membrane protein B29

C;Species: Mus musculus (house mouse)

C;Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 20-Mar-1998

C;Accession: B60228; B39398

R;Hombach, J.; Lottspeich, F.; Reth, M.

Eur. J. Immunol. 20, 2795-2799, 1990

A;Title: Identification of the genes encoding the IgM-alpha and Ig-beta components of th

A;Reference number: A60228; MUID:91099432; PMID:2269334

A;Accession: B60228

A;Molecule type: protein

A;Residues: 1-12 <HOM>

R;Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.

Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991

A;Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g

A;Reference number: A39398; MUID:91219496; PMID:2023945

A;Accession: B39398

A;Molecule type: protein

A;Residues: 'XX', 3-10 <CAM>

C;Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 |||
 Db 4 LPL 6

RESULT 43

JX0315

aminotransferase chimera DY18 - synthetic (fragment)

C;Species: synthetic

C;Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999

C;Accession: JX0315

R;Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.

J. Biochem. 115, 568-577, 1994

A;Title: Construction of aminotransferase chimeras and analysis of their substrate sp

A;Reference number: JX0315; MUID:94334304; PMID:8056774

A;Accession: JX0315

A;Molecule type: DNA

A;Residues: 1-12 <MIY>

C;Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransf

C;Comment: The parental enzymes catalyze the reversible amino group transfer reaction

C;Keywords: aminotransferase

Query Match 16.7%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
 |||
 Db 7 LTL 9

RESULT 44

S49073

frame shifted cytochrome accessory protein HMW3 - Mycoplasma pneumoniae (fragment)

N;Alternate names: H+-transporting ATP synthase (EC 3.6.3.14) alpha chain (misidentif

C;Species: Mycoplasma pneumoniae

C;Date: 28-Aug-1998 #sequence_revision 28-Aug-1998 #text_change 19-Apr-2002

C;Accession: S49073

R;Proft, T.; Herrmann, R.

Mol. Microbiol. 13, 337-348, 1994

A;Title: Identification and characterization of hitherto unknown Mycoplasma pneumonia

A;Reference number: S49059; MUID:95075318; PMID:7984111

A;Accession: S49073

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-12 <PRO>

A;Cross-references: EMBL:Z32665; NID:9474163; PIDN:CAA83583.1; PID:G591348

A;Experimental source: clone D2-16

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994

A;Note: the GenBank entry MPPASAI, release 106.0, translates the ATC codon, 1 in this

C;Comment: The nucleotide sequence translated in an alternative reading frame is iden

C;Genetics:

A;Genetic code: SGC3

Query Match 16.7%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 |||
 Db 3 TLT 5

RESULT 45

PQ0491

self-incompatibility locus glycoprotein delta - wild cabbage (fragment)

C;Species: Brassica oleracea (wild cabbage)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Oct-1997

C;Accession: PQ0491

R;Gaude, T.; Friiry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.

Plant Cell 5, 75-86, 1993

A;Title: Expression of a self-incompatibility gene in a self-compatible line of Brass

A;Reference number: JQ1733; MUID:93177215; PMID:8439745

A;Accession: PQ0491

A;Molecule type: protein

A;Residues: 1-13 <GAU>

A;Experimental source: stigma, var. acephala p57s1

C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot

C;Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT 3
|||
Db 9 SLT 11

RESULT 46

A60856
inhibin alpha chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60856
R;Levensha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenthal
J. Endocrinol. 113, 213-221, 1987
A;Title: Isolation of inhibin from ovine follicular fluid.
A;Reference number: A60856; MUID:87224684; PMID:3585232
A;Accession: A60856
A;Molecule type: protein
A;Residues: 1-13 <LEV>
C;Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C;Superfamily: inhibin
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15
|||
Db 4 PLP 6

RESULT 47

S15755
actin 7 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C;Accession: S15755
R;Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A;Reference number: S15754; MUID:91346640; PMID:2102831
A;Accession: S15755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <PEA>
A;Cross-references: EMBL:X17120; NID:gi18527; PIDN:CAA34980.1; PID:gi18528
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17
|||
Db 9 PLV 11

RESULT 48

JZVHP1
crabrolin - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A01781
R;Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A;Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,

A;Reference number: A92441; MUID:84289390; PMID:6206053

A;Accession: A01781
A;Molecule type: protein
A;Residues: 1-13 <ARG>
C;Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; venom
F;13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
|||
Db 2 LPL 4

RESULT 49

PN0125
serine proteinase (EC 3.4.21.-) - Actinomyces sp. (fragment)
C;Species: Actinomyces sp.
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 27-Jan-1995
C;Accession: PN0125
R;Mosolova, O.V.; Rudenskaya, G.N.; Stepanov, V.M.; Khodova, O.M.; Tsaplina, I.A.
Biochimia 52, 414-422, 1987
A;Title: Glu, Asp-specific proteinase from Actinomyces.
A;Reference number: PN0125
A;Accession: PN0125
A;Molecule type: protein
A;Residues: 1-13 <MOS>
A;Note: article in Russian with English abstract
C;Keywords: hydrolase; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TDV 7
|||
Db 5 TDV 7

RESULT 50

PC4055
hypothetical 13 protein - Frankia sp. (fragment)
C;Species: Frankia sp.
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 27-Oct-1995
C;Accession: PC4055
R;Harriott, O.T.; Hosted, T.J.; Benson, D.R.
Gene 161, 63-67, 1995
A;Title: Sequences of nifX, nifZ, nifH, nifB and two ORF in the Frankia nitrogen fix:
A;Reference number: JC4203; MUID:95369734; PMID:7642138
A;Accession: PC4055
A;Molecule type: DNA
A;Residues: 1-13 <HAR>
A;Cross-references: GB:L29299

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTD 6
|||
Db 10 LTD 12

RESULT 51

D56661
S-locus specific glycoprotein (allele S3) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: D56661

```

R;Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal seq
A;Reference number: A56661; MUID:92090397; PMID:1752245
A;Accession: D56661
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <GAU>
A;Experimental source: stigma extracts, var. acephala
A;Note: sequence extracted from NCBI backbone (NCBIP:72300)
C;Comment: This glycoprotein, expressed only in stigmas, plays an important role in the
C;Keywords: glycoprotein; polymorphism

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
Db 9 SLT 11

RESULT 52
S09019
hemolytic protein B9 - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S09019
R;Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erpamer, G.F.; Barra, D.; Bossa, F.
Biochim. Biophys. Acta 1033, 318-323, 1990
A;Title: Purification and characterization of bioactive peptides from skin extracts of R
A;Reference number: S09018; MUID:90198965; PMID:2317508
A;Accession: S09019
A;Molecule type: protein
A;Residues: 1-13 <STM>

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
Db 2 LPL 4

RESULT 53
I84603
deoxynucleotidyltransferase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I84603
R;Koikwai, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A;Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in mam
A;Reference number: I45884; MUID:87213162; PMID:3579900
A;Accession: I84603
A;Status: preliminary; translated from GB/EMBL/DDJ
A;Molecule type: mRNA
A;Residues: 1-13 <RES>
A;Cross-references: GB:M26144; NID:G951194; PIDN:AAA74588.1; PID:G951195
C;Genetics:
A;Gene: GDB:DNTT
A;Cross-references: GDB:I19100; OMIM:187410
A;Map position: 10q23-10q24

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 9 PLP 11

```

```

RESULT 54
A61458
Ig kappa chain V-I region (BOU) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C;Accession: A61458; ELO156
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A;Title: Expression of a public idotype by human monoclonal IgM directed to myelin-a
A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: A61458
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Comment: This protein is one of monoclonal IgM reactive with myeloma-associated gly
C;Keywords: heterotetramer; immunoglobulin

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
Db 10 TLT 12

RESULT 55
S57571
T cell receptor alpha chain V-J region (clone PP7 and others) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57571; S57573; S57576
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversifie
A;Reference number: S57494
A;Accession: S57571
A;Molecule type: mRNA
A;Residues: 1-13 <BUR>
A;Cross-references: EMBL:Z49948; NID:G887496; PIDN:CAA90219.1; PID:G887497
A;Experimental source: clone PP7
A;Accession: S57573
A;Molecule type: mRNA
A;Residues: 1-13 <BUL>
A;Cross-references: EMBL:Z49952; NID:G887512; PIDN:CAA90223.1; PID:G887513
A;Experimental source: clone RL16
C;Keywords: T-cell receptor

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EXL 10
Db 8 EXL 10

RESULT 56
PH0138
T-cell receptor beta chain V-D-J region C8 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C;Accession: PH0138
R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.;
J. Exp. Med. 173, 19-24, 1991
A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the con
A;Reference number: PH0135; MUID:91086843; PMID:1702137
A;Accession: PH0138

```

A;Molecule type: mRNA
A;Residues: 1-13 <MAR>
C;Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
|||
Db 11 EKL 13
|||

RESULT 57

JN0390
histamine-releasing peptide II - oriental hornet
N;Alternate names: venom protein HR-2
C;Species: Vespa orientalis (oriental hornet)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
C;Accession: JN0390; S10919
R;Miroschnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus
Bioorg. Khim. 7, 1467-1477, 1981
A;Title: Structure and properties of histamine releasing peptides from the venom of Vesp
A;Reference number: JN0389
A;Accession: JN0390
A;Molecule type: protein
A;Residues: 1-14 <MIR>
R;Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St
A;Reference number: S06445
A;Accession: S10919
A;Molecule type: protein
A;Residues: 1-14 <TUI>
C;Superfamily: crabrolin
C;Keywords: amidated carboxyl end; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 2 LPL 4
|||

RESULT 58

S19803
ubiquitin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-Sep-1993
C;Accession: S19803
R;Belknap, W.
submitted to the EMBL Data Library, January 1992
A;Reference number: S19798
A;Accession: S19803
A;Molecule type: mRNA
A;Residues: 1-14 <BEL>
A;Cross-references: EMBL:Z11667
C;Superfamily: ubiquitin; ubiquitin homology

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 7 TLT 9
|||

RESULT 59

B29743
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)

translation initiation factor eIF-2 alpha chain-associated kinase phosphopeptide - re
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Oct-1997
C;Accession: B29743
R;Rose, D.W.; Wettenhall, R.E.H.; Kudlicki, W.; Kramer, G.; Hardesty, B.
Biochemistry 26, 6583-6587, 1987
A;Title: The 90-kilodalton peptide of the heme-regulated eIF-2-alpha kinase has sequ
A;Reference number: A9521; MUID:88107571; PMID:3427028
A;Accession: B29743
A;Molecule type: protein
A;Residues: 1-14 <ROS>
A;Experimental source: reticulocyte
C;Superfamily: heat shock protein 90

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
|||
Db 3 SLT 5
|||

RESULT 60

C33098
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: C33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098
A;Accession: C33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
|||
Db 6 EKL 8
|||

RESULT 61

D61308
hemocyanin chain 5A - Sahara scorpion (fragment)
C;Species: Androctonus australis (Sahara scorpion)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: D61308
R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
FEBS Lett. 106, 289-291, 1979
A;Title: Structural characterization of seven different subunits in Androctonus aust:
A;Reference number: A61308; MUID:80047238; PMID:499512
A;Accession: D61308
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 10 LPL 12
|||

RESULT 62

PT0259
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0259
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
C:Accession: PT0259
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
|||
Db 2 TLT 4
|||

RESULT 63
S57572
T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57572
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified
A:Reference number: S57494
C:Accession: S57572
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-14 <BUR>
A:Cross-references: EMBL:Z49957; NID:G887478; PIDN:CAA90228.1; PID:G887479
C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
|||
Db 10 PLV 12
|||

RESULT 64
PC4382
dehydrin 4.5K polypeptide - Soybean (fragment)
N:Alternate names: acid soluble 26K protein
C:Species: Glycine max
C:Date: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 18-Jul-2001
C:Accession: PC4382
R:Momma, M.; Haraguchi, K.; Saito, M.; Chikuni, K.; Harada, K.
Biosci. Biotechnol. Biochem. 61, 1286-1291, 1997
A:Title: Purification and characterization of the acid soluble 26-kDa polypeptide from
A:Reference number: PC4380; MUID:97446521; PMID:9301109
C:Accession: PC4382
A:Molecule type: protein
A:Residues: 1-14 <MOM>
A:Experimental source: seed
C:Comment: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
|||
Db 6 EKL 8
|||

RESULT 65
A26997
unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)
N:Alternate names: cytochrome P450B
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-Mar-1999
C:Accession: A26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha
A:Reference number: A26997; MUID:8800604; PMID:3651420
C:Accession: A26997
A:Molecule type: protein
A:Residues: 1-15 <GRA>
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembr

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
|||
Db 7 LTL 9
|||

RESULT 66
B56661
S-locus specific glycoprotein P57 beta - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 31-Oct-1997
C:Accession: B56661
R:Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal
A:Reference number: A56661; MUID:92090397; PMID:1752245
C:Accession: B56661
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <GAU>
A:Experimental source: stigma extracts, var. acephala, self-compatible line P57
A:Note: sequence extracted from NCBI backbone (NCBIP:72302)
C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in t
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
|||
Db 11 SLT 13
|||

RESULT 67
PQ0681
photosystem I 19.0K D1 chain - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C:Accession: PQ0681
R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyama, M.
Plant Physiol. 102, 1259-1267, 1993
A:Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal ar
A:Reference number: PQ0667; MUID:94105345; PMID:8278548
C:Accession: PQ0681
A:Molecule type: protein
A:Residues: 1-15 <OBO>
C:Superfamily: photosystem I chain II
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
|||
Db 2 VEK 4

RESULT 68

PQ0545
capsid protein VP19C - human herpesvirus 1 (fragment)
C;Species: human herpesvirus 1
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PQ0545
R;Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
A;Reference number: PQ0544; MUID:93019027; PMID:1328483
A;Accession: PQ0545
A;Molecule type: protein
A;Residues: 1-15 <DAV>
A;Experimental source: strain 17
C;Genetics:
A;Gene: UL38
C;Keywords: capsid protein

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 5 PLP 7

RESULT 69

B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A;Reference number: B39109; MUID:91156678; PMID:1705704
A;Accession: B39109
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <HAN>
A;Cross-references: GB:M58406
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative core
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Accession: JQ1585
A;Molecule type: genomic RNA
A;Residues: 1-15 <KUM>
A;Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 10 PLP 12

RESULT 70

A35232
gentisate 1,2-dioxygenase (EC 1.13.11.4) - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni

C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 23-Jun-1993
C;Accession: A35232
R;Harpel, M.R.; Lipscomb, J.D.
J. Biol. Chem. 265, 6301-6311, 1990
A;Title: Gentisate 1,2-dioxygenase from Pseudomonas. Purification, characterization,
A;Reference number: A35232; MUID:90202907; PMID:2156846
A;Accession: A35232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <HAR>
C;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LVQ 18
|||
Db 2 LVQ 4

RESULT 71

S61284
phosphoprotein, 80K - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 25-Apr-1997
C;Accession: S61284
R;Freestone, P.; Grant, S.; Toth, I.; Norris, V.
Mol. Microbiol. 15, 573-580, 1995
A;Title: Identification of phosphoproteins in Escherichia coli.
A;Reference number: S61284; MUID:95302968; PMID:7783627
A;Accession: S61284
A;Molecule type: protein
A;Residues: 1-15 <PRE>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
|||
Db 3 EKL 5

RESULT 72

S62620
protein disulfide-isomerase (EC 5.3.4.1) - castor bean (fragment)
C;Species: Ricinus communis (castor bean)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 17-Mar-1999
C;Accession: S62620
R;Coughlan, S.J.; Hastings, C.; Winfrey Jr., R.J.
Eur. J. Biochem. 235, 215-224, 1996
A;Title: Molecular characterization of plant endoplasmic reticulum: identification o:
A;Reference number: S62620; MUID:96202938; PMID:8631332
A;Accession: S62620
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <COU>
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
|||
Db 11 LTL 13

RESULT 73

PA0051
protein QP200016 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C/Accession: PA0051
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0051
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEX 9
|||
Db 2 VEX 4

RESULT 74
PA0060
protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C/Accession: PA0060
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0060
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
|||
Db 4 PLP 6

RESULT 75
PA0106
protein QF200076 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C/Accession: PA0106
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0106
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
|||
Db 6 LTL 8

Search completed: November 25, 2003, 19:36:09
Job time : 13.3488 secs

GenCore version 5.1.1.6

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDEKHLPLPLVQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	13	1	TEJA_RANJA
2	4	22.2	17	1	PH3_ERAM
3	4	22.2	20	1	LPTR_BACST
4	3	16.7	8	1	ALL6_CYDPO
5	3	16.7	10	1	ESL_LACCA
6	3	16.7	10	1	NS1_MYCTU
7	3	16.7	10	1	URE3_MORMO
8	3	16.7	11	1	TIN4_HOPTI
9	3	16.7	12	1	PPK4_PERAM
10	3	16.7	12	1	TIN2_HOPTI
11	3	16.7	12	1	TIN3_HOPTI
12	3	16.7	12	1	TM2A_METWA
13	3	16.7	13	1	ACT7_SOYBN
14	3	16.7	13	1	CRBL_VESCR
15	3	16.7	13	1	CRIC_RANES
16	3	16.7	13	1	FR12_PEA
17	3	16.7	13	1	HPB9_RANES
18	3	16.7	13	1	IDHP_RAT
19	3	16.7	13	1	TEMA_RANTE
20	3	16.7	13	1	TEMF_RANTE
21	3	16.7	14	1	CRBL_VESOR
22	3	16.7	14	1	ECDC_LYMDI
23	3	16.7	15	1	CYSK_CLOPA
24	3	16.7	15	1	GTS_ASADI
25	3	16.7	15	1	ONCI_ONCMY
26	3	16.7	15	1	UC29_MAIZE
27	3	16.7	16	1	ARCD_PSEPU
28	3	16.7	16	1	FIBA_MELME
29	3	16.7	16	1	IBP4_PIG
30	3	16.7	16	1	MMPX_SOLTU
31	3	16.7	17	1	ACT6_SOYBN
32	3	16.7	17	1	EPG_THRAQ
33	3	16.7	18	1	RL23_HALCU

RESULT 1

34	3	16.7	18	1	UC21_MAIZE
35	3	16.7	19	1	H170_RAT
36	3	16.7	19	1	LANA_ACTLG
37	3	16.7	19	1	LPGE_ECOTI
38	3	16.7	19	1	MIFH_TRISP
39	3	16.7	20	1	FIBB_SHERP
40	3	16.7	20	1	FRHA_METRA
41	3	16.7	20	1	HET1_RADMG
42	3	16.7	20	1	M117_BOVIN
43	3	16.7	20	1	TENA_ACTTE
44	3	16.7	20	1	TENB_ACTTE
45	3	16.7	20	1	TL22_SPIOL
46	3	16.7	20	1	YPRB_SERMA
47	2	11.1	5	1	BIOA_CITPR
48	2	11.1	5	1	PRCT_PERAM
49	2	11.1	6	1	TMOF_SAREU
50	2	11.1	6	1	TRPI_PSEBU
51	2	11.1	6	1	VP19_HSVIK
52	2	11.1	7	1	CCF1_ENTFA
53	2	11.1	7	1	MNP1_LEPDE
54	2	11.1	7	1	UN06_PINPS
55	2	11.1	8	1	ACT_CARMA
56	2	11.1	8	1	AXH_TABAT
57	2	11.1	8	1	CAD1_ENTFA
58	2	11.1	8	1	COM2_CONFU
59	2	11.1	8	1	CPD1_ENTFA
60	2	11.1	8	1	HTF2_PERAM
61	2	11.1	8	1	PLP_BRANA
62	2	11.1	8	1	PKP3_PERAM
63	2	11.1	8	1	RT34_BOVIN
64	2	11.1	8	1	UPAA_HUMAN
65	2	11.1	9	1	ALC_CHLRE
66	2	11.1	9	1	BUK_CLOPA
67	2	11.1	9	1	FAR5_PANRE
68	2	11.1	9	1	FAR5_PENMO
69	2	11.1	9	1	FAR9_ASCSU
70	2	11.1	9	1	FIBB_MACTU
71	2	11.1	9	1	MGMT_BOVIN
72	2	11.1	9	1	MOSH_CLYQA
73	2	11.1	9	1	OXYA_SQUAC
74	2	11.1	9	1	OKYT_RABIT
75	2	11.1	9	1	PH1_LYCSB
76	2	11.1	9	1	RT33_BOVIN
77	2	11.1	9	1	SAMP_MUSCA
78	2	11.1	9	1	TAL1_PICUA
79	2	11.1	9	1	TAL3_PICUA
80	2	11.1	9	1	UHA2_HUMAN
81	2	11.1	9	1	ULAD_HUMAN
82	2	11.1	9	1	ULAE_HUMAN
83	2	11.1	9	1	UPA3_HUMAN
84	2	11.1	9	1	UPA6_HUMAN
85	2	11.1	9	1	UPA7_HUMAN
86	2	11.1	10	1	AH3_PRUSE
87	2	11.1	10	1	AL15_CARMA
88	2	11.1	10	1	ANGT_BOVIN
89	2	11.1	10	1	ANGT_CHICK
90	2	11.1	10	1	APF_CAPGI
91	2	11.1	10	1	BRK_ONCMY
92	2	11.1	10	1	CATB_SHERP
93	2	11.1	10	1	COXA_ONCMY
94	2	11.1	10	1	COXK_ONCMY
95	2	11.1	10	1	FARP_LOCMY
96	2	11.1	10	1	FARP_MANSE
97	2	11.1	10	1	GAJU_HUMAN
98	2	11.1	10	1	GONI_PETWA
99	2	11.1	10	1	GON2_CHEPR
100	2	11.1	10	1	GON3_ONCKB

ALIGNMENTS

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TEJA_RANJA
ID TEJA_RANJA STANDARD; PRT; 13 AA.
AC P83307;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tempurin-1Ja.
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=21826910; PubMed=11835990;
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT "Antimicrobial peptides with atypical structural features from the
RL skin of the Japanese brown frog Rana japonica.";
RL Peptides 23:419-425(2002).
CC -1- FUNCTION: Antibacterial activity against the Gram-negative
CC bacterium E.coli and the Gram-positive bacterium S.aureus.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=1405; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13
SQ SEQUENCE 13 AA; 1407 MW; 3EF713EA610A2448 CRC64;

Query Match 22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
Db 2 LPLV 5

RESULT 2
PH3_PERAM
ID PH3_PERAM STANDARD; PRT; 17 AA.
AC P82696;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide hormone 3 (Pee-VEAcid 1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20140865; PubMed=10676456;
RA Predel R., Eckert M., Holman G.M.;
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs
RT of insects.";
RL Ann. N.Y. Acad. Sci. 897:282-290(1999).
CC -1- FUNCTION: UNKNOWN.
CC -1- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.
KW Neuropeptide.
SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F86E8EB CRC64;

Query Match 22.2%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTLT 5
Db 3 LTLT 6

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RESULT 3
LPTR_BACST
ID LPTR_BACST STANDARD; PRT; 20 AA.
AC P05658;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tetracycline resistance leader peptide.
DE TETL.
GN Bacillus stearothermophilus,
OS Bacillus cereus, and
OS Staphylococcus hyicus.
OG Plasmid pTHT15, Plasmid pBC16, and Plasmid pSTEL.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422, 1396, 1284;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=B.stearothermophilus; PLASMID=pTHT15;
RX MEDLINE=86031344; PubMed=2996983;
RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
RT "Nucleotide sequence of the tetracycline resistance gene of pTHT15, a
RT thermophilic Bacillus plasmid: comparison with staphylococcal TcR
RT controls.";
RL Gene 37:131-138(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=B.cereus; PLASMID=pBC16;
RX MEDLINE=90221899; PubMed=2109312;
RA Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;
RT "Nucleotide sequence of the tetracycline resistance gene of pBC16
RT from Bacillus cereus.";
RL Nucleic Acids Res. 18:1635-1635(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=S.hyicus; PLASMID=pSTEL;
RX MEDLINE=92321725; PubMed=1622166;
RA Schwarz S., Cardoso M., Wegener H.C.;
RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline
RT resistance determinant encoded by plasmid pSTEL from Staphylococcus
RT hyicus.";
RL Antimicrob. Agents Chemother. 36:580-588(1992).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; D00006; BAA00004.1; -
CC EMBL; M11036; AAA22850.1; -
CC EMBL; X51366; CAA35750.1; -
CC EMBL; X60828; CAA43219.1; -
CC PIR; S09233; LFBSTU.
CC PIR; S23742; S23742.
CC Leader peptide; Antibiotic resistance; Plasmid.
KW SEQUENCE 20 AA; 2253 MW; 18D0F4A6CA231CAL CRC64;

Query Match 22.2%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 17 SLTL 20

RESULT 4
ALL6_CYDPO
ID ALL6_CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiaastatin 6.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Dave H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.,
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
 Db 1 LPL 3

RESULT 5
 ESL_LACCA
 ID -ESL_LACCA STANDARD; PRT; 10 AA.
 AC P81758;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Putative esterase/lipase (EC 3.1.1.-) (Fragment).
 OS Lactobacillus casei.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1582;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=IFPL731;
 RA Lopez de Felipe F.;
 RL Submitted (MAR-1999) to the SWISS-PROT data bank.
 KW Hydrolase; Serine esterase.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TDV 7
 Db 4 TDV 6

RESULT 6
 NSI_MYCTU
 ID -NSI_MYCTU STANDARD; PRT; 10 AA.
 AC P81135;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 1 (Fragment).
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]

RP SEQUENCE.
 RC STRAIN=H37Rv;
 RA Prasad H.K., Annapurna P.S.;
 RL Submitted (DEC-1997) to the SWISS-PROT data bank.
 CC -!- CAUTION: We are unable to find this protein in the translation of
 CC the genome of strain H37Rv.
 FT NON TER 1
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1042 MW; 8767FB6AB2C73771 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17
 Db 4 PLV 6

RESULT 7
 URE3_MORMO
 ID -URE3_MORMO STANDARD; PRT; 10 AA.
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DE amidohydrolase) (Fragment).
 GN UREA.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences."
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR, C35389; C35389.
 KW Hydrolase.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9
 Db 8 VEK 10

RESULT 8
 TIN4_HOPTI
 ID -TIN4_HOPTI STANDARD; PRT; 11 AA.
 AC P82654;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tigerin-4.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;

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RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
FT MOD_RES 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 7 PLP 9

RESULT 9
ID PPK4_PERAM STANDARD; PRT; 12 AA.
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (pea-PK-4) (YXPRL-amide).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OC NCBI_TaxID=6978;
RN [1]
SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
TISSUE SPECIFICITY.
RP TISSUE=20189894; PubMed=10723010;
RX Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRlamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -|- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -|- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12 12
FT SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13
Db 2 HLP 4

RESULT 10
ID TIN2_HOFTI STANDARD; PRT; 12 AA.

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AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerinin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OC NCBI_TaxID=103373;
RN [1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RP TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD_RES 12 12
FT SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 7 PLP 9

RESULT 11
ID TIN3_HOFTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerinin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OC NCBI_TaxID=103373;
RN [1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RP TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD_RES 12 12
FT SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 13 PLP 15
DB 7 PLP 9

RESULT 12
TM2A METMA
ID TM2A METMA STANDARD; PRT; 12 AA.
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT coenzyme M methyltransferase from Methanosarcina mazei Go1
RT reconstituted in ether lipid liposomes.";
RL Eur. J. Biochem. 239:857-864(1996).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
DB 2 EKL 4

RESULT 13
ACT7 SOYBN
ID ACT7 SOYBN STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SAC7;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";

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RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17120; CAA34980.1; -.
CC PIR; S15755; S15755.
CC InterPro; IPR004001; Actin.
CC DR PROSITE; PS00406; ACTINS_1; PARTIAL.
CC DR PROSITE; PS00432; ACTINS_2; PARTIAL.
CC DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
CC KW Structural protein; Multigene family.
CC FT NON_TER 13 13
CC SQ SEQUENCE 13 AA; 1420 MW; 8BEFE3C36D4FD05A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
DB 9 PLV 11

RESULT 14
CRBL VESCR
ID CRBL VESCR STANDARD; PRT; 13 AA.
AC P01518;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Crabrolin.
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=84289390; PubMed=6206053;
RA Argolas A., Pisano J.J.;
RT "Isolation and characterization of two new peptides, mastoparan C and
RT crabrolin, from the venom of the European hornet, Vespa crabro.";
RL J. Biol. Chem. 259:10106-10111(1984).
RN [2]
RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.
RX MEDLINE=97419326; PubMed=9273892;
RA Krishnakumari V., Nagaraj R.;
RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue
RT peptide from the venom of the European hornet, Vespa crabro, and its
RT analogs.";
RL J. Pept. Res. 50:88-93(1997).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils. Has antimicrobial and hemolytic activity.
CC PIR; A01781; JZVHP1.
CC KW Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.
CC MOD_RES 13 13 AMIDATION.

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SQ SEQUENCE 13 AA; 1497 MW; 5155F8FCEA8D2407 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
DB 2 LPL 4

RESULT 15
CRIC RANES
ID CRIC RANES STANDARD; PRT; 13 AA.
AC P31832;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Calreticulin (Major microsomal calcium-binding protein) (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RC MEDLINE=91207333; PubMed=2018493;
RA Treveso S., Zorzato F., Chiozzi P., Melandri P., Volpe P., Pozzan T.;
RA "Frog brain expresses a 60 kDa Ca2+ binding protein similar to
RT mammalian calreticulin."
RL Biochem. Biophys. Res. Commun. 175:444-450(1991).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1510 MW; D0F62AD09EAE339 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
DB 2 PLV 4

RESULT 16
FR12_PEA
ID FR12_PEA STANDARD; PRT; 13 AA.
AC P83445;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ferritin 2, chloroplast (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC STRAIN=cv. Laxton's Progress; TISSUE=Leaf;
RA Shingles R., McCarty R.E.;
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
contains a central cavity into which the polymeric ferric iron
core is deposited.
CC -1- SUBCELLULAR LOCATION: Chloroplast (inner envelope membrane), and
CC other plastids.
CC -1- TISSUE SPECIFICITY: Leaves.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
CC 4.74, its MW is: 25.7 kDa.
CC -1- SIMILARITY: BELONGS TO THE FERRITIN FAMILY.
DR InterPro; IPR001519; Ferritin.
DR PROSITE; PS00204; FERRITIN_2; PARTIAL.
DR PROSITE; PS00540; FERRITIN_1; PARTIAL.
DR PROSITE; PS00905; FERRITIN-LIKE; PARTIAL.
KW Iron storage; Iron; Metal-binding; Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1246 MW; 26C9DC25F334ADC7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
DB 8 TLT 10

RESULT 17
HPB9 RANES
ID HPB9 RANES STANDARD; PRT; 13 AA.
AC P32416;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein B9 (fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RC MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.;
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta."
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -1- FUNCTION: Shows hemolytic activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
DR PIR; S09019; S09019.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD_RES 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
DB 2 LPL 4

RESULT 18
IDHP RAT
ID IDHP RAT STANDARD; PRT; 13 AA.
AC P56574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)
DE (Oxalosuccinate decarboxylase) (IDH) (NADP-specific IDH) (IDP) (ICD-
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Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
Db 2 LPL 4

RESULT 22
ECDC LYMDI
ID ECDC LYMDI STANDARD; PRT; 14 AA.
AC P80940;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide C (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -1- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 9 PLP 11

RESULT 23
CYSK CLOPA
ID CYSK CLOPA STANDARD; PRT; 15 AA.
AC P81340;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulphydrylase) (O-acetylserine (thiol)-lyase) (CSase) (CP 27) (Fragment).
GN CYSK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- CATALYTIC ACTIVITY: O(3)-acetyl-L-serine + H(2)S = L-cysteine +
CC acetate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: Cysteine biosynthesis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-SYNTHASE FAMILY.
CC InterPro; IPR001216; Cys_synthase.

DR PROSITE; PS00901; CYS SYNTHASE; PARTIAL.
KW Lyase; Cysteine biosynthesis; Pyridoxal phosphate.
FT NON TER 15
SQ SEQUENCE 15 AA; 1625 MW; 0196582B9671A352 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
Db 10 PLV 12

RESULT 24
GTS ASADI
ID GTS ASADI STANDARD; PRT; 15 AA.
AC P83246;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST) (Fragment).
DE Asaphis dichotoma.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Tellinoidea; Psammobiidae; Asaphis.
OX NCBI_TaxID=184428;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM ANALYSIS.
RC TISSUE=Intestine, and Liver;
RX MEDLINE=22135252; PubMed=12139969;
RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;
RT "Purification and characterization of a novel glutathione S-transferase from Asaphis dichotoma.";
RL Arch. Biochem. Biophys. 403:202-208(2002).
CC -1- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-dinitrobenzene and etharynic acid.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Homodimer.
CC -1- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.
CC -1- MISCELLANEOUS: In A. dichotoma there are at least two isozymes of glutathione S-transferase.
CC -1- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene as the substrate.
CC -1- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme, respectively.
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. SIGMA FAMILY.
DR GO; GO:0004364; F:glutathione transferase activity; NAS.
DR GO; GO:0006803; P:glutathione conjugation reaction; NAS.
KW Transferase.
FT NON TER 15
SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB0B9 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLH 11
Db 4 KLH 6

RESULT 25
ONCL ONCMY
ID ONCL ONCMY STANDARD; PRT; 15 AA.
AC P83287;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Oncorhynchus 1 (Fragment).


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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP TISSUE=Skin;
RC Fernandes J.M.O., Smith V.J., Kemp G.D.;
RT "Purification and N-terminal sequencing of a 3 kDa antibacterial
RT peptide from skin secretions of rainbow trout."
RL Submitted (MAY-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antibacterial activity against Gram positive
CC bacterium P.citreus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003795; F:antimicrobial peptide activity; NAS.
DR GO; GO:0006805; P: xenobiotic metabolism; NAS.
KW Antibiotic.
FT UNSURE 4 4 OR G.
FT UNSURE 9 9 OR T.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1601 MW; 43C25028DBC12B7C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVE 8
   |||
DB 9 DVE 11

RESULT 26
UC29 MAIZE
ID UC29 MAIZE STANDARD; PRT; 15 AA.
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 37.6 kDa.
DR Maize-2DPAGE; P80635; COLEOPTILE.
DR MaizeDB; 123960; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
   |||
DB 8 PLV 10

RESULT 27
ARCD_PSEPU
ID ARCD_PSEPU STANDARD; PRT; 16 AA.
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginine/ornithine antiporter (Fragment).
GN ARCD.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DDbj databases.
CC -!- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
CC ARGinine DEIMINASE PATHWAY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
CC PERMEASES.
CC -----
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CC -----
DR EMBL; U07185; AAA16963.1; -.
KW Transport; Antiport; Amino-acid transport; Transmembrane;
KW Inner membrane.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
   |||
DB 14 LTL 16

RESULT 28
FIBA_MELME
ID FIBA_MELME STANDARD; PRT; 16 AA.
AC P14456;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Meles meles (Eurasian badger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OC Meles.
OX NCBI_TaxID=9662;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

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CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7
DB 1 TDV 3

RESULT 29
IBP4_PIG STANDARD; PRT; 16 AA.
ID IBP4_PIG
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E.; Pan Y.-C.E.; Ehterton T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 IGFBP domain.
CC -1- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac_pr.
DR PROSITE; PS000716; Thyroglobulin_1.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
DB 12 EKL 14

RESULT 30
MMPX_SOLTU STANDARD; PRT; 16 AA.
ID MMPX_SOLTU
AC P80501;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unidentified mitochondrial matrix protein (Fragment).
OS Solanum tuberosum (Potato).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=41113;
RN [1]
RP SEQUENCE.
RC TISSUE=Tuber;
RC MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Kruft V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
RT of the protein complexes of plant mitochondria.";
RL Plant J. 9:357-368(1996).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Mitochondrion.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1768 MW; C59D4DB48AA18B8D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEX 9
DB 9 VEX 11

RESULT 31
ACT6_SOYBN STANDARD; PRT; 17 AA.
ID ACT6_SOYBN
AC P15986;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 6 (Fragment).
GN SAC6.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Wayne;
RC MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOSOLIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -1- SIMILARITY: Belongs to the actin family.
-----
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CC EMBL; X17119; CAA34979.1; -.
CC PIR; S15754; S15754.
CC InterPro; IPR004001; Actin.
CC PIR; IPR004000; Actin_like.
CC PIR; PF00022; actin; 1.
CC PROSITE; PS00406; ACTINS_1; PARTIAL.

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DR PROSITE; PS00432; ACTINS 2; PARTIAL.
 KW PROSITE; PS01132; ACTINS_ACT-LIKE; PARTIAL.
 DR Structural protein; Multigene family.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
 DB 9 PLV 11

RESULT 32
 EFG THEAQ STANDARD; PRT; 17 AA.
 AC Q01697;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (Fragment).
 GN FUSA OR FUS.
 OS Thermus aquaticus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=271;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EP 02276;
 RX MEDLINE=92362620; PubMed=1499561;
 RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O., Erdmann V.;
 RT "Sequence of the tufA gene encoding elongation factor EF-Tu from Thermus aquaticus and overproduction of the protein in Escherichia coli.";
 RL Eur. J. Biochem. 207:839-846(1992).
 CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE RIBOSOME.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. EF-G/EF-2 SUBFAMILY.

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DR EMBL; X66322; CAA46997.1; -.
 DR HAMAP; MF 00054; -; 1.
 DR InterPro; IPR000795; EF_GTPbind.
 DR PROSITE; PS00301; EFATOR GTP; PARTIAL.
 KW Elongation factor; Protein biosynthesis; GTP-binding.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2094 MW; EA46E1EF05F86E1D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
 DB 11 EKL 13

RESULT 33
 RL23_HALCU STANDARD; PRT; 18 AA.
 ID RL23_HALCU

AC P05975;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S ribosomal protein L23P (HL31) (Fragment).
 GN RPL23P.
 OS Halobacterium cutirubrum.
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=2242;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84282108; PubMed=6467081;
 RA Matheson A.I., Yeguchi M., Christensen P., Rollin C.F., Hasnain S.;
 RT "Purification, properties, and N-terminal amino acid sequence of certain 50S ribosomal subunit proteins from the archaebacterium Halobacterium cutirubrum."
 RT Halobacterium cutirubrum.
 RL Can. J. Biochem. Cell Biol. 62:426-433(1984).
 CC -!- FUNCTION: BINDS TO A SPECIFIC REGION ON THE 23S RRNA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS. InterPro; IPR001014; Ribosomal L23.
 DR PROSITE; PS00050; RIBOSOMAL L23; PARTIAL.
 KW Ribosomal protein; rRNA-binding.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2041 MW; 3B61DC53F8B4DD4C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
 DB 7 PLV 9

RESULT 34
 UC21_MAIZE STANDARD; PRT; 18 AA.
 ID UC21_MAIZE
 AC P80627;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riscardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
 CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
 CC Maize-2DPAGE; P80627; COLEOPTILE.
 DR MaizeDB; 123953; -.
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
 DB 11

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Db      15 VEK 17

RESULT 35
HI70_RAT
ID HI70_RAT STANDARD; PRT; 19 AA.
AC P21794,
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Hormone-induced protein 70 kDa (HIP-70) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX MEDLINE=90208308; PubMed=2181662;
RA Mobbs C.V., Fink G., Pfaff D.W.;
RT "HIP-70: a protein induced by estrogen in the brain and LH-RH in the
RT pituitary.";
RL Science 247:1477-1479(1990).
CC -!- INDUCTION: MOST PROMINENT PROTEIN INDUCED BY ESTROGEN IN
CC HYPOTHALAMUS AND MOST PROMINENT PROTEIN INDUCED BY LH-RH IN
CC PITUITARY.
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2113 MW; F793A98720B68E3C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
Db 5 LTD 7

RESULT 36
LANA_ACTLG
ID LANA_ACTLG STANDARD; PRT; 19 AA.
AC P56650;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lantibiotic actagardine (Gardimycin).
OS Actinoplanes liguriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micromonosporineae; Micromonosporaceae; Actinoplanes.
OX NCBI_TaxID=69484;
RN [1]
RP PRELIMINARY SEQUENCE, AND STRUCTURE BY NMR.
RX MEDLINE=91008698; PubMed=2211371;
RA Kettnering J.K., Malabarba A., Vekey K., Cavallieri B.;
RT "Sequence determination of actagardine, a novel lantibiotic, by
RT homonuclear 2D NMR spectroscopy.";
RL J. Antibiot. 43:1082-1088(1990).
RN [2]
RP SEQUENCE, AND STRUCTURE BY NMR.
RX MEDLINE=95255286; PubMed=7737178;
RA Zimmermann N., Metzger J.W., Jung G.;
RT "The tetracyclic lantibiotic actagardine. 1H-NMR and 13C-NMR
RT assignments and revised primary structure.";
RL Eur. J. Biochem. 228:786-797(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=97363218; PubMed=9219543;
RA Zimmermann N., Jung G.;
RT "The three-dimensional solution structure of the lantibiotic murein-
RT biosynthesis-inhibitor actagardine determined by NMR.";
RL Eur. J. Biochem. 246:809-819(1997).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST SOME GRAM-POSITIVE
CC BACTERIA. HAS GOOD ANTISTREPTOCOCCAL ACTIVITY.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of

Thr, and Ser into dehydrated AA and the formation of thioether
bonds with cysteine. The 14-19 beta-methylanthionine thioether
bond is oxidized to a sulfoxide. This is followed by membrane
translocation and cleavage of the modified precursor.
PIR; A58700; A58700.
DR PDB; 1AJ1; 15-OCT-97.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Oxidation;
KW 3D-structure; Thioether bond. Lanthionine (Ser-Cys).
FT CROSSLINK 1 6 Beta-methylanthionine (Thr-Cys).
FT CROSSLINK 7 12 Beta-methylanthionine (Thr-Cys).
FT CROSSLINK 9 17 Beta-methylanthionine sulfoxide
FT CROSSLINK 14 19 (Cys-Thr).
SQ SEQUENCE 19 AA; 1946 MW; 5C138C7CEB8765B3 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
Db 7 TLT 9

RESULT 37
LPGE_ECOLI
ID LPGE_ECOLI STANDARD; PRT; 19 AA.
AC P33236;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gef leader peptide.
DE GEFL OR B0018.
GN Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92048481; PubMed=1943701;
RA Poulsen L.K., Refn A., Molin S., Andersson P.;
RT "The gef gene from Escherichia coli is regulated at the level of
RT translation.";
RL Mol. Microbiol. 5:1639-1648(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -----
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CC -----
DR EMBL; AE000112; AAC73129.1; ALT_TERM.
DR EcoGene; EG12074; GefL.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0BEB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6

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Db      |||
        9 LTD 11

RESULT 38
MIFH_TRISP      STANDARD;      PRT;      19 AA.
AC P81529;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-dopachrome-methyl ester tautomerase (Macrophage migration inhibitory
factor homolog) (Fragment).
OS Trichinella spiralis (Trichina worm).
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
OC Trichinellidae; Trichinella.
OX NCBI_TaxID=6334;
RN [1]
RP SEQUENCE.
RX MEDLINE=99013685; PubMed=9794786;
RA Pennock J.L., Behnke J.M., Selkirk Q.D., Devaney E., Grenais R.K.,
RA Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
RT "Rapid purification and characterization of L-dopamine-methyl-ester
RT tautomerase (macrophage migration inhibitory factor) from Trichinella
RT spiralis, Trichuris muris and Brugia pahangi.";
RL Biochem. J. 335:495-498(1998).
CC -!- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
CC -!- INDUCTION: INHIBITED BY FREE FATTY ACIDS AND HAEMATIN.
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR InterPro; IPR001398; MIF.
DR PROSITE; PS01158; MIF; PARTIAL.
KW Cycokine.
FT NON TER      19
SQ SEQUENCE      19 AA; 2106 MW; F7CAA05F112A628D CRC64;

Query Match      16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 TDV 7
        |||
Db      12 TDV 14

RESULT 39
FIBB_SHEEP
ID FIBB_SHEEP      STANDARD;      PRT;      20 AA.
AC P14470;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Ovis aries (Sheep), and
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

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DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE      1 20 FIBRINOPEPTIDE B.
FT MOD_RES      5 5 SULFATION.
FT NON_TER      20 20
SQ SEQUENCE      20 AA; 2338 MW; FCF5B6FF0DEC6627 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 LPL 14
        |||
Db      15 LPL 17

RESULT 40
FRHA_METBA
ID FRHA_METBA      STANDARD;      PRT;      20 AA.
AC P80489;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coenzyme F420 hydrogenase alpha subunit (EC 1.12.98.1) (8-hydroxy-5-
DE deazaflavin-reducing hydrogenase alpha subunit) (FRH) (Fragment).
GN FRHA.
OS Methanosarcina barkeri.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2208;
RN [1]
RP SEQUENCE.
RC STRAIN=Fusaro / DSM 804;
RX MEDLINE=96085134; PubMed=8521835;
RA Michel R., Massanz C., Kostka S., Richter M., Fiebig K.;
RT "Biochemical characterization of the 8-hydroxy-5-deazaflavin-reactive
RT hydrogenase from Methanosarcina barkeri Fusaro.";
RL Eur. J. Biochem. 233:727-735(1995).
CC -!- FUNCTION: REDUCES THE PHYSIOLOGICAL LOW-POTENTIAL TWO-ELECTRON
CC ACCEPTOR COENZYME F420, AND THE ARTIFICIAL ONE-ELECTRON
CC METHYLVIIOGEN.
CC -!- CATALYTIC ACTIVITY: H(2) + coenzyme F420 = reduced coenzyme F420.
CC -!- COFACTOR: FRH CONTAINS NICKEL, IRON-SULFUR, AND FAD COFACTORS.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS AND A
CC GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE
CC SUBUNIT FAMILY.
DR PIR; S63483; S63483.
DR InterPro; IPR001501; N1_hdl.
DR PROSITE; PS00507; N1_HGENASE_L_1; PARTIAL.
DR PROSITE; PS00508; N1_HGENASE_L_2; PARTIAL.
KW Oxidoreductase; Metal-binding; Nickel; FAD.
FT NON TER      20
SQ SEQUENCE      20 AA; 2233 MW; OD6597417D776D03 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LTL 4
        |||
Db      18 LTL 20

RESULT 41
HETI_RADMG
ID HETI_RADMG      STANDARD;      PRT;      20 AA.
AC P58689;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Cytolysin I (HMG I) (Magnificalyisin I) (Fragment).
 OS Radianthus magnifica (Magnificent sea anemone) (Heteractis magnifica).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Stichodactylidae; Heteractis.
 ON NCBI_TaxID=38281;
 RN [1]
 RP SEQUENCE AND CHARACTERIZATION.
 RX MEDLINE=94196594; PubMed=8146870;
 RA Khoo K.S., Kam W.K., Khoo H.E., Gopalakrishnakone P., Chung M.C.;
 RT "Purification and partial characterization of two cytolysins from a
 RT tropical sea anemone, Heteractis magnifica.";
 RL Toxicon 31:1567-1579(1993).
 CC -!- FUNCTION: Has both cytolytic and hemolytic activity. Pore forming
 CC protein.
 CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
 CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
 KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2003 MW; ED9ABD98AC7C4EBC CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
 ||||
 Db 11 SLT 13

RESULT 42
 ID MIL7 BOVIN STANDARD; PRT; 20 AA.
 AC P3545l;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 17 kDa milk glycoprotein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Milk;
 RX MEDLINE=93308294; PubMed=8320368;
 RA Soerensen E.S., Petersen T.E.;
 RT "Purification and characterization of three proteins isolated from
 RT the proteose peptone fraction of bovine milk.";
 RL J. Dairy Res. 60:189-197(1993).
 CC -!- PTM: N-GLYCOSYLATED.
 CC -!- SIMILARITY: TO CAMEL WHEY PROTEIN.
 KW Glycoprotein; Milk.
 FT NON TER 1
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
 ||||
 Db 12 LPL 14

RESULT 43
 ID TENA ACTTE STANDARD; PRT; 20 AA.
 AC P30833;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tenebrosin A (Fragment).
 OS Actinia tenebrosa (Australian red waratah sea anemone).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Actinia.
 ON NCBI_TaxID=6105;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90232538; PubMed=1970442;
 RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
 RA Moritz R.L., Simpson R.J.;
 RT "Purification and characterisation of proteins with cardiac
 RT stimulatory and haemolytic activity from the anemone Actinia
 RT tenebrosa.";
 RL Toxicon 28:29-41(1990).
 CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a
 CC channel-forming and/or membrane-penetrating protein.
 CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
 CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
 KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 1974 MW; FA32AC8BDAAFF5FA CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 ||||
 Db 13 TLT 15

RESULT 44
 ID TENB ACTTE STANDARD; PRT; 20 AA.
 AC F30834;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tenebrosin B (Fragment).
 OS Actinia tenebrosa (Australian red waratah sea anemone).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Actinia.
 ON NCBI_TaxID=6105;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90232538; PubMed=1970442;
 RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
 RA Moritz R.L., Simpson R.J.;
 RT "Purification and characterisation of proteins with cardiac
 RT stimulatory and haemolytic activity from the anemone Actinia
 RT tenebrosa.";
 RL Toxicon 28:29-41(1990).
 CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a
 CC channel-forming and/or membrane-penetrating protein.
 CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
 CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
 KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 ||||
 Db 13 TLT 15

RESULT 45
 TL22 SPIOL

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ID TL22 SPIOL STANDARD; PRT; 20 AA.
AC P82756;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylakoid lumenal 22 kDa protein (P22) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RA Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;
RL Submitted (SEP-2000) to the SWISS-PROT data bank.
KW -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2409 MW; 78F5B5069BBE620 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
DB 17 SLT 19

RESULT 46
YPRB SERMA STANDARD; PRT; 20 AA.
ID YPRB_SERMA
AC P22581;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in prob 5' region (Fragment).
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Str41;
RX MEDLINE=91237315; PubMed=1851803;
RA Omori K., Suzuki S., Imai Y., Komatsubara S.;
RT "Analysis of the Serratia marcescens proBA operon and feedback
control of proline biosynthesis.";
RL J. Gen. Microbiol. 137:509-517(1991).
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DR EMBL; D90351; BAAL4363.1; -
DR EMBL; X53086; CAA37253.1; -
DR PIR; C49753; C49753.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2248 MW; 4DD777735276674 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EXL 10
DB 13 EXL 15

RESULT 47
BIOA CITFR STANDARD; PRT; 5 AA.
ID BIOA_CITFR
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
(EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
aminotransferase) (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shivan D., Campbell A.;
RL "Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
diaminononanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
aminotransferases.
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DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAAB1B1AGF00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TD 6
DB 3 TD 4

RESULT 48
PRCT PERAM STANDARD; PRT; 5 AA.
ID PRCT_PERAM
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;

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RN SEQUENCE
 RP SPECIES=P.americana;
 RC MEDLINE=76074708; PubMed=576;
 RX Starratt A.N., Brown B.E.;
 RA "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 in insects.";
 RL Life Sci. 17:1253-1256(1975).
 RN [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RL "Pentapeptide (proctolin) associated with an identified neuron.";
 RN Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillinghaast E.K., Townley M.A., Vetrovs A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RL "Identification of proctolin in the central nervous system of the
 horseshoe crab, Limulus polyphemus.";
 RL Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=86232789; PubMed=2872661;
 RA Stangler J., Dirksen H., Keller R.;
 RL "Identification and immunocytochemical localization of proctolin in
 pericardial organs of the shore crab, Carcinus maenas.";
 RL Peptides 7:67-72(1986).
 CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR PIR; A01644; HOROHA.
 DR PIR; A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 LP 13
 Db 3 LP 4
 RESULT 49
 ID TMOF_SARBU STANDARD; PRT; 6 AA.
 AC P41495;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOF).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 RA de Loof A.;
 RL "Sequencing and characterization of trypsin modulating oostatic
 factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
 (Sarcophaga) bullata.";

RL Regul. Pept. 50:61-72(1994).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 CC DEVELOPMENT.
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 CC EPITHELIUM AFTER A BLOOD MEAL.
 KW Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 LP 11
 Db 5 LP 6
 RESULT 50
 ID TRPI_PSEPU STANDARD; PRT; 6 AA.
 AC P36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TrpBA operon transcriptional activator (fragment).
 GN TRPI.
 OS Pseudomonas putida.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG1 C15;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Ederly L., Crawford I.P.;
 RL "DNA sequence of the tryptophan synthase genes of Pseudomonas
 putida.";
 RL Biochimie 71:521-531(1989).
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
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 CC -----
 CC EMBL; X13299; CAA31660.1; -
 DR InterPro; IPR000847; HTH_LySR.
 DR PROSITE; PS00044; HTH_LYSR FAMILY; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 LP 13
 Db 5 LP 6
 RESULT 51

VP19 HSV1K
 ID VP19 HSV1K STANDARD; PRT; 6 AA.
 AC P23210;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)
 DE (Capsid protein VP19C) (Fragment).
 GN UL38.
 OS Herpes simplex virus (type 1 / strain KOS).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
 RA Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 RT expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 CC EMBEDDED. BINDS DNA.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
 CC
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 CC
 CC -----
 DR EMBL; M57646; AAA45830.1; -;
 KW Capsid assembly; Coat protein; DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PL 14
 Db 5 PL 6
 RESULT 52
 CCF1_ENTFA
 ID CCF1_ENTFA STANDARD; PRT; 7 AA.
 AC P20104;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone cCF10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=89008313; PubMed=3139659;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adsit J.C., Dunn G.M., Suzuki A.;
 RT "Structure of cCF10, a peptide sex pheromone which induces
 RT conjugative transfer of the Streptococcus faecalis tetracycline
 RT resistance plasmid, pCF10.";
 RL J. Biol. Chem. 263:14574-14578(1988).
 CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PCF10.
 DR PIR; A30812; A30812.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TL 4
 Db 3 TL 4
 RESULT 53
 MNPI_LEPDE
 ID MNPI_LEPDE STANDARD; PRT; 7 AA.
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuropeptide 1 (Leu-MNP-I).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropic neuropeptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata.";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 CC Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PL 14
 Db 5 PL 6
 RESULT 54
 UN06_PINFS
 ID UN06_PINFS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 7
 NON_TER 7

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SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LP 13
DB 5 LP 6

RESULT 55
ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Carinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 kDa.
CC -!- SIMILARITY: Belongs to the actin family.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin like.
DR PROSITE; PS00406; ACTINS 1; PARTIAL.
DR PROSITE; PS00432; ACTINS 2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein.
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE83 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DV 7
DB 3 DV 4

RESULT 56
AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RA TISSUE=Corpora cardiaca;
```

OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=99388839; PubMed=10461743;
 RA Jacobson R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 RT dynamics in the contryphan family.";
 RL J. Pept. Res. 54:93-99(1999).
 CC -!- SUPRACELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 8
 FT MOD RES 4 4 D-LEUCINE.
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 LP 13
 Db ||
 5 LP 6
 RESULT 59
 CPD1_ENTFA
 ID CPD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, cPD1.";
 RL Science 226:849-850(1984).
 CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC BACTERIOCIN PLASMID PP1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 LV 17
 Db ||
 2 LV 3
 RESULT 60
 HTF2_PERAM
 ID HTF2_PERAM STANDARD; PRT; 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypertrehalosemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
 DE (PeA-CAH-II) (LeD-CC-II) (Hypertrehalosemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana.";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blattella orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; B44960; B44960.
 DR PIR; B49823; B49823.
 DR PIR; S08996; S08996.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LT 3
 Db ||
 2 LT 3
 RESULT 61
 P1P_BRANA
 ID P1P_BRANA STANDARD; PRT; 8 AA.
 AC P81707;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Plastidial lipid-associated protein (fragment).

OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV, TOPAZ; TISSUE=Tapetum;
 RX MEDLINE=99349136; PubMed=10420651;
 RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
 RA Murphy D.J.;
 RT "Composition and role of tapetal lipid bodies in the biogenesis of the
 RT pollen coat of Brassica napus";
 RL Planta 208:588-598(1999).
 CC -!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOTPLAST, A TAPETUM-
 CC SPECIFIC PLASTIDIAL LIPID ORGANELLE.
 CC -!- TISSUE SPECIFICITY: TAPETUM OF ANTHERS.
 CC NON_TER 8
 FT SEQUENCE 8 AA; 989 MW; 957B1AA452CAA042 CRC64;
 SQ SEQUENCE 8 AA; 989 MW; 957B1AA452CAA042 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 DV 7
 DB ||
 3 DV 4
 RESULT 62
 ID PPK3_PERAM STANDARD; PRT; 8 AA.
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FAPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Ragm-specific distribution of FXPLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8
 FT AMIDATION.
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D72C7 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 LV 17
 DB ||
 1 LV 2

RESULT 63
 ID RT34_BOVIN STANDARD; PRT; 8 AA.
 AC P82929;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
 GN MRP34.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=21276436; PubMed=11279123;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LT 3
 DB ||
 5 LT 6
 RESULT 64
 ID UPAA_HUMAN STANDARD; PRT; 8 AA.
 AC P30096;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
 CC SWISS-2DPAGE; P30096; HUMAN.
 DR NON_TER 1
 FT NON_TER 5
 FT VARIANT 5 5 F -> P.
 FT /FTID=VAR_000004.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LT 3
||
Db 3 LT 4

RESULT 65
ALC_CHLRE
ID _ALC_CHLRE STANDARD; PRT; 9 AA.
AC P82678;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Allantoicase (EC 3.5.3.4) (Allantoate amidohydrolase) (Fragment).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RC STRAIN=6145C;
RX MEDLINE=20318328; PubMed=10860551;
RA Piedras P., Munoz A., Aguilar M., Pineda M.;
RT "Allantoate amidohydrolase (Allantoicase) from Chlamydomonas
reinhardtii: its purification and catalytic and molecular
characterization.";
RL Arch. Biochem. Biophys. 378:340-348(2000).
CC -!- FUNCTION: Catalyzes the degradation of allantoate to (-)-
ureidoglycolate and (+)-ureidoglycolate to glyoxylate.
CC -!- CATALYTIC ACTIVITY: Allantoate + H(2)O = (-)-ureidoglycolate +
urea.
CC -!- PATHWAY: Degradation of allantoin (purine catabolism); second
step.
CC -!- SUBUNIT: Homohexamers.
CC -!- MISCELLANEOUS: Optimum pH is 6.5 and 8 for the reactions with
allantoate and ureidoglycolate, respectively.
CC -!- SIMILARITY: BELONGS TO THE ALLANTOICASE FAMILY.
KW Hydrolase; Purine metabolism. OR Y.
FT UNSURE 5 5
FT NON TER 9 9
SQ SEQUENCE 9 AA; 943 MW; D934ADD9D6D871F2 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TL 4
||
Db 8 TL 9

RESULT 66
BUK_CLOPA
ID _BUK_CLOPA STANDARD; PRT; 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetokinase family.
DR HAMAP; MF 00542; -; 1.
DR InterPro; IPR000890; Acetate kin.
DR PROSITE; PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON TER 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KL 10
||
Db 3 KL 4

RESULT 67
FAR5_PANRE
ID _FAR5_PANRE STANDARD; PRT; 9 AA.
AC P82661;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF5 (AMRNALVRF-amide).
OC Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimodea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of FMRFamide-related
peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9
FT NON TER 9
SQ SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LV 17
||
Db 6 LV 7

RESULT 68
FAR5_PENMO
ID _FAR5_PENMO STANDARD; PRT; 9 AA.
AC P83320;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP5 (SMPSLRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Eyestalk; MEDLINE=21956277; PubMed=11959015;
 RA Sthigongul P., Pupum J., Krungkasem C., Longyant S.,
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn *Penaeus monodon*.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1121.1; METHOD=WALDI.
 CC -1- SIMILARITY: BELONGS TO THE FAP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SL 2
 DB 4 SL 5

RESULT 69
 FAR9 ASCSU STANDARD; PRT; 9 AA.
 AC P43172;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AF9.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OS Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]

RESULT 70
 FIBB MACFU STANDARD; PRT; 9 AA.
 AC P19345;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Macaca fuscata fuscata (Japanese macaque).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9543;
 RN [1]

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PL 14
 DB 6 PL 7

RP SEQUENCE.
 RX MEDLINE=85289140; PubMed=3928610;
 RA Nakamura S., Takenaka O., Takahashi K.;
 RT "Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and
 RT patas monkey (*Erythrocebus patas*): their amino acid sequences,
 RT restricted mutations, and a molecular phylogeny for macaques,
 RT guenons, and baboons.";
 RL J. Biochem. 97:1487-1492(1985).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR; C24180; C24180.
 DR InterPro; IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SL 2
 DB 4 SL 5

RESULT 71
 MGMT BOVIN STANDARD; PRT; 9 AA.
 AC P29177;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
 DE methylguanine-DNA methyltransferase) (Fragment).
 GN MGMT.
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

RESULT 72
 TISSUE=Thymus; MEDLINE=90174912; PubMed=2308822;
 RX MEDLINE=90174912; PubMed=2308822;
 RA Rydberg B., Hall J., Karran P.;
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
 RT methyltransferase.";
 RL Nucleic Acids Res. 18:17-21(1990).
 CC -1- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
 CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
 CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
 CC IRREVERSIBLY INACTIVATED.
 CC -1- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
 CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
 CC S-methyl-L-cysteine.
 CC -1- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
 DR InterPro; IPR001497; Methyltransf_1.
 DR PROSITE; PS00374; MGMT; PARTIAL.
 KW DNA repair; Transferase; Methyltransferase.
 FT NON TER 1 1
 FT ACT SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

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Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LT 3
      ||
Db      6 LT 7

RESULT 72
MOSH CLYJA
ID MOSH CLYJA STANDARD; PRT; 9 AA.
AC P198E2;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sperm-activating peptide SAP-b ([His6]-mosact).
OS Clypeaster japonicus (Sand dollar).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_TaxID=7644;
RN [1]
RN SEQUENCE.
RC TISSUE=Egg jelly;
RC Suzuki N., Kurita M., Yoshino K.I., Kajiura H., Nomura K.,
RA Yamaguchi M.;
RT "Purification and structure of mosact and its derivatives from the
RT egg jelly of the sea urchin Clypeaster japonicus.";
RL Zool. Sci. 4:649-656(1987).
RN [2]
RN BROMINATION OF HIS-6.
RX MEDLINE=91167743; PubMed=2076468;
RA Takao T., Yoshino K., Suzuki N., Shimonishi Y.;
RT "Analysis of post-translational modifications of proteins by accurate
RT mass measurement in fast atom bombardment mass spectrometry.";
RL Biomed. Environ. Mass Spectrom. 19:705-712(1990).
CC -!- FUNCTION: Stimulates sperm respiration and motility.
DR PIR; JN0026;
KW Bromination.
FT MOD RES
SQ SEQUENCE 9 AA; 914 MW; 93245721EDC5BAB5 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 HL 12
      ||
Db      6 HL 7

RESULT 73
OXVA_SQUAC
ID OXVA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RN SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]

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RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PL 14
      ||
Db      7 PL 8

RESULT 74
OXYT_RABIT
ID OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamys amphibius (Hippopotamus),
OS Balanoptera phyllis (Finback whale) (Common rorqual),
OS Tachyglottus aculeatus aculeatus (Australian echidna), and
OS Hydrologus collii (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986; 9833, 9770, 49271, 7873;
RN [1]
RN SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RN SEQUENCE.
RC SPECIES=H.amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RN SEQUENCE.
RC SPECIES=B.phyllis;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RN SEQUENCE.
RC SPECIES=A.aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophyseal hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RN SEQUENCE.
RC SPECIES=H.collii;

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RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holoccephalian
RL elasmobranch fish, Hydrolagus collei.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PL 14
Db 7 PL 8

RESULT 75
PPH1 LYCES
ID PPH1 LYCES STANDARD; PRT; 9 AA.
AC P83380;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LesAPI (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=2361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RT esculentum) cell cultures.";
PT esculentum) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In L.esculentum there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1005 MW; 3F17C04B5042CAA8 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DV 7
Db 11
```

Db 3 DV 4

Search completed: November 25, 2003, 19:28:22
Job time : 6.45515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDVEXKLHPLPLVQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	27.8	17	4	Q96P96
2	5	27.8	19	4	Q9UCK6
3	4	22.2	8	8	P93963
4	4	22.2	8	8	P92384
5	4	22.2	8	8	P93973
6	4	22.2	8	8	P92215
7	4	22.2	8	8	P93957
8	4	22.2	8	8	P92222
9	4	22.2	8	8	P92388
10	4	22.2	8	8	P92441
11	4	22.2	8	8	P92404
12	4	22.2	8	8	P93961
13	4	22.2	8	8	P93970
14	4	22.2	8	8	P93955
15	4	22.2	8	8	P93965
16	4	22.2	8	8	P92394

17	4	22.2	8	8	P92382	hordeum bra
18	4	22.2	8	8	P93966	aequilops sp
19	4	22.2	8	8	P92227	crithopsis
20	4	22.2	8	8	P92373	haynaldia v
21	4	22.2	8	8	P92211	agropyron c
22	4	22.2	8	8	P92428	peridictyon
23	4	22.2	8	8	P93959	hordeum ere
24	4	22.2	8	8	P92219	australopyr
25	4	22.2	8	8	P93985	aequilops co
26	4	22.2	8	8	P92443	taeniatheru
27	4	22.2	8	8	P92391	heteranthel
28	4	22.2	8	8	P93981	crithodium
29	4	22.2	8	8	P93992	australopyr
30	4	22.2	8	8	P92426	pseudoroegn
31	4	22.2	8	8	P92431	aequilops ta
32	4	22.2	8	8	P92422	psathyrosta
33	4	22.2	9	4	Q16220	homo sapien
34	4	22.2	11	4	Q9UEL0	homo sapien
35	4	22.2	13	12	Q9WMG5	sigma virus
36	4	22.2	15	8	Q9T2K8	spinacia ol
37	4	22.2	15	12	Q66174	human coron
38	4	22.2	16	4	Q9NNZ2	homo sapien
39	4	22.2	16	4	O00497	homo sapien
40	4	22.2	17	8	Q9TDO2	macaca sylv
41	4	22.2	17	8	Q9T379	macaca sylv
42	4	22.2	18	4	Q16244	homo sapien
43	4	22.2	18	6	Q8WN06	bos taurus
44	4	22.2	19	8	Q31687	artemia par
45	4	22.2	19	15	Q905P5	human immu
46	4	22.2	20	2	Q9R9A5	nitrospir
47	4	22.2	20	2	Q9R987	nitrospir
48	4	22.2	20	4	Q6T45	homo sapien
49	4	22.2	20	10	Q9S900	vigna sinen
50	4	22.2	20	11	Q9QW2	rattus sp.
51	4	22.2	20	15	Q85636	moloney mur
52	3	16.7	5	13	P83308	gallus gall
53	3	16.7	7	10	P93233	lycopersico
54	3	16.7	7	12	Q66205	transmissib
55	3	16.7	7	13	O42564	fugu rubrip
56	3	16.7	8	2	Q9R9C2	borrelia bu
57	3	16.7	8	6	Q9XSY1	canis famil
58	3	16.7	8	6	Q95M23	sus scrofa
59	3	16.7	8	9	Q8SBU0	bacterioph
60	3	16.7	8	9	Q8H9K1	bacterioph
61	3	16.7	9	2	O31363	borrelia ga
62	3	16.7	9	2	P83157	anabaena sp
63	3	16.7	9	4	Q16605	homo sapien
64	3	16.7	9	5	Q9TWV0	anthopleura
65	3	16.7	9	8	Q94VD8	varanus nil
66	3	16.7	9	8	Q94VC6	varanus pil
67	3	16.7	9	8	Q94VE1	varanus mer
68	3	16.7	9	10	Q9S8J8	oryza sativ
69	3	16.7	9	11	Q61723	mus musculu
70	3	16.7	9	15	Q85723	simian sarc
71	3	16.7	9	15	Q935G1	salmonella
72	3	16.7	10	2	Q9XBH3	bacillus ce
73	3	16.7	10	2	Q9R5T2	acetobacter
74	3	16.7	10	2	P83154	anabaena sp
75	3	16.7	10	8	Q9TG86	diploglossu
76	3	16.7	10	8	Q94V97	varanus spe
77	3	16.7	10	8	Q94VD5	varanus oli
78	3	16.7	10	8	Q94VC9	varanus pan
79	3	16.7	10	8	Q94VF0	varanus kin
80	3	16.7	10	8	P92771	varanus var
81	3	16.7	10	8	Q94V85	varanus sca
82	3	16.7	10	8	Q94PD8	ophisaurus
83	3	16.7	10	8	Q9TG38	bipes bipor
84	3	16.7	10	8	Q9TG35	ophisaurus
85	3	16.7	10	8	Q94VD2	varanus pan
86	3	16.7	10	10	Q9FS93	silene pent
87	3	16.7	10	11	Q9QVF7	rattus sp.
88	3	16.7	10	11	Q9ESU5	mus musculu
89	3	16.7	10	11	Q9ESU5	mus musculu

90 3 16.7 10 15 Q88082 chimpanzee
 91 3 16.7 11 2 Q47606 escherichia
 92 3 16.7 11 2 Q9K332 ataphylococ
 93 3 16.7 11 2 Q47569 escherichia
 94 3 16.7 11 6 Q8HYM4 felis silve
 95 3 16.7 11 7 Q9TOR3
 96 3 16.7 11 8 Q94V94
 97 3 16.7 11 8 Q94V98 varanus gou
 98 3 16.7 11 8 Q9G616 ceratophora
 99 3 16.7 11 8 Q9G610 lyriocephal
 100 3 16.7 11 8 Q9G5V3 phrynoceph

ALIGNMENTS

RESULT 1
 Q96P96 PRELIMINARY; PRT; 17 AA.
 AC Q96P96
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NHP2-like protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
 RT "Characterization of TPA-responsive genes in U937 cells using ordered
 RT differential display PCR."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401217; AAL02173.1; -.
 FT NON TER 1
 SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEF CRC64;

Query Match 27.8%; Score 5; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPPL 16
 DB 13 LPPL 17

RESULT 2
 Q9UCK6 PRELIMINARY; PRT; 19 AA.
 AC Q9UCK6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Aspartylglucosaminidase beta 1 subunit (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=931111925; PubMed=1281977;
 RA Rip J.W., Coulter-Mackie M.B., Rupa C.A., Gordon B.A.;
 RT "Purification and structure of human liver aspartylglucosaminidase."
 RL Biochem. J. 288:1005-1010(1992).
 DR HSP; P20933; 1APV.
 SQ SEQUENCE 19 AA; 2127 MW; BC2F148525610300 CRC64;

Query Match 27.8%; Score 5; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17

Db 2 PLPLV 6

RESULT 3
 P93963 PRELIMINARY; PRT; 8 AA.
 ID P93963
 AC P93963
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD
 OS Psathyrostachys stoloniformis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Psathyrostachys.
 OX NCBI_TaxID=58873;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H9182; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77754; CAB01341.1; -.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 878 MW; 1BC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 DB 2 SLTL 5

RESULT 4
 P92384 PRELIMINARY; PRT; 8 AA.
 ID P92384
 AC P92384
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD
 OS Hordeum murinum subsp. glaucum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=98113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H801; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77762; CAB01365.1; -.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
|||||
Db 2 SLTL 5

RESULT 5

P93973 ID P93973 PRELIMINARY; PRT; 8 AA.
AC P93973; AC P93973; PRELIMINARY; PRT; 8 AA.
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Eremopyrum distans.
OS Eremopyrum distans.
OG Chloroplast.
OG Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Eremopyrum.
OX NCBI_TaxID=58936;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H552; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77745; CAB01314.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
|||||
Db 2 SLTL 5

RESULT 6

P92215 ID P92215 PRELIMINARY; PRT; 8 AA.
AC P92215; AC P92215; PRELIMINARY; PRT; 8 AA.
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Amblyopyrum muticum.
OG Chloroplast.
OG Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H552; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77756; CAB01347.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
|||||
Db 2 SLTL 5

RESULT 7

P93957 ID P93957 PRELIMINARY; PRT; 8 AA.
AC P93957; AC P93957; PRELIMINARY; PRT; 8 AA.
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Festucopsis serpentini.
OG Chloroplast.
OG Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Festucopsis.
OX NCBI_TaxID=72456;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6511; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z79501; CAB01777.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
|||||
Db 2 SLTL 5

RESULT 8

P92222 ID P92222 PRELIMINARY; PRT; 8 AA.
AC P92222; AC P92222; PRELIMINARY; PRT; 8 AA.
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OG Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromus.
OX NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSM414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01356.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
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Db 2 SLTL 5

RESULT 9

P92388 ID P92388 PRELIMINARY; PRT; 8 AA.
AC P92388;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Henrardia.
OC NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01323.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
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Db 2 SLTL 5

RESULT 10

P92441 ID P92441 PRELIMINARY; PRT; 8 AA.
AC P92441;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Thinopyrum bessarabicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Thinopyrum.
OC NCBI_TaxID=4601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6725; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77769; CAB01386.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
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|
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Db 2 SLTL 5

RESULT 11

P92404 ID P92404 PRELIMINARY; PRT; 8 AA.
AC P92404;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Lophopyrum.
OC NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6692; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77743; CAB01308.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
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Db 2 SLTL 5

RESULT 12

P93961 ID P93961 PRELIMINARY; PRT; 8 AA.
AC P93961;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Peathrostachys rupestris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Peathrostachys.
OC NCBI_TaxID=58938;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6703; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77755; CAB01344.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

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Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 13
P93970 PRELIMINARY; PRT; 8 AA.
AC P93970;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Bremopyrum triticeum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Bremopyrum.
OX NCBI_TaxID=58937;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5553; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77746; CAB01315.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 14
P93955 PRELIMINARY; PRT; 8 AA.
AC P93955;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Festucopsis festucoeides.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Festucopsis.
OX NCBI_TaxID=72455;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6731; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77770; CAB01389.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 15
P93965 PRELIMINARY; PRT; 8 AA.
AC P93965;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Secale strictum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=58866;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4342; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77765; CAB01373.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 16
P92394 PRELIMINARY; PRT; 8 AA.
AC P92394;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H3139; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77764; CAB01371.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

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SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;
Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 17
P92382
ID P92382 PRELIMINARY; PRT; 8 AA.
AC P92382;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01362.1; -.
KW Chloroplast.
FT NON-TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 18
P93966
ID P93966 PRELIMINARY; PRT; 8 AA.
AC P93966;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Aegilops speltoides (Goat grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=4573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4523; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77766; CAB01377.1; -.
KW Chloroplast.

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;
Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 19
P92227
ID P92227 PRELIMINARY; PRT; 8 AA.
AC P92227;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Crithopsis delileana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Crithopsis.
OX NCBI_TaxID=37674;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5558; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77751; CAB01332.1; -.
KW Chloroplast.
FT NON-TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 20
P92373
ID P92373 PRELIMINARY; PRT; 8 AA.
AC P92373;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Haynaldia villosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5561; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01302.1; -.

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KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 21

P92211
 ID P92211 PRELIMINARY; PRT; 8 AA.
 AC P92211;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Agropyron cristatum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Agropyron.
 OX NCBI_TaxID=4593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H4349; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; 277771; CAB01392.1; -.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 22

P92428
 ID P92428 PRELIMINARY; PRT; 8 AA.
 AC P92428;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Peridictyon sanctum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Peridictyon.
 OX NCBI_TaxID=37683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H5575; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; 277749; CAB01326.1; -.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 23

P93959
 ID P93959 PRELIMINARY; PRT; 8 AA.
 AC P93959;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Hordeum erectifolium.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=58926;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H1150; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; 279500; CAB01776.1; -.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 24

P92219
 ID P92219 PRELIMINARY; PRT; 8 AA.
 AC P92219;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Australopyrum retrofractum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Australopyrum.
 OX NCBI_TaxID=4597;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6723; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";

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RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77767; CAB01380.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 860 MW; 1EC7287731A735AA CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 25
P93985 PRELIMINARY; PRT; 8 AA.
ID P93985;
AC P93985;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Aegilops comosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=4485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6673; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77742; CAB01305.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 26
P92443 PRELIMINARY; PRT; 8 AA.
ID P92443;
AC P92443;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Taeniatherum caput-medusae (Medusahead).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Taeniatherum.
OX NCBI_TaxID=37687;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H10254; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01359.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 27
P92391 PRELIMINARY; PRT; 8 AA.
ID P92391;
AC P92391;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Heteranthellium piliferum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Heteranthellium.
OX NCBI_TaxID=37679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5557; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01329.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 28
P93981 PRELIMINARY; PRT; 8 AA.
ID P93981;
AC P93981;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Crithodium monococtum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Crithodium.
OX NCBI_TaxID=72428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4547; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;

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RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data.",
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z7775; CAB01350.1; -.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 29

P93992
 ID P93992 PRELIMINARY; PRT; 8 AA.
 AC P93992;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Australopyrum velutinum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Australopyrum.
 OX NCBI_TaxID=58935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6724; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G.; Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data.",
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77768; CAB01383.1; -.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 30

P92426
 ID P92426 PRELIMINARY; PRT; 8 AA.
 AC P92426;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Pseudoroegneria.
 OX NCBI_TaxID=4604;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H9082; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G.; Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data.",
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77744; CAB01311.1; -.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 31

P92431
 ID P92431 PRELIMINARY; PRT; 8 AA.
 AC P92431;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Aegilops tauschii (Aegilops squarrosa).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Aegilops.
 OX NCBI_TaxID=37682;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6668; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G.; Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data.",
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77758; CAB01353.1; -.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
 ||||
 Db 2 SLTL 5

RESULT 32

P92422
 ID P92422 PRELIMINARY; PRT; 8 AA.
 AC P92422; P92420;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
 DE Chloroplast RPOA gene (Fragment).
 GN PETD.
 OS Psathyrostachys fragilis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Psathyrostachys.
 OX NCBI_TaxID=37729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H4372, and H917; TISSUE=Leaf;

RA Petersen G., Seberg O.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z77753; CAB01338.1; -;
 DR EMBL; Z77752; CAB01335.1; -;
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
 Db 2 SLTL 5

RESULT 33

Q16220 PRELIMINARY; PRT; 9 AA.
 AC Q16220;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE HGRP protein (Fragment).
 GN HGRP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RL [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94320083; PubMed=8044796;
 RA Nagalla S.R., Spindel E.R.;
 RT "Functional analysis of the 5'-flanking region of the human gastrin-releasing peptide gene in small cell lung carcinoma cell lines.";
 RL Cancer Res. 54:4461-4467(1994).
 DR EMBL; S73265; AADI4116.1; -;
 FT NON TER
 SQ SEQUENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
 Db 6 LPLV 9

RESULT 34

Q9UELO PRELIMINARY; PRT; 11 AA.
 AC Q9UELO;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE FAS antigen (CD95 antigen) (Fragment).
 GN CD95.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RL [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95355401; PubMed=7543095;
 RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
 RA Nakanishi Y.;
 RT "Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection.";
 RL J. Biol. Chem. 270:18007-18012(1995).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
 RA Koppers R., Rajewsky K.;
 RT "Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg cells.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Koppers R.;
 RT "Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22404279; PubMed=12516573;
 RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chlorazzi N.,
 RA Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
 RT "Lack of deleterious somatic mutations in the CD95 gene of plasmablasts from systemic lupus erythematosus patients and autoantibody-producing cell lines.";
 RL Eur. J. Immunol. 32:3785-3792(2002).
 DR EMBL; D31968; BAA20850.1; -;
 DR EMBL; AJ279011; CAC35539.1; -;
 DR EMBL; AJ279012; CAC35540.1; -;
 DR EMBL; AJ279013; CAC35541.1; -;
 DR EMBL; AJ509179; CAD48929.1; -;
 DR EMBL; AJ509180; CAD48930.1; -;
 FT NON TER
 SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
 Db 8 LPLV 11

RESULT 35

Q9MMG5 PRELIMINARY; PRT; 13 AA.
 AC Q9MMG5;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE 3 protein (Fragment).
 GN GENE 3.
 OS Sigma virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.
 OX NCBI_TaxID=11301;
 RL [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212481; PubMed=8384742;
 RA Teninges D., Bras F., Dezelee S.;
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene overlap.";
 RL Virology 193:1018-1023(1993).
 DR EMBL; S57850; AAD40700.1; -;
 FT NON TER
 SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75E32D5 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
 Db 8 LPLV 11

RESULT 36

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Q9T2K8
ID Q9T2K8 PRELIMINARY; PRT; 15 AA.
AC Q9T2K8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LHCII kinase, 64 kDa kinase (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE
RX MEDLINE=92183823; PubMed=1544419;
RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
RL FERS Lett. 298:33-35(1992).
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

Query Match 22.2%; Score 4; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db |||||
6 DVEK 9

RESULT 37
Q66174 PRELIMINARY; PRT; 15 AA.
ID Q66174
AC Q66174
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Surface protein (Fragment).
OS Human coronavirus (strain 229E)
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11137;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=229E;
RX MEDLINE=89366667; PubMed=2701946;
RA Raabe T., Siddell S.;
RT "Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA
RL 5 unique regions.";
RL Nucleic Acids Res. 17:6387-6387(1989).
DR EMBL; X15654; CAA33680.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1834 MW; 8CE369AE77DC4015 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db |||||
8 DVEK 11

RESULT 38
Q9NNZ2 PRELIMINARY; PRT; 16 AA.
ID Q9NNZ2
AC Q9NNZ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

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DE Integrin alpha-2 subunit (Fragment).
GN ITGA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98421383; PubMed=9746778;
RA Kritzik M., Savage B., Nugent D.J., Santos S., Ruggeri Z.M.,
RA Kunicki T.J.;
RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
RT that are associated with differences in platelet alpha2 beta1
RT density.";
RL Blood 92:2382-2388(1998).
DR EMBL; AF062039; AAF77577.1; -.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db |||||
10 PLPL 13

RESULT 39
O00497 PRELIMINARY; PRT; 16 AA.
ID O00497
AC O00497
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA mismatch repair protein (Fragment).
GN HMLH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Palmirotta R., Veri M.C., Curia M.C., Aceto G., D'Amico F.,
RA Esposito D.L., Mariani-Costantini R., Messerini L., Mori S., Cama A.,
RA Battista P.;
RT "Transcripts with splicings of exons 15 and 16 of the hMLH1 gene in
RT normal lymphocytes: implications in RNA-based mutation screening of
RT hereditary nonpolyposis colorectal cancer.";
RL Submitted (APR-1997) to the EMBL/GenBank/DDRJ databases.
DR EMBL; AF001359; AAB58936.1; -.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1850 MW; 996602B4FF583D2 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db |||||
9 SLTL 12

RESULT 40
Q9TDQ2 PRELIMINARY; PRT; 17 AA.
ID Q9TDQ2
AC Q9TDQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Macaca sylvanus (Barbary ape).

```

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=20028760; PubMed=10563020;
 RA Bailey J.F., Henneberg M., Colson I.B., Ciarallo A., Hedges R.E.,
 RA Sykes B.;
 RT "Monkey business in Pompeii--unique find of a juvenile Barbary macaque
 RT skeleton in Pompeii identified using osteology and ancient DNA
 RT techniques.";
 RL Mol. Biol. Evol. 16:1410-1414 (1999).
 DR EMBL; AF064450; AAF09257.1; -.
 KW Mitochondrion.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2002 MW; CE16F446963413D2 CRC64;
 Query Match 22.2%; Score 4; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SLTL 4
 Db 14 SLTL 17
 RESULT 41
 Q9T379
 ID Q9T379 PRELIMINARY; PRT; 17 AA.
 AC Q9T379;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE NADH dehydrogenase subunit 5 (Fragment).
 GN ND5.
 OS Macaca sylvanus (Barbary ape).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=20028760; PubMed=10563020;
 RA Bailey J.F., Henneberg M., Colson I.B., Ciarallo A., Hedges R.E.M.,
 RA Sykes B.;
 RT "Monkey business in Pompeii - unique find of a juvenile Barbary
 RT macaque skeleton in Pompeii identified using osteology and ancient DNA
 RT techniques.";
 RL Mol. Biol. Evol. 16:1410-1414 (1999).
 DR EMBL; AF064452; AAF09259.1; -.
 DR EMBL; AF064451; AAF09258.1; -.
 KW Mitochondrion.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1974 MW; CE16F45DE01D13D2 CRC64;
 Query Match 22.2%; Score 4; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SLTL 4
 Db 14 SLTL 17
 RESULT 42
 Q16244
 ID Q16244 PRELIMINARY; PRT; 18 AA.
 AC Q16244;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE STS protein (Fragment).
 GN STS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95038775; PubMed=7951263;
 RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
 RT "Characterization of the deletion breakpoints in a patient with
 RT steroid sulfatase deficiency.";
 RL Hum. Mutat. 4:76-78 (1994).
 DR EMBL; S74383; AAD14153.1; -.
 FT NON_TER 1
 SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;
 Query Match 22.2%; Score 4; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 PLPL 16
 Db 2 PLPL 5
 RESULT 43
 Q8WN06
 ID Q8WN06 PRELIMINARY; PRT; 18 AA.
 AC Q8WN06;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Neuronal nicotinic receptor beta 4 subunit (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Valor L.M., Campos-Caro A., Carrasco-Serrano C., Ortiz J.A.,
 RA Ballesta J.J., Criado M.;
 RT "Transcription Factors NF-Y and Sp1 are Important Determinants of the
 RT Promoter Activity of the Bovine and Human Neuronal Nicotinic Receptor
 RT Beta4 Subunit Genes.";
 RL J. Biol. Chem. 0:0-0 (2002).
 DR EMBL; AF453876; AAL57839.1; -.
 KW Receptor.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1946 MW; 43BB1157148CEB76 CRC64;
 Query Match 22.2%; Score 4; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 14 LPLV 17
 Db 5 LPLV 8
 RESULT 44
 Q31687
 ID Q31687 PRELIMINARY; PRT; 19 AA.
 AC Q31687;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN ATP8.

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OS Artemia parthenogenetica.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_TaxID=6663;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=La Mata;
RC MEDLINE=94223692; PubMed=8169960;
RX Perez M.I., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
RA "Speciation in the artemia genus: mitochondrial DNA analysis of
RT bisexual and parthenogenetic brine shrimps.";
RL J. Mol. Evol. 38:156-168(1994).
DR EMBL; X67263; CAA47685.1; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2246 MW; 41922AD313E087E3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLP 15
DB |||||
5 LPLP 8

RESULT 45
Q905F5 PRELIMINARY; PRT; 19 AA.
AC Q905F5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG311;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410450; AAL10267.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2221 MW; BE83B262BA711903 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDVE 8
DB |||||
2 TDVE 5

RESULT 46
Q9R9A5 PRELIMINARY; PRT; 20 AA.
AC Q9R9A5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Ammonia monooxygenase 1 subunit C (Fragment).
GN AMOCl.
OS Nitrosospira sp. NpAV.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;

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OC Nitrosomonadaceae; Nitrosospira.
OX NCBI_TaxID=58133;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NpAV;
RC MEDLINE=96001263; PubMed=7557469;
RX Klotz M.G., Norton J.M.;
RA "Sequence of an ammonia monooxygenase subunit A-encoding gene from
RT Nitrosospira sp. NpAV.";
RL Gene 163:159-160(1995).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=NpAV;
RC MEDLINE=96275998; PubMed=8674986;
RX Norton J.M., Low J.M., Klotz M.G.;
RA "The gene encoding ammonia monooxygenase subunit A exists in three
RT nearly identical copies in Nitrosospira sp. NpAV.";
RL FEMS Microbiol. Lett. 139:181-188(1996).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=NpAV;
RC MEDLINE=97306641; PubMed=9163908;
RX Klotz M.G., Alzerreca J., Norton J.M.;
RT "A gene encoding a membrane protein exists upstream of the amoA/amoB
RT genes in ammonia oxidizing bacteria; a third member of the amo
RT operon?";
RL FEMS Microbiol. Lett. 150:65-73(1997).
DR EMBL; AF032438; AAB8680.1; -.
KW Monooxygenase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2266 MW; A745DC66ACC3F2A9 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTQV 7
DB |||||
1 LTQV 4

RESULT 47
Q9R987 PRELIMINARY; PRT; 20 AA.
ID Q9R987;
AC Q9R987;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Ammonia monooxygenase subunit C1 (Fragment).
GN AMOCl.
OS Nitrosospira sp. Np39-19.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosospira.
OX NCBI_TaxID=61907;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Np39-19;
RA Norton J.M., Alzerreca J.J., Klotz M.G.;
RT "Diversity of the genes encoding ammonia monooxygenase in autotrophic
RT ammonia-oxidizing bacteria.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Np39-19;
RA Shiozawa T.L., Norton J.M., Alzerreca J.J., Klotz M.G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042170; AAC25054.1; -.
KW Monooxygenase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2266 MW; A745DC66ACC3F2A9 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTV 7
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|
Db 1 LTV 4

RESULT 48

Q96T45 ID Q96T45 PRELIMINARY; PRT; 20 AA.
AC Q96T45;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MER receptor tyrosine kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517330; PubMed=11062461;
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,
RA Apfelstedt-Sylla E., Vollrath D.;
RT "Mutations in MERTK, the human orthologue of the RCS rat retinal
RT dystrophy gene, cause retinitis pigmentosa.";
RL Nat. Genet. 26:270-271 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,
RA Apfelstedt-Sylla E., Vollrath D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366903; AAK54121.1; -.
KW Kinase; Receptor.
FT NON TER 20
SQ SEQUENCE 20 AA; 2232 MW; A853BEF7EECE2910 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
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|
Db 5 PLPL 8

RESULT 49

Q9S900 ID Q9S900 PRELIMINARY; PRT; 20 AA.
AC Q9S900;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C7 peptide (Fragment).
OS Vigna sinensis (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3920;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735 (1992).
DR HSP; P02248; 1UBI.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
FT NON TER 20
SQ SEQUENCE 20 AA; 2211 MW; BAA7DDE7501B659E CRC64;

Query Match 22.2%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTV 5
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|
|
Db 6 LTV 9

RESULT 50

Q9QUW2 ID Q9QUW2 PRELIMINARY; PRT; 20 AA.
AC Q9QUW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 22 kDa INTRALYSOSOMAL lipid-transfer protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=97104296; PubMed=8948454;
RA Kuwana T., Mullock B.M., Luzio J.P.;
RT "Identification of a lysosomal protein causing lipid transfer, using a
RT fluorescence assay designed to monitor membrane fusion between rat
RT liver endosomes and lysosomes.";
RL Biochem. J. 308:937-946 (1995).
DR HSP; P17900; IG13.
SQ SEQUENCE 20 AA; 2211 MW; 3A160591EA5542C5 CRC64;

Query Match 22.2%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTV 4
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|
|
Db 17 LTV 20

RESULT 51

Q85636 ID Q85636 PRELIMINARY; PRT; 20 AA.
AC Q85636;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Revertant mutant dl587rev patch region including partial LTR and gag
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroviruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86089316; PubMed=2416955;
RA Colicelli J., Goff S.P.;
RT "Isolation of a recombinant murine leukemia virus utilizing a new
RT primer tRNA.";
RL J. Virol. 57:37-45 (1986).
RN [2]
RP SEQUENCE OF 1-5 FROM N.A.
RX MEDLINE=88019205; PubMed=3660592;
RA Colicelli J., Goff S.P.;
RT "Identification of endogenous retroviral sequences as potential donors
RT for recombinational repair of mutant retroviruses: Positions of
RT crossover points.";
RL Virology 160:518-522 (1987).
DR EMBL; M12275; AAA46501.1; -.
DR InterPro; IPR000840; Gag_MA.
DR Pfam; PF01140; Gag_MA; 1.
FT NON TER 20
SQ SEQUENCE 20 AA; 2214 MW; FB14F3F0FB11AC31 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRTL 4
|||
Db 10 SRTL 13

RESULT 52
P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE FMRPamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRPamide";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
|||
Db 1 LPL 3

RESULT 53
P93233
ID P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN LE-ACS1B;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843;
RA Ootiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
KW Lyase.
FT NON TER 1
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
|||
Db 3 PLV 5

RESULT 54
Q66205
ID Q66205 PRELIMINARY; PRT; 7 AA.
AC Q66205;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Membrane protein (1 is 3rd base in codon) (Fragment).
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FS772/70;
RX MEDLINE=88216185; PubMed=2835592;
RA Britton P., Carnes R.S., Page K.W., Garves D.J., Parra F.;
RT "Sequence of the Nucleoprotein Gene from a Virulent British Field
RT Isolate of Transmissible Gastroenteritis Virus and its Expression in
RT Saccharomyces Cerevisiae";
RL Mol. Microbiol. 2:89-99(1988).
DR EMBL; Y00542; CAA68606.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 869 MW; 72C691E727233B70 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
|||
Db 1 EKL 3

RESULT 55
O42564
ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodonidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
KW Ionic channel.
FT NON TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17

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Db      11 HLP 13
      |||
      2 HLP 4

RESULT 56
Q9R9C2 PRELIMINARY; PRT; 8 AA.
ID Q9R9C2
AC Q9R9C2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Plasmid cp32-3, possible partition proteins (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]_TaxID=139;
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Castjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022480; AAC35445.1; -.
KW Plasmid.
FT NON TER
SQ SEQUENCE 8 AA; 985 MW; E8B41B41A735B446 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
   |||
Db 3 SLT 5

RESULT 57
Q9XSX1 PRELIMINARY; PRT; 8 AA.
ID Q9XSX1
AC Q9XSX1
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Retinoblastoma protein (Fragment).
GN RB1
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_TaxID=9615;
RP SEQUENCE FROM N.A.
RX MEDLINE=97049323; PubMed=8894053;
RA Venter P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
RT "Gene-specific universal mammalian sequence-tagged sites: application
RT to the canine genome.";
RL Biochem. Genet. 34:321-341(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Venter P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;
RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RB1)
RT gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF155737; AAD38807.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 8 AA; 895 MW; 1425BB18C676721E3 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      2 PLV 4
      |||
      2 PLV 4

RESULT 58
Q9SM23 PRELIMINARY; PRT; 8 AA.
ID Q9SM23
AC Q9SM23
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).
GN ATP1A1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_TaxID=9823;
RP SEQUENCE FROM N.A.
RC STRAIN=Pietrain;
RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
RA Geldermann H., Kopecky M.;
RT "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and
RT linkage assignments of ATP1A1 and IVL to chromosome 4.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344138; CAC51422.1; -.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
   |||
Db 2 VEK 4

RESULT 59
Q8SBJ0 PRELIMINARY; PRT; 8 AA.
ID Q8SBJ0
AC Q8SBJ0
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gp30.2 (Fragment).
GN G30.2.
OS Bacteriophage RB69.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=12353;
RN [1]_TaxID=12353;
RP SEQUENCE FROM N.A.
RA Piesniene L., Kolesinskiene G., Truncaite L., Zajackauskaite A.,
RA Nivinskas R.;
RT "Genomic region with genes 30.6-30.3 of T4-related bacteriophages.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439452; CAD28423.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 16.7%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
   |||
Db 6 LTD 8

RESULT 60

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Q8H9K1
ID Q8H9K1 PRELIMINARY; PRT; 8 AA.
AC Q8H9K1;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Gp30.2 protein (Fragment).
GN 30.2.
OS Bacteriophage L210.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=192973;
RN [1]_TaxID=192973;
RP SEQUENCE FROM N.A.
RA Kolesinskien G., Nivinskas R.;
RT "A pair of overlapping genes 30.3 and 30.3' of T4-related
RT bacteriophages.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458400; CAD30256.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 16.7%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
Db |||
6 LTD 8

RESULT 61
ID O31363 PRELIMINARY; PRT; 9 AA.
AC O31363;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Outer surface protein C (Fragment).
OS OSCP.
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-PBI;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "ne Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93699; AAC45533.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1019 MW; 4864C1A731A44333 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
Db |||
5 TLT 7

RESULT 62
P83157
ID P83157 PRELIMINARY; PRT; 9 AA.
AC P83157;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).

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OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -! FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -! CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -! SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -! SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Iron; Metal-binding.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db |||
6 PLP 8

RESULT 63
Q16605
ID Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 OR GST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330756; PubMed=3138230;
RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
RT "Human glutathione S-transferases. The Ha multigene family encodes
RT products of different but overlapping substrate specificities.";
RL J. Biol. Chem. 263:12797-12800(1988).
DR EMBL; M21867; AAA52617.1; -.
DR EMBL; M21866; AAA35938.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;

Query Match 16.7%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLH 11
Db |||
6 KLH 8

RESULT 64
Q9TWV0
ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Antho-REPAMIDE-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

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OC Nynanthaeae; Actiniidae; Anthopleura.
 RN NCBI_TaxID=6110;
 RP SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
 RT "Isolation of leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH₂ (Antho-RPamide),
 an N-terminally protected, biologically active neuropeptide from sea
 anemones.";
 RL Peptides 13:851-857(1992).
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
 DB 5 PLP 7

RESULT 65
 ID Q94VD8 PRELIMINARY; PRT; 9 AA.
 AC Q94VD8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus niloticus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=62046;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407514; AAL10096.1; -.
 KW Mitochondrion.
 FT NON-TER
 SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 DB 2 TLT 4

RESULT 66
 ID Q94VC6 PRELIMINARY; PRT; 9 AA.
 AC Q94VC6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus pilbarensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=62048;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).

DR EMBL; AF407518; AAL10108.1; -.
 KW Mitochondrion.
 FT NON-TER
 SQ SEQUENCE 9 AA; 1064 MW; 874CA5A36411A735 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3
 DB 2 SLT 4

RESULT 67
 ID Q94VE1 PRELIMINARY; PRT; 9 AA.
 AC Q94VE1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus mertensi.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=62044;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407512; AAL10090.1; -.
 KW Mitochondrion.
 FT NON-TER
 SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
 DB 2 TLT 4

RESULT 68
 ID Q988J8 PRELIMINARY; PRT; 9 AA.
 AC Q988J8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORYZATENSIN-BIOACTIVE peptide.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95102521; PubMed=7804141;
 RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
 RT "Isolation and characterization of oryzatensin: a novel bioactive
 peptide with ileum-contracting and immunomodulating activities derived
 from rice albumin.";
 RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
 DR Gramene; Q988J8; -.
 SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 16.7%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15

Db 6 PLP 8

RESULT 69

Q61723 Q61723 PRELIMINARY; PRT; 9 AA.
AC Q61723;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE NF-kappa-B DNA-binding subunit (Fragment).
GN NFkB1 OR NF-KAPPA-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cBYJ; TISSUE=Spleen;
RX MEDLINE=94156215; PubMed=2203532;
RA Ghosh S., Gifford A.M., Riviere L.R., Tempst P., Nolan G.P.,
RA Baltimore D.;
RT "Cloning of the p50 DNA binding subunit of NF-kappa-B: Homology to rel
and dorsal.";
RL Cell 62:1019-1029(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cBYJ; TISSUE=Spleen;
RX MEDLINE=94156215; PubMed=8112620;
RA Huo L., Chung W.H., Rothstein T.L.;
RT "C-terminal sequence of the NF-kappa-B p50 precursor from primary
murine B-lymphocytes.";
RL Gene 139:287-288(1994).
DR EMBL; L13466; AAC37644.1; -.
DR MGD; MGI:97312; Nfkb1.
KW DNA-binding.
FT NON TER 1 1
FT CONFLICT 5 5 A -> P (IN REF. 1).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 925 MW; 300821E72DC1B408 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LHL 12

Db 6 LHL 8

RESULT 70

Q85723 Q85723 PRELIMINARY; PRT; 9 AA.
AC Q85723;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE V-sis and p28-sis genes (Fragment).
OS Simian sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11817;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84106822; PubMed=6319011;
RA Devare S.G., Shatzman A., Robbins K.C., Rosenberg M., Aaronson S.A.;
RT "Expression of the PDGF-related transforming protein of simian sarcoma
virus in E. coli";
RL Cell 36:43-49(1984).
DR EMBL; K01473; AAA46816.1; -.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1048 MW; 9C53A86C6C361A731 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5

Db 2 TLT 4

RESULT 71

Q935G1 Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1.O1C.
OS Salmonella typhi.
OG Plasmid pHCMI.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
RA Cronin A., Davies P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL513393; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON TER 9 9

SQ SEQUENCE 9 AA; 904 MW; 5FDCD77776D86767 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15

Db 1 PLP 3

RESULT 72

Q9XBH3 Q9XBH3 PRELIMINARY; PRT; 10 AA.
AC Q9XBH3;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Celf-like protein (Fragment).
GN CELF.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 10987;
RC MEDLINE=99231848; PubMed=10217496;
RA Oktad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "Genome organisation is not conserved between Bacillus cereus and

```

RT Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL; AJ000394; CAB40625.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1264 MW; D3757BC33339C9D6 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 2; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEX 9
   |||
Db 8 VEX 10

RESULT 73
Q9R5T2 PRELIMINARY; PRT; 10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]
RP SEQUENCE
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
RL dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RA Arch. Biochem. Biophys. 291:161-167(1991).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 2; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13
   |||
Db 2 HLP 4

RESULT 74
P83154 PRELIMINARY; PRT; 10 AA.
AC P83154;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Phycobilisome rod-core linker polypeptide cpcG3 (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlenann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -!- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.

```

```

CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
KW Phycobilisome; Photosynthesis; Thylakoid; Membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; 2F9B662B5B172737 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 2; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
   |||
Db 2 LPL 4

RESULT 75
Q9TG86 PRELIMINARY; PRT; 10 AA.
AC Q9TG86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
OS COI.
GN Diploglossus bilobatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguillidae;
OC Diploglossus.
OX NCBI_TaxID=102183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343613; PubMed=10413621;
RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
RA Papenfuss T.J.;
RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
RT in anquid lizards and related taxonomic families.";
RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL; AF085608; AAD51514.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1255 MW; 5DEE80C7336411A7 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 8; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
   |||
Db 2 TLT 4

Search completed: November 25, 2003, 19:34:02
Job time : 35.8023 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLDVEXKHLPLVQ 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A.Geneseq 19Jun03.*

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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Ewe colostrinin pe
5	18	100.0	18	23	Colostrinin consti
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Neural cell regula
8	6	33.3	6	11	Hypotensive peptid
9	6	33.3	6	21	Bioactive peptide

10	6	33.3	8	22	AAE07194	Colostrinin peptid
11	6	33.3	9	11	AAE03874	Hypotensive peptid
12	6	33.3	9	22	AAE07204	Modified colostrin
13	5	27.8	9	22	AAE98809	HIV gp120 protein
14	5	27.8	9	22	AAE98810	HIV gp120 protein
15	5	27.8	9	22	AAE98811	HIV gp120 protein
16	5	27.8	9	22	AAE98811	HIV gp120 protein
17	5	27.8	9	22	AAE98811	HIV gp120 protein
18	5	27.8	9	22	AAE98811	HIV gp120 protein
19	5	27.8	9	22	AAE98811	HIV gp120 protein
20	5	27.8	10	22	AAE98811	HIV gp120 protein
21	5	27.8	10	22	AAE98811	HIV gp120 protein
22	5	27.8	10	22	AAE98811	HIV gp120 protein
23	5	27.8	11	22	AAE98811	HIV gp120 protein
24	5	27.8	12	22	AAE98811	HIV gp120 protein
25	5	27.8	12	22	AAE98811	HIV gp120 protein
26	5	27.8	12	22	AAE98811	HIV gp120 protein
27	5	27.8	12	22	AAE98811	HIV gp120 protein
28	5	27.8	12	22	AAE98811	HIV gp120 protein
29	5	27.8	12	22	AAE98811	HIV gp120 protein
30	5	27.8	12	22	AAE98811	HIV gp120 protein
31	5	27.8	12	22	AAE98811	HIV gp120 protein
32	5	27.8	12	22	AAE98811	HIV gp120 protein
33	5	27.8	12	22	AAE98811	HIV gp120 protein
34	5	27.8	12	22	AAE98811	HIV gp120 protein
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45	5	27.8	12	22	AAE98811	HIV gp120 protein
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55	5	27.8	12	22	AAE98811	HIV gp120 protein
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57	5	27.8	12	22	AAE98811	HIV gp120 protein
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59	5	27.8	12	22	AAE98811	HIV gp120 protein
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81	5	27.8	12	22	AAE98811	HIV gp120 protein
82	5	27.8	12	22	AAE98811	HIV gp120 protein

83 5 27.8 18 22 AAB89449 HIV gp120 protein
 84 5 27.8 18 22 AAB89663 HIV gp120 protein
 85 5 27.8 18 22 AAB89664 HIV gp120 protein
 86 5 27.8 18 22 AAB89665 HIV gp120 protein
 87 5 27.8 18 22 AAB89666 HIV gp120 protein
 88 5 27.8 18 22 AAB89667 HIV gp120 protein
 89 5 27.8 19 23 ABG62441 Eubacterial DNA po
 90 5 27.8 19 23 ABG53241 Desulfobulbus sp p
 91 5 27.8 20 20 AAY03008 Fragment of human
 92 4 22.2 5 15 AAS8329 Hypotensive polype
 93 4 22.2 5 19 AAM45571 Amino-terminal pro
 94 4 22.2 5 23 ABO8941 Peptide #4 used in
 95 4 22.2 6 21 AAB12610 Halovir A peptide
 96 4 22.2 6 22 AAU04587 Human G-protein co
 97 4 22.2 6 22 AAB55480 Human elastase var
 98 4 22.2 7 21 AAB17246 SH3 antagonist pep
 99 4 22.2 7 21 AAY91412 Human secreted pro
 100 4 22.2 7 22 AAE09140 Bacteriophage type

ALIGNMENTS

RESULT 1
 AAB72268
 ID AAB72268 standard; peptide; 18 AA.
 XX
 AC AAB72268;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Colostrinin derived cytokine inducing peptide SEQ ID 23.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 XX 22-FEB-2001.
 XX
 XX 17-AUG-2000; 2000WO-US22818.
 XX
 XX 17-AUG-1999; 99US-0149311.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 SLTLTDVEKHLPLPLVQ 18
 |||||
 Db 1 SLTLTDVEKHLPLPLVQ 18
 |||||
 RESULT 2
 AAB72521
 ID AAB72521 standard; Peptide; 18 AA.
 XX
 AC AAB72521;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #22.
 XX
 KW Dermatological; oxidative stress regulator; colostrinin.
 XX
 OS Unidentified.
 XX
 PN WO200112650-A2.
 XX
 XX 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22665.
 XX
 XX 17-AUG-1999; 99US-0149310.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 PS Claim 6; Page 26; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 SLTLTDVEKHLPLPLVQ 18
 |||||
 Db 1 SLTLTDVEKHLPLPLVQ 18
 |||||
 RESULT 3
 AAB72553
 ID AAB72553 standard; Peptide; 18 AA.
 XX
 AC AAB72553;
 XX
 DT 09-MAY-2001 (first entry)
 XX

DE Colostrinin peptide #22.
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 XX Unidentified.
 OS
 XX WO200112651-A2.
 FN
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX 17-AUG-1999; 99US-0149633.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I;
 PI
 XX WPI; 2001-226545/23.
 DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 PT
 XX Claim 6; Page 21; 35pp; English.
 PS
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 CC
 XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLTDVEKHLPLPLVQ 18
 Db 1 SLTLTDVEKHLPLPLVQ 18
 RESULT 4
 ID AAB59331 standard; Peptide; 18 AA.
 AC AAB59331;
 XX 21-MAR-2001 (first entry)
 DT
 XX Ewe colostrinin peptide fragment C-6.
 DE
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX WO200075173-A2.
 PN
 XX 14-DEC-2000.
 PD
 XX 02-JUN-2000; 2000WO-GB02128.
 PF
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGE-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 XX characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLTDVEKHLPLPLVQ 18
 Db 1 SLTLTDVEKHLPLPLVQ 18
 RESULT 5
 ID AAE20250 standard; peptide; 18 AA.
 XX
 AC AAE20250;
 XX 18-JUN-2002 (first entry)
 DT
 XX Colostrinin constituent peptide #22.
 DE
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 18 /note= "Optionally C-terminal amide"
 FT
 XX WO200213850-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22776.
 PF
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI
 XX WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 PS Claim 6; Page 26; 51pp; English.
 XX
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLTDVEKHLPLPLVQ 18
 |||||
 Db 1 SLTLTDVEKHLPLPLVQ 18

RESULT 6
 AAM51057
 ID AAM51057 standard; Peptide; 18 AA.
 XX
 AC AAM51057;
 DT 30-MAY-2002 (first entry)
 DE Colostrinin constituent peptide (casein amino acids 139-156).
 XX
 XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "optional C-terminal amidation"

PN WO200213849-A1.
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22775.
 XX 17-AUG-2000; 2000WO-US22775.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 XX Stanton GU, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2002-269150/31.
 DR
 XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX
 PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 139-156. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent.. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLTDVEKHLPLPLVQ 18
 |||||
 Db 1 SLTLTDVEKHLPLPLVQ 18

RESULT 7
 AAO14599
 ID AAO14599 standard; peptide; 18 AA.
 XX
 AC AAO14599;
 DT 27-MAY-2002 (first entry)
 DE Neural cell regulatory colostrinin peptide 22.
 XX
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 XX neural cell treatment.

Unidentified.
 Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optional C-terminal amide"

PN WO200213851-A1.
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22777.
 XX 17-AUG-2000; 2000WO-US22777.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I, Stanton JG, Hughes TK;
 XX WPI; 2002-269152/31.
 DR
 XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -
 XX
 PS Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in


```

CC the method of the invention.
XX
SQ Sequence 18 AA;

Query Match      100.0%; Score 18; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTDVEKHLPLPLVQ 18
Db 1 SLTLTDVEKHLPLPLVQ 18

RESULT 8
AAR03868
ID AAR03868 standard; Protein; 6 AA.
XX
AC AAR03868;
XX
DT 17-FEB-1993 (first entry)
XX
DE Hypotensive peptide (7).
XX
KW Hypotensor; salt.
XX
OS Synthetic.
XX
PN JP02062828-A.
XX
PD 02-MAR-1990.
XX
PF 26-AUG-1988; 88JP-0211696.
XX
PR 26-AUG-1988; 88JP-0211696.
XX
PA (AJIN ) AJINOMOTO KK.
XX
WPI; 1990-111933/15.
XX
New peptide used as active ingredient of hypotensive agent -
PT which may be prep'd. e.g. as tablets, capsules, powder, syrup,
PT injection prepn. etc.
XX
PS Claim; Page ?; 9pp; Japanese.
XX
XX The peptides given in AAR03862-76 and their salts can be used as
XX components of hypotensive agents.
CC The hypotensor may be in the form of tablets, capsules, powder,
CC syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of
CC the peptide.
XX
SQ Sequence 6 AA;

Query Match      33.3%; Score 6; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPLP 15
Db 1 LHLPLP 6

RESULT 9
AAV69541
ID AAV69541 standard; peptide; 6 AA.
XX
AC AAV69541;
XX
DT 19-APR-2000 (first entry)
XX
DE Bioactive peptide #7 from whey protein hydrolysate.
XX
WY Whey protein hydrolysate; bioactive peptide; non bitter flavour;

KW food product; digestible; hypotensive.
XX
OS Unidentified.
XX
WO9965326-A1.
XX
PD 23-DEC-1999.
XX
PF 14-JUN-1999; 99WO-NZ00084.
XX
PR 17-JUN-1998; 98NZ-0330710.
XX
PA (NZDA-) NEW ZEALAND DAIRY BOARD.
XX
PI Schlothauer R, Schollum LM, Singh AM, Reid JR;
XX WPI; 2000-116705/10.
XX
PT Preparation of whey protein hydrolysate containing bioactive peptides
PT but does not have bitter flavor -
XX
PS Claim 19; Page 21; 32pp; English.
XX
XX Sequences AAV69535-Y69536 represent bioactive peptides which are
XX components of whey protein hydrolysate. The invention relates to the
XX preparation of whey protein hydrolysate containing such bioactive
XX peptides by treating a whey protein containing substrate with one or more
XX enzymes capable of hydrolysing whey proteins to produce the whey protein
XX hydrolysate containing bioactive peptides, and terminating the hydrolysis
XX before substantial production of unacceptable bitter flavours. The
XX invention also encompasses a non bitter product produced by partial
XX hydrolysis of a substrate containing whey proteins, where the product
XX comprises bioactive peptides and has a degree of hydrolysis of the whey
XX proteins of below 10%, a food product containing the non bitter product,
XX any one or a combination of two or more of the bioactive peptides of the
XX invention, and a method for reducing systolic blood pressure in a patient
XX which comprises administering the non bitter product to the patient. The
XX peptides, products and food products are useful in a method for the
XX reduction of systolic blood pressure. The whey protein products are free
XX from bitter flavours and contain bioactive peptides. The products of the
XX process have high digestibility and good organoleptic properties. The
XX products may have bland or slightly sweet taste and are free of soapy
XX and/or brothy flavours.
XX
SQ Sequence 6 AA;

Query Match      33.3%; Score 6; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPLP 15
Db 1 LHLPLP 6

RESULT 10
AAE07194
ID AAE07194 standard; peptide; 8 AA.
XX
AC AAE07194;
XX
DT 06-NOV-2001 (first entry)
XX
DE Colostrin peptide 10.
XX
KW Colostrin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW central nervous system disorder; neurodegenerative disorder; weight loss;
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW acquired immunological deficiency; neurological disorder; dementia;
XX antiviral.
XX
OS Unidentified.

```


QY 1 SLTTLT 5
 DB 4 SLTTLT 8

RESULT 15

AAB89811 ID AAB89811 standard; Peptide; 9 AA.

XX AC AAB89811;

XX DT 23-MAY-2001 (first entry)

XX DE HIV gp120 protein binding peptide #904.

XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;

XX KW replication; CCR5; CXCR4; CD4; STRL33.

XX OS Synthetic.

XX PN WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US23505.

XX PR 27-AUG-1999; 99US-0151270.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Saxinger C;

XX DR WPI; 2001-244398/25.

XX PT Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions

XX PS Example 10; Page 68; 114pp; English.

XX CC The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 9 AA;

Query Match 27.8%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
 DB 3 SLTTLT 7

RESULT 16

AAM24655 ID AAM24655 standard; Peptide; 9 AA.

XX AC AAM24655;

XX DT 04-DEC-2001 (first entry)

XX DE Human MHC class I molecule HLA-A2 binding 83P5G4 peptide #32.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytotstatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.

XX

OS Homo sapiens.

XX PN WO200159115-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX PR 09-FEB-2000; 2000US-0181261.

XX PA (UROG-) UROGENESYS INC.

XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX PI Mitchell SC, Jakobovits A;

XX DR WPI; 2001-514669/56.

XX AN An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone cancer

XX PS Example 15; Page 77; 112pp; English.

XX CC The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 9 AA;

Query Match 27.9%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
 DB 2 LPLPL 6

RESULT 17

AAM24955 ID AAM24955 standard; Peptide; 9 AA.

XX AC AAM24955;

XX DT 04-DEC-2001 (first entry)

XX DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #32.

XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytotstatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.

XX OS Homo sapiens.

XX PN WO200159115-A2.

XX PR 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04426.

XX 09-FEB-2000; 2000US-0181261.
XX (UROC-) UROGENESYS INC.
XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX Mitchell SC, Jakobovits A;
XX WPI; 2001-514669/56.
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
XX therapeutic agent in multiple cancers such as prostate, bladder and
XX bone cancer -
XX Example 15; Page 85; 112pp; English.
XX The polypeptide sequences represent the 83P5G4-related protein and
XX peptide fragments of the protein. 83P5G4 exhibits prostate specific
XX expression in normal adult tissue, but it is also aberrantly expressed in
XX many cancers including tumours of the prostate, testis, bladder, kidney,
XX brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
XX liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
XX peptide fragments and specific PCR primers are therefore useful for
XX diagnosing and treating cancer. A vector comprising a polynucleotide
XX which encodes a single chain monoclonal antibody, that immunospecifically
XX binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
XX polynucleotide having the 83P5G4 coding sequence, are both useful in the
XX preparation of a composition for treating a patient with a cancer that
XX expresses 83P5G4. The sequences can be used in diagnostic methods to
XX monitor the level of 83P5G4 gene products in serum, blood, urine and
XX tissue and to thereby detect the presence of cancerous cells.
XX Sequence 9 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 LPLPL 16
DB 5 LPLPL 9
RESULT 18
AAM25052
ID AAM25052 standard; Peptide; 9 AA.
XX AAM25052;
XX 04-DEC-2001 (first entry)
XX Human MHC class I molecule HLA-B7 binding 83P5G4 peptide #29.
XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
XX cytotstatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
XX single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
XX chromosome 1q31-q32.
XX Homo sapiens.
XX OS
XX WO200159115-A2.
XX 16-AUG-2001.
XX 09-FEB-2001; 2001WO-US04426.
XX 09-FEB-2000; 2000US-0181261.
XX (UROC-) UROGENESYS INC.
XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX Mitchell SC, Jakobovits A;

XX WPI; 2001-514669/56.
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
XX therapeutic agent in multiple cancers such as prostate, bladder and
XX bone cancer -
XX Example 15; Page 87; 112pp; English.
XX The polypeptide sequences represent the 83P5G4-related protein and
XX peptide fragments of the protein. 83P5G4 exhibits prostate specific
XX expression in normal adult tissue, but it is also aberrantly expressed in
XX many cancers including tumours of the prostate, testis, bladder, kidney,
XX brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
XX liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
XX peptide fragments and specific PCR primers are therefore useful for
XX diagnosing and treating cancer. A vector comprising a polynucleotide
XX which encodes a single chain monoclonal antibody, that immunospecifically
XX binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
XX polynucleotide having the 83P5G4 coding sequence, are both useful in the
XX preparation of a composition for treating a patient with a cancer that
XX expresses 83P5G4. The sequences can be used in diagnostic methods to
XX monitor the level of 83P5G4 gene products in serum, blood, urine and
XX tissue and to thereby detect the presence of cancerous cells.
XX Sequence 9 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 LPLPL 16
DB 5 LPLPL 9
RESULT 19
AAM25004
ID AAM25004 standard; Peptide; 10 AA.
XX AAM25004;
XX 04-DEC-2001 (first entry)
XX Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #81.
XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
XX cytotstatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
XX single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
XX chromosome 1q31-q32.
XX Homo sapiens.
XX OS
XX WO200159115-A2.
XX 16-AUG-2001.
XX 09-FEB-2001; 2001WO-US04426.
XX 09-FEB-2000; 2000US-0181261.
XX (UROC-) UROGENESYS INC.
XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX Mitchell SC, Jakobovits A;
XX WPI; 2001-514669/56.
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
XX therapeutic agent in multiple cancers such as prostate, bladder and
XX bone cancer -

PS Example 15; Page 86; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 20
AAM25103
ID AAM25103 standard; Peptide; 10 AA.
XX
AC AAM25103;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-B7 binding 83P5G4 peptide #80.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix; single chain monoclonal antibody; urine; uterus; rectum; stomach; human; chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN WO200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PA (UROC-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin B; Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
PT An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone cancer -
XX
PS Example 15; Page 89; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 21
AAM25203
ID AAM25203 standard; Peptide; 10 AA.
XX
AC AAM25203;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC molecule HLA-B35 binding 83P5G4 peptide #80.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix; single chain monoclonal antibody; urine; uterus; rectum; stomach; human; chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN WO200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PA (UROC-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin B; Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
PT An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone cancer -
XX
PS Example 15; Page 91; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.

XX
SQ Sequence 10 AA;

Query Match 27.8%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 22
AAB20470
ID AAB20470 standard; Peptide; 11 AA.
XX
AC AAB20470;
XX
DT 21-JUN-2001 (first entry)
XX
DE Mouse CD166 peptide isolated in database screening.
XX
KW CD166; ALCAM; mouse; PSK; seizure related protein; epilepsy;
KW neurological disorder; diagnosis; therapy.
XX
OS Mus sp.
XX
PN WO200125268-A1.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-DK00556.
XX
PR 04-OCT-1999; 99DK-0001420.
XX
PA (SCHR/) SCHROTZ-KING P.
PA (KING/) KING A.
PA (MANN/) MANN M.
PA (ANDE/) ANDERSEN J.
PA (KUES/) KUESTER B.
XX
PI Schrotz-King P, King A, Mann M, Andersen J, Kuester B;
XX
DR WPI; 2001-290605/30.
XX
PT Novel human seizure related proteins useful for controlling epileptic
PT seizures and neurological disorders, and for identifying potential drug
PT targets for use in diagnosis and/or prognosis of neurological disorders
PT -
XX
PS Disclosure; Page 58; 150pp; English.
XX

CC The present sequence is that of a mouse CD166 (ALCAM) peptide
CC identified during a proteomics screening approach for membrane
CC receptors in the brain. 9 Proteins from an RP-HPLC preparation
CC from the mouse E16 brain plasma membrane were analyzed by
CC nanoelectrospray tandem mass spectrometry. Peptide sequences were
CC found by searching NRDB or EST databases with peptide sequence tags.
CC Sample 8 was identified as CD166. Sample 7 was novel, and named
CC PSK-1. Human PSKs (see AAB20446-48) were subsequently identified.
CC These are novel transmembrane receptor or secreted proteins that
CC are potentially involved in the control or generation of seizures
CC such as epileptic seizures or other neurological disorders.
CC PSK-1, -2 and -3 polynucleotides and polypeptides can be used to
CC identify potential drug targets. They can also be used in the
CC diagnosis of seizure related conditions or other neurodegeneration
CC such as Alzheimer, Rasmussen's Encephalitis, Parkinson's disease,
CC multiple sclerosis, cerebrovascular disorders (stroke syndromes)
CC like ischaemia, Huntington's disease or schizophrenia (Claimed),
CC and in the treatment of conditions caused by PSK upregulation,
CC

CC deficiency or impaired function.
XX
SQ Sequence 11 AA;

Query Match 27.8%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLTDV 7
|||||
Db 6 TLTDV 10

RESULT 23
ABU03415
ID ABU03415 standard; Protein; 11 AA.
XX
AC ABU03415;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #195.
XX
KW Translational profiling; expressed protein tag; EPT; kinase;
KW phosphatase; protease; protease inhibitor; transporter;
KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer;
KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PR 28-MAR-2002; 2002WO-US09671.
XX
PR 28-MAR-2001; 2001US-279495P.
PR 21-MAY-2001; 2001US-292544P.
PR 08-AUG-2001; 2001US-310801P.
PR 01-OCT-2001; 2001US-326370P.
PR 04-DEC-2001; 2001US-336780P.
PR 20-FEB-2002; 2002US-358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
PT or leukemia -
XX
PS Claim 10; SEQ ID No 195; 134pp; English.
XX

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor.
CC The polypeptide is useful as an immunogenic composition for eliciting
CC in a mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to
CC this polypeptide, is useful for treating cancer. The polypeptide is
CC also useful for identifying compounds that binds to a naturally
CC processed class I or class II MHC-binding polypeptide. The polypeptides
CC and polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling.

CC Note: This sequence does not appear in the printed specification but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 11 AA;

Query Match 27.8%; Score 5; DB 24; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLTDV 7
 |||||
 Db 6 TLTDV 10

RESULT 24

AAB89415
 ID AAB89415 standard; Peptide; 12 AA.

XX AC AAB89415;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #508.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.

PN WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US23505.

XX 27-AUG-1999; 99US-0151270.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -

XX Example 9; Page 57; 114pp; English.

XX The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.

XX Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
 |||||
 Db 6 SLTLT 10

RESULT 25

AAB89855
 ID AAB89855 standard; Peptide; 12 AA.

XX AC AAB89855;

XX Saxinger C;

DT 23-MAY-2001 (first entry)
 XX HIV gp120 protein binding peptide #948.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.

PN WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US23505.

XX 27-AUG-1999; 99US-0151270.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 69; 114pp; English.

XX The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.

XX Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
 |||||
 Db 8 SLTLT 12

RESULT 26

AAB89856
 ID AAB89856 standard; Peptide; 12 AA.

XX AC AAB89856;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #949.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.

PN WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US23505.

XX 27-AUG-1999; 99US-0151270.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX

DR WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 69; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
|||||
Db 7 SUTLTL 11

RESULT 27
AAB89857
ID AAB89857 standard; Peptide; 12 AA.
XX
XX AAB89857;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #950.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 69; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 12 AA;

Query Match 27.8%; Score 5; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5

Db 6 SLTTLT 10
|||||
RESULT 28
AAAY30295
ID AAAY30295 standard; peptide; 14 AA.
XX
XX AAAY30295;
AC
XX 23-NOV-1999 (first entry)
DT
XX Angiopoietin derived peptide #10.
DE
XX
KW Angiogenesis; tumour; metastasis; wound healing; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; cancer; blood supply; imaging;
KW treatment; angiopoietin; Tie-1; Tie-2; TPCK Trypsin; protease;
KW receptor tyrosine kinase.
XX
OS Synthetic.
XX
XX WO9940947-A2.
PN
XX 19-AUG-1999.
PD
XX 11-FEB-1999; 99WO-CA00101.
PF
XX 11-FEB-1998; 98US-0074420.
PR
XX (RESO-) RESOLUTION PHARM INC.
PA
XX Eshima D, Fauconnier T, Pollak A, Thornback J;
PI
XX WPI; 1999-527342/44.
DR
XX Angiogenesis targeting molecules, for, e.g. detecting and treating
PT cancer
PT
XX
PS Example 16; Page 50; 70pp; English.
XX
CC Sequences AAAY30286-Y30310 and AAAY34151-Y34156 are peptides derived from
CC the angiopeptins through cleavage by the proteases TPCK Trypsin or
CC Staphylococcus aureus protease. The angiopeptins bind to the receptor
CC tyrosine kinase Tie-2 which is upregulated during angiogenesis.
CC Angiopoietin 1 (Ang 1) is ubiquitously expressed and interacts with
CC Tie-2 on endothelial cells and early haemopoietic cells. Angiopoietin 2
CC (Ang 2) is homologous to Ang 1 and competitively inhibits Ang 1
CC interaction with Tie-2. Angiogenesis is the process involved in creating
CC a blood supply to a tumour. The peptides are used in a compound that
CC binds to sites of angiogenesis. The compound consists of a chelator
CC moiety capable of complexing a radionuclide metal or a moiety capable of
CC binding to a halogen group, and an angiogenesis targeting molecule. The
CC peptides are incorporated in the angiogenesis targeting molecule. The
CC compounds are used for imaging and treating angiogenesis, and also to
CC detect, stage and treat tumours and metastases. Angiogenesis is also
CC required for wound healing and conditions such as diabetic retinopathy,
CC rheumatoid arthritis and psoriasis, therefore the compounds may also be
CC useful in the treatment of these conditions.
XX
SQ Sequence 14 AA;

Query Match 27.8%; Score 5; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTDVE 8
|||||
Db 1 LTDVE 5

RESULT 29
AAE03935
ID AAE03935 standard; peptide; 14 AA.

XX AAE03935;
XX 09-AUG-2001 (first entry)
XX Human gene 38 encoded secreted protein fragment HBJFJ14, SEQ ID NO:98.
XX
XX Human; secreted protein; proliferative disorder; cancer; tumour;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angioecnic disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder;
XX endocrine disorder; infection; wound healing; vulnery;
XX cell culture; chemotaxis; food additive; gene therapy;
XX binding partner identification.
XX
XX Homo sapiens.
XX
XX W0200077022-A1.
XX
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US15136.
XX
XX 11-JUN-1999; 99US-0138629.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX
XX WPI; 2001-367020/38.
XX N-PSDB; RAD08382.
XX
XX Nucleic acids encoding 50 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's
XX disease, botulism, cancers and Scimitar syndrome -
XX
XX Claim 11; Page 546; 614pp; English.
XX
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
XX protein genes and AAE03898-AAE03947 represent the proteins they encode.
XX AAE03948-AAE03996 represent human secreted protein fragments or variants.
XX The genes and their secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 50 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angioecnic disorders, kidney disorders,
XX gastrointestinal disorders, pregnancy-related disorders, endocrine
XX disorders, and infections. The proteins can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin aging due to
XX sunburn, to maintain organs before transplantation, for supporting cell
XX culture of primary tissues, to regenerate tissues, to identify their
XX cognate ligands or binding partners, and in chemotaxis, and can be used
XX as a food additive or preservative to modify storage properties.
XX Antibodies specific for a protein of the invention can be used in
XX alleviating symptoms associated with the disorders mentioned above, and
XX in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX immunosorbent assay (ELISA). The present sequence represents a human
XX secreted protein fragment of the invention.
XX
XX Sequence 14 AA;

Query Match 27.8%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 LHLPL 14
Db 5 LHLPL 9
RESULT 30
AAW39008
ID AAW39008 standard; peptide; 15 AA.
XX AAW39008;
XX AC
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:407.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX (UTNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX Sparks AB, Thorn JM;
XX WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
Query Match 27.8%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
 Db 3 LPLPL 7

RESULT 31
 AAW38988
 ID AAW38988 standard; peptide; 15 AA.
 AC AAW38988;
 XX
 XX
 XX 27-MAR-1998 (first entry)
 XX
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:385.
 XX
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 XX
 XX WO9730074-A1.
 PN
 XX
 XX 21-AUG-1997.
 XX
 XX 14-FEB-1997; 97WO-US02298.
 XX
 XX 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX
 XX WPI; 1997-424972/39.
 DR
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 PS Claim 22; Page 92; 131pp; English.
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 SQ Sequence 15 AA;
 XX

Query Match 27.8%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
 Db 10 LPLPL 14

RESULT 32
 AAB89429
 ID AAB89429 standard; Peptide; 15 AA.
 XX
 AC AAB89429;
 XX
 XX 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #522.
 XX
 XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 XX WO200116182-A2.
 PN
 XX
 XX 08-MAR-2001.
 XX
 XX 25-AUG-2000; 2000WO-US23505.
 XX
 XX 27-AUG-1999; 99US-0151270.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Saxinger C;
 PI
 XX
 XX WPI; 2001-244398/25.
 DR
 XX
 XX Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX
 XX Example 9; Page 58; 114pp; English.
 PS
 XX
 CC The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.
 XX
 SQ Sequence 15 AA;
 XX

Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SUTLT 5
 Db 9 SUTLT 13

RESULT 33
 AAB89430
 ID AAB89430 standard; Peptide; 15 AA.
 XX
 AC AAB89430;
 XX
 XX 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #523.
 XX
 XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 XX WO200116182-A2.
 PN
 XX
 XX 08-MAR-2001.
 XX
 XX 25-AUG-2000; 2000WO-US23505.
 XX

Query Match 27.8%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
PR 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX |||||
XX Db 8 SLTLT 12
XX
XX RESULT 34
XX AAB89431
XX ID AAB89431 standard; Peptide; 15 AA.
XX
XX AC AAB89431;
XX
XX XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #524.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US233505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX |||||
XX Db 8 SLTLT 12
XX
XX RESULT 34
XX AAB89431
XX ID AAB89431 standard; Peptide; 15 AA.
XX
XX AC AAB89431;
XX
XX XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #524.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US233505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX |||||
XX Db 11 SLTLT 15
XX
XX RESULT 36
XX AAB89620
XX ID AAB89620 standard; Peptide; 15 AA.
XX
XX AC AAB89620;
XX
XX XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #713.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX Sequence 15 AA;
```


AAB89623
ID AAB89623 standard; Peptide; 15 AA.
XX AC AAB89623;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #716.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
XX PS Example 10; Page 64; 114pp; English.
XX FS The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
PR Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTTLT 5
DB 7 SLTTLT 11
RESULT 40
AAB90009
ID AAB90009 standard; Peptide; 15 AA.
XX AC AAB90009;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1102.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
XX PS Example 10; Page 73; 114pp; English.
XX CC The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
PR Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTTLT 5
DB 8 SLTTLT 12
RESULT 41
AAB90010
ID AAB90010 standard; Peptide; 15 AA.
XX AC AAB90010;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1103.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -
XX PS Example 10; Page 73; 114pp; English.
XX CC The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 S1TLT 5
 |||||
 8 S1TLT 12

Db

RESULT 42
 AAB90011
 ID AAB90011 standard; Peptide; 15 AA.
 AC AAB90011;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #1104.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 PD 08-MAR-2001.
 PF 25-AUG-2000; 2000WO-US23505.
 PR 27-AUG-1999; 99US-0151270.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Saxinger C;
 XX
 DR WPI; 2001-244398/25.
 XX
 DE Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX
 PS Example 10; Page 73; 114pp; English.
 XX
 CC The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 S1TLT 5
 |||||
 8 S1TLT 12

Db

RESULT 44
 AAB90013
 ID AAB90013 standard; Peptide; 15 AA.
 XX
 AC AAB90013;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #1106.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 PD 08-MAR-2001.
 PF 25-AUG-2000; 2000WO-US23505.
 PR 27-AUG-1999; 99US-0151270.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Saxinger C;
 XX
 DR WPI; 2001-244398/25.
 XX
 DE Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX

Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 S1TLT 5
 |||||
 8 S1TLT 12

Db

RESULT 43
 AAB90012
 ID AAB90012 standard; Peptide; 15 AA.
 XX
 AC AAB90012;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #1105.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.
 OS WO200116182-A2.
 PN 08-MAR-2001.
 PD 25-AUG-2000; 2000WO-US23505.
 PF 27-AUG-1999; 99US-0151270.
 XX
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Saxinger C;
 XX
 DR WPI; 2001-244398/25.
 XX
 DE Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX
 PS Example 10; Page 73; 114pp; English.
 XX
 CC The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 S1TLT 5
 |||||
 8 S1TLT 12

Db

RESULT 44
 AAB90013
 ID AAB90013 standard; Peptide; 15 AA.
 XX
 AC AAB90013;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #1106.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 PD 08-MAR-2001.
 PF 25-AUG-2000; 2000WO-US23505.
 PR 27-AUG-1999; 99US-0151270.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Saxinger C;
 XX
 DR WPI; 2001-244398/25.
 XX
 DE Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX

```

PS Example 10; Page 73; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 45
AAB90014
ID AAB90014 standard; Peptide; 15 AA.
XX
AC AAB90014;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1107.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX
PS Example 10; Page 73; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 46
AAB90015

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ID AAB90015 standard; Peptide; 15 AA.
XX
AC AAB90015;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1108.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 47
AAB90016
ID AAB90016 standard; Peptide; 15 AA.
XX
AC AAB90016;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1109.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX

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PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX
PS Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTTLT 5
DB 8 SLTTLT 12
RESULT 48
AAB90022
ID AAB90022 standard; Peptide; 15 AA.
XX
XX AAB90022;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1115.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US233505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTTLT 5
DB 8 SLTTLT 12
RESULT 48
AAB90022
ID AAB90022 standard; Peptide; 15 AA.
XX
XX AAB90022;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1115.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US233505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTTLT 5
DB 8 SLTTLT 12
RESULT 49
AAB90023
ID AAB90023 standard; Peptide; 15 AA.
XX
XX AAB90023;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1116.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US233505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTTLT 5
DB 8 SLTTLT 12
RESULT 50
AAB90024
ID AAB90024 standard; Peptide; 15 AA.
XX
XX AAB90024;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1117.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.

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OS Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
DB 8 SLTTLT 12
XX
RESULT 51
AAB90025
ID AAB90025 standard; Peptide; 15 AA.
XX
AC AAB90025;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1118.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.

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XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
DB 8 SLTTLT 12
XX
RESULT 52
AAB90026
ID AAB90026 standard; Peptide; 15 AA.
XX
AC AAB90026;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1119.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 73; 114pp; English.
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
DB 8 SLTTLT 12
XX
RESULT 53
AAB90027
ID AAB90027 standard; Peptide; 15 AA.

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```
XX AAB90027;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #1120.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTILT 5
XX |||||
XX 8 SLTILT 12
XX
XX RESULT 54
XX AAB90028
XX ID AAB90028 standard; Peptide; 15 AA.
XX
XX AC AAB90028;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #1121.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
```

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XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTILT 5
XX |||||
XX 8 SLTILT 12
XX
XX RESULT 55
XX AAB90029
XX ID AAB90029 standard; Peptide; 15 AA.
XX
XX AC AAB90029;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #1122.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTILT 5
XX |||||
XX 8 SLTILT 12
XX
XX RESULT 56
XX AAB90030
XX ID AAB90030 standard; Peptide; 15 AA.
XX
XX AC AAB90030;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #1123.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
```


CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db |||||
8 SLTLT 12

RESULT 59
AAB90033
ID AAB90033 standard; Peptide; 15 AA.

XX AC AAB90033;
XX
XX 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1126.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX

XX PN WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX

XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 74; 114pp; English.
XX

XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db |||||
8 SLTLT 12

RESULT 60
AAB90039
ID AAB90039 standard; Peptide; 15 AA.

XX

AC AAB90039;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1132.
XX

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX

XX Synthetic.
XX
XX WO200116182-A2.
XX

XX PD 08-MAR-2001.
XX

XX PF 25-AUG-2000; 2000WO-US23505.
XX

XX PR 27-AUG-1999; 99US-0151270.
XX

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

XX PI Saxinger C;
XX

XX DR WPI; 2001-244398/25.
XX

XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 74; 114pp; English.
XX

XX CC The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db |||||
8 SLTLT 12

RESULT 61
AAB90040
ID AAB90040 standard; Peptide; 15 AA.

XX AC AAB90040;
XX

XX DT 23-MAY-2001 (first entry)
XX

XX DE HIV gp120 protein binding peptide #1133.
XX

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX

XX Synthetic.
XX

XX PN WO200116182-A2.
XX

XX PD 08-MAR-2001.
XX

XX PF 25-AUG-2000; 2000WO-US23505.
XX

XX PR 27-AUG-1999; 99US-0151270.
XX

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

PI Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 74; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLTLT 5
Db 8 SLTLT 12
RESULT 62
AAB90041
ID AAB90041 standard; Peptide; 15 AA.
XX AC AAB90041;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1134.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 74; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLTLT 5
Db 8 SLTLT 12
RESULT 64
AAB90101
ID AAB90101 standard; Peptide; 15 AA.
XX AC AAB90101;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1194.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12
RESULT 63
AAB90042
ID AAB90042 standard; Peptide; 15 AA.
XX AC AAB90042;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1135.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 74; 114pp; English.
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLTLT 5
Db 8 SLTLT 12
RESULT 64
AAB90101
ID AAB90101 standard; Peptide; 15 AA.
XX AC AAB90101;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1194.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US23505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
WPI; 2001-244398/25.
XX
DR Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 75; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLTLT 5
DB 8 SLTLT 12
RESULT 65
AAB90102
ID AAB90102 standard; Peptide; 15 AA.
XX
AC AAB90102;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1195.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
XX 1 SLTLT 5
DB 8 SLTLT 12
RESULT 66
AAB90103
ID AAB90103 standard; Peptide; 15 AA.
XX
AC AAB90103;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1196.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
XX 1 SLTLT 5
DB 8 SLTLT 12
RESULT 67
AAB90104
ID AAB90104 standard; Peptide; 15 AA.
XX
AC AAB90104;

```



```

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 70
AAB90112
ID AAB90112 standard; Peptide; 15 AA.
XX AAB90112;
AC
XX
XX 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1205.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 75; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 71
AAB90113
ID AAB90113 standard; Peptide; 15 AA.
XX AAB90113;
AC
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #1206.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX

```

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XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 75; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 72
AAB90114
ID AAB90114 standard; Peptide; 15 AA.
XX AAB90114;
AC
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #1207.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 75; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX

```

CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLT 5
 |||||
 Db 8 SLTLT 12

RESULT 73
 AAB90115
 ID AAB90115 standard; Peptide; 15 AA.
 XX AC
 XX AAB90115;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #1208.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 XX
 PD |||||
 XX
 PF 8 SLTLT 12
 XX
 PR 25-AUG-2000; 2000WO-US23505.
 XX
 PT 27-AUG-1999; 99US-0151270.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Saxinger C;
 XX
 DR WPI; 2001-244398/25.
 XX
 PT Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX
 PS Example 10; Page 75; 114pp; English.
 XX
 CC The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLT 5
 |||||
 Db 8 SLTLT 12

RESULT 74
 AAB90116
 ID AAB90116 standard; Peptide; 15 AA.
 XX AC
 XX AAB90116;
 XX

DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #1209.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 XX
 PD |||||
 XX
 PF 8 SLTLT 12
 XX
 PR 25-AUG-2000; 2000WO-US23505.
 XX
 PT 27-AUG-1999; 99US-0151270.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Saxinger C;
 XX
 DR WPI; 2001-244398/25.
 XX
 PT Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions -
 XX
 PS Example 10; Page 76; 114pp; English.
 XX
 CC The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the
 CC virus. The present sequence is an example of a peptide of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLTLT 5
 |||||
 Db 8 SLTLT 12

RESULT 75
 AAB90118
 ID AAB90118 standard; Peptide; 15 AA.
 XX AC
 XX AAB90118;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE HIV gp120 protein binding peptide #1211.
 XX
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.
 XX
 OS Synthetic.
 XX
 PN WO200116182-A2.
 XX
 PD |||||
 XX
 PF 8 SLTLT 12
 XX
 PR 25-AUG-2000; 2000WO-US23505.
 XX
 PT 27-AUG-1999; 99US-0151270.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Saxinger C;
 XX

DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 76; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTIT 5
 |||||
Db 8 SLTIT 12

Search completed: November 25, 2003, 19:27:10
Job time : 46.9419 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8937 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SUTLTDVEXLHPLPLVQ 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-Processing: Listing first 100 summaries

Database : Published Applications AA:
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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	16	33.3	14	15	US-10-148-936-8
3	5	27.8	9	10	US-09-780-053-148
4	5	27.8	9	10	US-09-780-053-448
5	5	27.8	9	10	US-09-780-053-548
6	5	27.8	9	15	US-10-084-813-916
7	5	27.8	9	15	US-10-084-813-917
8	5	27.8	9	15	US-10-084-813-918
9	5	27.8	10	10	US-09-780-053-497
10	5	27.8	10	10	US-09-780-053-596
11	5	27.8	10	10	US-09-780-053-696
12	5	27.8	12	12	US-10-286-457-346
13	5	27.8	12	15	US-10-084-813-537
14	5	27.8	12	15	US-10-084-813-962
15	5	27.8	12	15	US-10-084-813-963
16	5	27.8	12	15	US-10-084-813-963
17	5	27.8	12	15	US-10-084-813-963
18	5	27.8	12	15	US-10-084-813-963
19	5	27.8	12	15	US-10-084-813-963
20	5	27.8	12	15	US-10-084-813-963
21	5	27.8	12	15	US-10-084-813-963
22	5	27.8	12	15	US-10-084-813-963
23	5	27.8	12	15	US-10-084-813-963
24	5	27.8	12	15	US-10-084-813-963
25	5	27.8	12	15	US-10-084-813-963
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27	5	27.8	12	15	US-10-084-813-963
28	5	27.8	12	15	US-10-084-813-963
29	5	27.8	12	15	US-10-084-813-963
30	5	27.8	12	15	US-10-084-813-963
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37	5	27.8	12	15	US-10-084-813-963
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41	5	27.8	12	15	US-10-084-813-963
42	5	27.8	12	15	US-10-084-813-963
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44	5	27.8	12	15	US-10-084-813-963
45	5	27.8	12	15	US-10-084-813-963
46	5	27.8	12	15	US-10-084-813-963
47	5	27.8	12	15	US-10-084-813-963
48	5	27.8	12	15	US-10-084-813-963
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52	5	27.8	12	15	US-10-084-813-963
53	5	27.8	12	15	US-10-084-813-963
54	5	27.8	12	15	US-10-084-813-963
55	5	27.8	12	15	US-10-084-813-963
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62	5	27.8	12	15	US-10-084-813-963
63	5	27.8	12	15	US-10-084-813-963
64	5	27.8	12	15	US-10-084-813-963
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82	5	27.8	12	15	US-10-084-813-963
83	5	27.8	12	15	US-10-084-813-963
84	5	27.8	12	15	US-10-084-813-963
85	5	27.8	12	15	US-10-084-813-963
86	5	27.8	12	15	US-10-084-813-963
87	5	27.8	12	15	US-10-084-813-963
88	5	27.8	12	15	US-10-084-813-963

12	15	US-10-084-813-964	Sequence 964, App
15	9	US-09-829-855-223	Sequence 223, App
15	12	US-10-161-791-385	Sequence 385, App
15	15	US-10-161-791-407	Sequence 407, App
15	15	US-10-084-813-29	Sequence 29, Appl
15	15	US-10-084-813-521	Sequence 521, App
15	15	US-10-084-813-522	Sequence 522, App
15	15	US-10-084-813-523	Sequence 523, App
15	15	US-10-084-813-726	Sequence 726, App
15	15	US-10-084-813-727	Sequence 727, App
15	15	US-10-084-813-728	Sequence 728, App
15	15	US-10-084-813-729	Sequence 729, App
15	15	US-10-084-813-730	Sequence 730, App
15	15	US-10-084-813-1115	Sequence 1115, Ap
15	15	US-10-084-813-1116	Sequence 1116, Ap
15	15	US-10-084-813-1117	Sequence 1117, Ap
15	15	US-10-084-813-1118	Sequence 1118, Ap
15	15	US-10-084-813-1119	Sequence 1119, Ap
15	15	US-10-084-813-1120	Sequence 1120, Ap
15	15	US-10-084-813-1121	Sequence 1121, Ap
15	15	US-10-084-813-1128	Sequence 1128, Ap
15	15	US-10-084-813-1129	Sequence 1129, Ap
15	15	US-10-084-813-1130	Sequence 1130, Ap
15	15	US-10-084-813-1131	Sequence 1131, Ap
15	15	US-10-084-813-1132	Sequence 1132, Ap
15	15	US-10-084-813-1133	Sequence 1133, Ap
15	15	US-10-084-813-1134	Sequence 1134, Ap
15	15	US-10-084-813-1135	Sequence 1135, Ap
15	15	US-10-084-813-1136	Sequence 1136, Ap
15	15	US-10-084-813-1137	Sequence 1137, Ap
15	15	US-10-084-813-1138	Sequence 1138, Ap
15	15	US-10-084-813-1139	Sequence 1139, Ap
15	15	US-10-084-813-1145	Sequence 1145, Ap
15	15	US-10-084-813-1146	Sequence 1146, Ap
15	15	US-10-084-813-1147	Sequence 1147, Ap
15	15	US-10-084-813-1148	Sequence 1148, Ap
15	15	US-10-084-813-1207	Sequence 1207, Ap
15	15	US-10-084-813-1208	Sequence 1208, Ap
15	15	US-10-084-813-1209	Sequence 1209, Ap
15	15	US-10-084-813-1210	Sequence 1210, Ap
15	15	US-10-084-813-1216	Sequence 1216, Ap
15	15	US-10-084-813-1217	Sequence 1217, Ap
15	15	US-10-084-813-1218	Sequence 1218, Ap
15	15	US-10-084-813-1219	Sequence 1219, Ap
15	15	US-10-084-813-1220	Sequence 1220, Ap
15	15	US-10-084-813-1221	Sequence 1221, Ap
15	15	US-10-084-813-1222	Sequence 1222, Ap
15	15	US-10-084-813-1224	Sequence 1224, Ap
16	9	US-09-829-855-227	Sequence 227, App
17	12	US-10-299-003-14	Sequence 14, Appl
18	15	US-10-084-813-552	Sequence 552, App
18	15	US-10-084-813-553	Sequence 553, App
18	15	US-10-084-813-554	Sequence 554, App
18	15	US-10-084-813-770	Sequence 770, App
18	15	US-10-084-813-771	Sequence 771, App
18	15	US-10-084-813-772	Sequence 772, App
18	15	US-10-084-813-773	Sequence 773, App
18	15	US-10-084-813-774	Sequence 774, App
19	9	US-09-829-855-225	Sequence 225, App
20	11	US-09-983-802-664	Sequence 664, App
20	12	US-10-340-288-5	Sequence 5, Appli
4	9	US-09-804-866-12	Sequence 12, Appl
5	9	US-09-804-866-13	Sequence 13, Appl
7	9	US-09-739-254-132	Sequence 132, App
7	9	US-09-904-615-132	Sequence 132, App
7	12	US-10-055-098-132	Sequence 132, App
7	15	US-10-054-988-132	Sequence 132, App
8	9	US-09-358-423-23	Sequence 23, Appl
8	9	US-09-358-423-24	Sequence 24, Appl
8	12	US-10-224-125-32	Sequence 32, Appl
8	14	US-10-047-881-23	Sequence 23, Appl
8	14	US-10-047-881-24	Sequence 24, Appl
9	10	US-09-780-053-566	Sequence 566, App

89 4 22.2 9 10 US-09-894-018-312 Sequence 312, App
90 4 22.2 9 10 US-09-821-831-68 Sequence 68, Appl
91 4 22.2 9 10 US-09-919-048-84 Sequence 84, Appl
92 4 22.2 9 10 US-09-919-048-126 Sequence 126, App
93 4 22.2 9 10 US-09-919-048-170 Sequence 170, App
94 4 22.2 9 10 US-09-017-743C-16 Sequence 16, Appl
95 4 22.2 9 10 US-09-909-460-91 Sequence 91, Appl
96 4 22.2 9 12 US-10-155-883B-53 Sequence 53, Appl
97 4 22.2 9 12 US-09-793-451-122 Sequence 122, App
98 4 22.2 9 12 US-09-793-451-131 Sequence 131, App
99 4 22.2 9 12 US-09-793-451-142 Sequence 142, App
100 4 22.2 9 12 US-09-793-451-236 Sequence 236, App

ALIGNMENTS

RESULT 1
US-10-281-652-23
; Sequence 23, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-23

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLDVEKHLPLPLVQ 18
 |||||
DB 1 SLTLDVEKHLPLPLVQ 18

RESULT 2
US-10-148-936-8
; Sequence 8, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: P49963
; CURRENT APPLICATION NUMBER: US/10/148,936
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928674.2
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-10-148-936-8

Query Match 33.3%; Score 6; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPLV 17
 |||||
DB 5 LPLPLV 10

RESULT 3
US-09-780-053-148
; Sequence 148, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-148

Query Match 27.8%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
 |||||
DB 2 LPLPL 6

RESULT 4
US-09-780-053-448
; Sequence 448, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09

; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-448

Query Match 27.8%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
| | | | |
Db 5 LPLPL 9

RESULT 5

US-09-780-053-545
; Sequence 545, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Paris
; APPLICANT: Eliana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-545

Query Match 27.8%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
| | | | |
Db 5 LPLPL 9

RESULT 6

US-10-084-813-916
; Sequence 916, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 916
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-084-813-916

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-916

Query Match 27.8%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
| | | | |
Db 5 SLTLT 9

RESULT 7

US-10-084-813-917
; Sequence 917, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 917
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-917

Query Match 27.8%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
| | | | |
Db 4 SLTLT 8

RESULT 8

US-10-084-813-918
; Sequence 918, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 918
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-918

Query Match 27.8%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
|||||
Db 3 SLTLT 7

RESULT 9

US-09-780-053-497
; Sequence 497, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 497
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-497

Query Match 27.8%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 10

US-09-780-053-596
; Sequence 596, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-596

Query Match 27.8%; Score 5; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 11

US-09-780-053-696
; Sequence 696, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 696
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-696

Query Match 27.8%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
|||||
Db 6 LPLPL 10

RESULT 12

US-10-286-457-346
; Sequence 346, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR FILING DATE: 2002-11-01
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, be
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-346

Query Match 27.8%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHLP 13
|||||

Db 6 KLHLP 10

RESULT 13

US-10-084-813-537

; Sequence 537, Application US/10084813

; Publication No. US20030068615A1

; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL

; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

; FILE REFERENCE: 215875

; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/151,270

; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 1242

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 537

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-537

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT/LT 5

Db 6 SLT/LT 10

RESULT 14

US-10-084-813-962

; Sequence 962, Application US/10084813

; Publication No. US20030068615A1

; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL

; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

; FILE REFERENCE: 215875

; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/151,270

; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 1242

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 962

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-962

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT/LT 5

Db 8 SLT/LT 12

RESULT 15

US-10-084-813-963

; Sequence 963, Application US/10084813

; Publication No. US20030068615A1

; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL

; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

; FILE REFERENCE: 215875

; CURRENT APPLICATION NUMBER: US/10/084,813

; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/151,270

; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 1242

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 963

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-963

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT/LT 5

Db 7 SLT/LT 11

RESULT 16

US-10-084-813-964

; Sequence 964, Application US/10084813

; Publication No. US20030068615A1

; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL

; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

; FILE REFERENCE: 215875

; CURRENT APPLICATION NUMBER: US/10/084,813

; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/151,270

; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 1242

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 964

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-964

Query Match

Best Local Similarity 27.8%; Score 5; DB 15; Length 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT/LT 5

Db 6 SLT/LT 10

RESULT 17

US-09-829-855-223

; Sequence 223, Application US/09829855

; Patent No. US20020065609A1

; GENERAL INFORMATION:

; APPLICANT: Matthew, Ashby N.

; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations

FILE REFERENCE: ASHBY-1
CURRENT APPLICATION NUMBER: US/09/829,855
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/196063
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/196258
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 244
SOFTWARE: PatentIn version 3.1
SEQ ID NO 223
LENGTH: 15
TYPE: PRT
ORGANISM: Denitrobacter permanens
US-09-829-855-223

Query Match 27.8%; Score 5; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 13 LPLVL 17
Db 4 LPLVL 8

RESULT 18

US-10-161-791-385
Sequence 385, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 385:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-385

Query Match 27.8%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 12 LPLPL 16
Db 10 LPLPL 14

RESULT 19

US-10-161-791-407
Sequence 407, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 407:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-407

Query Match 27.8%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 12 LPLPL 16
Db 3 LPLPL 7

RESULT 20

US-10-084-813-29
Sequence 29, Application US/10084813
Publication No. US20030068615A1

```
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-29

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 21
US-10-084-813-521
; Sequence 521, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 521
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-521

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 22
US-10-084-813-522
; Sequence 522, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 521
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-521

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      9 SLTTLT 13

RESULT 23
US-10-084-813-523
; Sequence 523, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 523
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-523

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      7 SLTTLT 11

RESULT 24
US-10-084-813-726
; Sequence 726, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; FILE REFERENCE: 215875
```

```
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 522
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-522

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      8 SLTTLT 12

RESULT 23
US-10-084-813-523
; Sequence 523, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 523
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-523

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      7 SLTTLT 11

RESULT 24
US-10-084-813-726
; Sequence 726, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; FILE REFERENCE: 215875
```

```
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 726
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-726

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      11 SLTLT 15

RESULT 25
US-10-084-813-727
; Sequence 727, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 727
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-727

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      10 SLTLT 14

RESULT 26
US-10-084-813-728
; Sequence 728, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 728
; LENGTH: 15
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-728

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      9 SLTLT 13

RESULT 27
US-10-084-813-729
; Sequence 729, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 729
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-729

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      8 SLTLT 12

RESULT 28
US-10-084-813-730
; Sequence 730, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 730
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-730
```

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 7 SLTLT 11

RESULT 29

US-10-084-813-1115
; Sequence 1115, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1115
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1115

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

RESULT 30

US-10-084-813-1116
; Sequence 1116, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1116
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1116

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 7 SLTLT 11

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

RESULT 31

US-10-084-813-1117
; Sequence 1117, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1117
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1117

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

RESULT 32

US-10-084-813-1118
; Sequence 1118, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1118
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1118

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
|
|
|
|
|
Db 8 SLTLT 12

```
RESULT 33
US-10-084-813-1119
; Sequence 1119, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1119
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1119

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 34
US-10-084-813-1120
; Sequence 1120, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1120
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1120

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 35
US-10-084-813-1121
; Sequence 1121, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1121
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1121

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 36
US-10-084-813-1128
; Sequence 1128, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1128
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1128

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 37
US-10-084-813-1129
; Sequence 1129, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1129

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
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; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1131

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
Db       8 SLTLT 12

RESULT 40
US-10-084-813-1132
; Sequence 1132, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1132

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
Db       8 SLTLT 12

RESULT 41
US-10-084-813-1133
; Sequence 1133, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1133
; LENGTH: 15
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1133

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 42
US-10-084-813-1134
; Sequence 1134, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1134
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1134

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 43
US-10-084-813-1135
; Sequence 1135, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1135
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1135
```

```
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 44
US-10-084-813-1136
; Sequence 1136, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1136
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1136

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 45
US-10-084-813-1137
; Sequence 1137, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1137
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1137

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
```

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Db      8 SLLT 12
|||||
RESULT 46
US-10-084-813-1138
; Sequence 1138, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1138
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1138
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLT 5
|||||
Db      8 SLLT 12
|||||
RESULT 47
US-10-084-813-1139
; Sequence 1139, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1139
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1139
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLT 5
|||||
Db      8 SLLT 12
|||||
RESULT 48
US-10-084-813-1140
; Sequence 1140, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1140
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1140
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLT 5
|||||
Db      8 SLLT 12
|||||
RESULT 49
US-10-084-813-1146
; Sequence 1146, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1146
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1146
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLT 5
|||||
Db      8 SLLT 12
|||||
RESULT 50
US-10-084-813-1147
; Sequence 1147, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
```


; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1147

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 51
US-10-084-813-1148
; Sequence 1148, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1148
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1148

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 52
US-10-084-813-1207
; Sequence 1207, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1207
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1207

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 53
US-10-084-813-1208
; Sequence 1208, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1208
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1208

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5
Db 8 SLTLT 12

RESULT 54
US-10-084-813-1209
; Sequence 1209, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1209
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1209

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 55
US-10-084-813-1210
; Sequence 1210, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/084,813
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1210
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1210

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 56
US-10-084-813-1216
; Sequence 1216, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1216
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
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```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1216

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 57
US-10-084-813-1217
; Sequence 1217, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/084,813
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1217
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1217

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 58
US-10-084-813-1218
; Sequence 1218, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1218
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1218

Query Match          27.8%; Score 5; DB 15; Length 15;
```

```
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 SLT/TLT 5
Db 8 SLT/TLT 12

RESULT 59
US-10-084-813-1219
; Sequence 1219, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1219
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1219

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT/TLT 5
Db 8 SLT/TLT 12

RESULT 60
US-10-084-813-1220
; Sequence 1220, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1220
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1220

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1, SLT/TLT 5
|||
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```
Db 8 SLT/TLT 12

RESULT 61
US-10-084-813-1221
; Sequence 1221, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1221
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1221

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT/TLT 5
|||
Db 8 SLT/TLT 12

RESULT 62
US-10-084-813-1222
; Sequence 1222, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1222
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1222

Query Match 27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT/TLT 5
|||
Db 8 SLT/TLT 12

RESULT 63
US-10-084-813-1224
```

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; Sequence 1224, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1224
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1224

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 64
US-09-829-855-227
; Sequence 227, Application US/09829855
; Patent No. US20020065609A1
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Benzene mineralizing clone SB-1
US-09-829-855-227

Query Match          27.8%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17
Db 4 PLPLV 8

RESULT 65
US-10-299-003-14
; Sequence 14, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
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; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-14

Query Match          27.8%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPL 14
Db 3 LHLPL 7

RESULT 66
US-10-084-813-552
; Sequence 552, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 552
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-552

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 12 SLTLT 16

RESULT 67
US-10-084-813-553
; Sequence 553, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 552
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-553
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; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 553
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-553

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT/LT 5
Db 11 SLT/LT 15

RESULT 68
US-10-084-813-554
; Sequence 554, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 554
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-554

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT/LT 5
Db 10 SLT/LT 14

RESULT 69
US-10-084-813-770
; Sequence 770, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
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; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 770
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-770

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT/LT 5
Db 14 SLT/LT 18

RESULT 70
US-10-084-813-771
; Sequence 771, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 771
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-771

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT/LT 5
Db 13 SLT/LT 17

RESULT 71
US-10-084-813-772
; Sequence 772, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
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```

; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-772

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 12 SLTLT 16

RESULT 72
US-10-084-813-773
; Sequence 773, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 773
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-773

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 11 SLTLT 15

RESULT 73
US-10-084-813-774
; Sequence 774, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 774
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

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US-10-084-813-774

Query Match          27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 10 SLTLT 14

RESULT 74
US-09-829-855-225
; Sequence 225, Application US/09829855
; Patent No. US20020065609A1
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Desulfobulbus sp. BG25
US-09-829-855-225

Query Match          27.8%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17
Db 4 PLPLV 8

RESULT 75
US-09-983-802-664
; Sequence 664, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
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;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
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;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
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;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
;; NUMBER OF SEQ ID NOS: 672
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 664
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-983-802-664

Query Match 27.8%; Score 5; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
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|
|
Db 1 LPLPL 5

Search completed: November 25, 2003, 20:37:00
Job time : 28.8837 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLDVEKHLPLVQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	4	US-09-641-803-23
2	5	27.8	15	3	US-08-602-999A-385
3	5	27.8	15	3	US-08-602-999A-407
4	5	27.8	15	4	US-09-500-124-385
5	5	27.8	15	4	US-09-500-124-407
6	5	27.8	17	4	US-09-140-749-14
7	5	27.8	20	4	US-09-227-357-664
8	4	22.2	5	3	US-09-202-832-6
9	4	22.2	6	1	US-08-212-433A-32
10	4	22.2	6	3	US-08-716-256-32
11	4	22.2	6	4	US-09-211-877-1
12	4	22.2	6	5	PCT-US95-03239-32
13	4	22.2	7	1	US-08-081-539-113
14	4	22.2	7	1	US-08-466-647-113
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16	4	22.2	7	4	US-08-320-373-78
17	4	22.2	9	1	US-08-454-207A-44
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35	4	22.2	10	3	US-08-159-339A-353
36	4	22.2	10	3	US-08-908-643C-17
37	4	22.2	11	2	US-08-637-759B-220
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43	4	22.2	12	1	US-08-249-322A-164
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50	4	22.2	12	3	US-08-602-999A-253
51	4	22.2	12	3	US-08-735-021-164
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55	4	22.2	12	4	US-09-500-124-253
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60	4	22.2	13	3	US-08-602-999A-92
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64	4	22.2	14	1	US-07-956-700B-82
65	4	22.2	14	1	US-08-258-851-6
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71	4	22.2	14	2	US-08-475-879-82
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75	4	22.2	14	3	US-09-516-704-34
76	4	22.2	14	4	US-09-433-043B-82
77	4	22.2	14	4	US-09-549-090-34
78	4	22.2	14	4	US-08-832-230A-34
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83	4	22.2	15	1	US-08-185-432-10
84	4	22.2	15	3	US-08-602-999A-330
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88	4	22.2	16	1	US-08-320-373-77
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92	4	22.2	16	1	US-07-942-245-154
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96	4	22.2	16	3	US-08-602-999A-234
97	4	22.2	16	4	US-09-180-100-25
98	4	22.2	16	4	US-08-182-967-28
99	4	22.2	16	4	US-08-500-124-234
100	4	22.2	17	1	US-07-798-776-16

Sequence 174, App
Sequence 157, App
Sequence 38, Appl
Sequence 9, Appl
Patent No. 5223606
Sequence 351, App
Sequence 352, App
Sequence 353, App
Sequence 17, Appl
Sequence 220, App
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Sequence 3, Appl
Sequence 1, Appl
Sequence 164, App
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Sequence 253, App
Sequence 160, App
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Sequence 3, Appl
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Sequence 77, Appl
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Sequence 93, Appl
Sequence 154, App
Sequence 9, Appl
Sequence 18, Appl
Sequence 5, Appl
Sequence 234, App
Sequence 25, Appl
Sequence 28, Appl
Sequence 234, App
Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-23
; Sequence 23, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDGOH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-23

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLTDVEKHLPLPLVQ 18
Db 1 SLTLTDVEKHLPLPLVQ 18

RESULT 2
US-08-602-999A-385
; Sequence 385, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385

Query Match 27.8%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
Db 10 LPLPL 14

RESULT 3
US-08-602-999A-407
; Sequence 407, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-407

Query Match 27.8%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
Db 3 LPLPL 7

RESULT 4
US-09-500-124-385
; Sequence 385, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-385

Query Match 27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
Db 10 LPLPL 14

RESULT 5
US-09-500-124-407
; Sequence 407, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-407

Query Match 27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
Db 3 LPLPL 7

RESULT 6
US-09-140-749-14
; Sequence 14, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-14

Query Match 27.8%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPL 14
| | | | |
Db 3 LHLPL 7

RESULT 7

US-09-227-357-664
; Sequence 664, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-664

Query Match 27.8%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
| | | | |
Db 1 LPLPL 5

RESULT 8

US-09-202-832-6
; Sequence 6, Application US/09202832
; Patent No. 6194190
; GENERAL INFORMATION:
; APPLICANT: IZU, Yukiko
; APPLICANT: TANAKA, Tetsuki
; APPLICANT: MIYAGI, Masaru
; APPLICANT: TANIGAWA, Tetsuo
; APPLICANT: TOMONO, Jun
; APPLICANT: TSUNASAWA, Susumu
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
; FILE REFERENCE: 1422-368P
; CURRENT APPLICATION NUMBER: US/09/202,832
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa = N-acetyl-glycine
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Peptide
US-09-202-832-6

Query Match 22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
| | | | |
Db 2 DVEK 5

```
RESULT 9
US-08-212-433A-32
; Sequence 32, Application US/08212433A
; Patent No. 5538897
; GENERAL INFORMATION:
; APPLICANT: Yates, III, John R.
; APPLICANT: Eng, James K.
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
; TITLE OF INVENTION: DATABASES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,433A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Hughes, Richard L.
; REGISTRATION NUMBER: 31,264
; REFERENCE/DOCKET NUMBER: 16336-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-433A-32

Query Match 22.2%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 10
US-08-716-256-32
; Sequence 32, Application US/08716256
; Patent No. 6017693
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,256
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:

Query Match 22.2%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 11
US-09-211-877-1
; Sequence 1, Application US/092111877
; Patent No. 6458766
; GENERAL INFORMATION:
; APPLICANT: Penical, William
; APPLICANT: Jensen, Paul R.
; APPLICANT: Rowley, David C.
; TITLE OF INVENTION: Halovir, An Antiviral Marine Natural Product, and
; TITLE OF INVENTION: Derivatives Thereof
; FILE REFERENCE: P-UD 3148
; CURRENT APPLICATION NUMBER: US/09/211,877
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Scytalidium CML240
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Aib;
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: leucinol
US-09-211-877-1

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLVQ 18
Db 2 PLVQ 5

RESULT 12
PCT-US95-03239-32
; Sequence 32, Application PC/TUS9503239
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
```

;; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
;; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
;; TITLE OF INVENTION: ORGANISMS
;; NUMBER OF SEQUENCES: 46
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/03239
;; FILING DATE: 14-MAR-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/212,433
;; FILING DATE: 14-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 16336-2PC
;; TELEPHONE: 206-467-9600
;; TELEFAX: 415-543-5043
;; INFORMATION FOR SEQ ID NO: 32:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; PCT-US95-03239-32

Query Match 22.2%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 13
US-08-081-539-113
; Sequence 113, Application US/08081539
; Patent No. 5501962
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Orlins, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,539
; FILING DATE: 19930621
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.

;; REGISTRATION NUMBER: 28623
;; REFERENCE/DOCKET NUMBER: 2724
;; TELEPHONE: (708)470-6501
;; TELEFAX: (708)470-6881
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-081-539-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 14
US-08-466-647-113
; Sequence 113, Application US/08466647
; Patent No. 5543141
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Orlins, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,647
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,539
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-647-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
|||
Db 3 PLPL 6

RESULT 15

US-09-904-615-132
; Sequence 132, Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-615-132

Query Match 22.2%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 LTLT 5
|||
Db 3 LTLT 6

RESULT 16

US-08-320-373-78
; Sequence 78, Application US/08320373
; Patent No. 5559025
; GENERAL INFORMATION:
; APPLICANT: Rhorn, Horst
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Sommergruber, Wolfgang
; APPLICANT: Zophel, Andreas
; APPLICANT: Blaas, Dieter
; APPLICANT: Kuchler, Ernst
; APPLICANT: Liebig, Hans-Dieter
; APPLICANT: Skern, Timothy
; TITLE OF INVENTION: Expression of Mature Proteinase 2A, the
; TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates
; TITLE OF INVENTION: Having an Inhibitory Effect
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,373
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/971,619
; FILING DATE: 06-NOV-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-320-373-78

Query Match 22.2%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 14 LPLV 17
|||
Db 4 LPLV 7

RESULT 17

US-08-454-207A-44
; Sequence 44, Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123tris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997,771
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0183
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-454-207A-44

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 9 KLHL 12
|||

Db 4 KLHL 7

RESULT 18

US-08-787-547-91

Sequence 91, Application US/08787547

Patent No. 5783567

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Curley, Joanne M.

APPLICANT: Langer, Robert S.

TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY

TITLE OF INVENTION: OF NUCLEIC ACID

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,547

FILING DATE: 22-JAN-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 91:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-787-547-91

Query Match 22.2%; Score 4; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12

Db 1 KLHL 4

RESULT 19

US-08-630-645-9

Sequence 9, Application US/08630645

Patent No. 5948763

GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio

APPLICANT: BAUMANN, Marc

APPLICANT: FRANGIONE, Blas

TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED

TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 400

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,645

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/478,326

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971

REFERENCE/DOCKET NUMBER: SOTO-JARA-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-630-645-9

Query Match 22.2%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db 5 PLPL 8

RESULT 20

US-09-510-738A-84

Sequence 84, Application US/09510738A

Patent No. 6268165

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP-A

CURRENT APPLICATION NUMBER: US/09/510,738A

CURRENT FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 09/039,211

PRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 188

SEQ ID NO 84

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Residues 264-272 of the hepsin protein

US-09-510-738A-84

Query Match 22.2%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db 3 PLPL 6

RESULT 21

```
US-09-510-738A-126
; Sequence 126, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 126
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 265-273 of the hepsin protein
US-09-510-738A-126
Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 2 PLPL 5

RESULT 22
US-09-510-738A-170
; Sequence 170, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 170
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 264-272 of the hepsin protein
US-09-510-738A-170
Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 23
US-08-197-484-38
; Sequence 38, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
```

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US-09-510-738A-126
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,692
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-38
Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
Db 1 KLHL 4

RESULT 24
US-08-766-596A-9
; Sequence 9, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
```


ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-9

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 5 PLPL 8

RESULT 25
US-08-661-966-84
Sequence 84, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-A/Div
CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 09/510,738
PRIOR FILING DATE: 2000-02-22
SEQ ID NO 84
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 264-272 of the hepsin protein
US-08-661-966-84

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 26

US-09-861-966-126
Sequence 126, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-A/Div
CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 09/510,738
PRIOR FILING DATE: 2000-02-22
SEQ ID NO 126
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 265-273 of the hepsin protein
US-09-861-966-126

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 2 PLPL 5

RESULT 27
US-09-861-966-170
Sequence 170, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-A/Div
CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 09/510,738
PRIOR FILING DATE: 2000-02-22
SEQ ID NO 170
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 264-272 of the hepsin protein
US-09-861-966-170

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 28
US-09-311-784A-174
Sequence 174, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.

```

; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV pol 489 (peptide 927.46)
US-09-311-784A-174

Query Match      22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KLHL 12
DB      1 KLHL 4

RESULT 29
US-09-369-247-157
; Sequence 157, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-157

Query Match      22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 EKHL 11
DB      3 EKHL 6

RESULT 30
PCT-US95-02121-38
; Sequence 38, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV pol 489 (peptide 927.46)
US-09-311-784A-174

Query Match      22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KLHL 12
DB      1 KLHL 4

RESULT 31
PCT-US96-10220-9
; Sequence 9, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
PCT-US95-02121-38

Query Match      22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KLHL 12
DB      1 KLHL 4

RESULT 31
PCT-US96-10220-9
; Sequence 9, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326

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; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10220-9

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 5 PLPL 8

RESULT 32
5223606-10
; Patent No. 5223606
; APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS,
; PIERRE; DEJEAN, ANNE
; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/134,130
; FILING DATE: 17-DEC-1987
; PRIOR APPLICATION DATA:
; SEQ ID NO: 10
; LENGTH: 9
5223606-10

Query Match 22.2%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLVQ 18
Db 6 PLVQ 9

RESULT 33
US-08-159-339A-351
; Sequence 351, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
Db 6 KLHL 9

RESULT 34
US-08-159-339A-352
; Sequence 352, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-351

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
Db 6 KLHL 9

RESULT 34
US-08-159-339A-352
; Sequence 352, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
```

APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-352

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
DB 6 KLHL 9

RESULT 35
US-08-159-339A-353
Sequence 353, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 353:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-353

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12
DB 6 KLHL 9

RESULT 36
US-08-908-643C-17
Sequence 17, Application US/08908643C
Patent No. 6120995
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
Pearlman, Joshua M.
Barber, Michael T.
Schultz, Stephanie
Parkinson, Scott J.
TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO
COLORECTAL CANCER CELLS AND METHODS OF
USING THE SAME
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,643C
FILING DATE: 07-AUG-1997
CLASSIFICATION: N/A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJJU-2209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-908-643C-17

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLP 13
DB 6 KLHL 9

Db 4 HLPL 7

RESULT 37

US-08-637-759B-220
; Sequence 220, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: US/08/637,759B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-637-759B-220

Query Match 22.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLPL 14
Db 5 HLPL 8

RESULT 38

US-08-637-759B-220
; Sequence 220, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: US/08/637,759B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-637-759B-220

Query Match 22.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLPL 14
Db 5 HLPL 8

RESULT 39

US-09-201-945-220
; Sequence 220, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101

QY 11 HLPL 14
Db 5 HLPL 8

RESULT 39

US-09-201-945-220
; Sequence 220, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101

TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-201-945-220

Query Match 22.2%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLPL 14
||||
DB 5 HLPL 8

RESULT 40
US-07-756-250-3
Sequence 3, Application US/07756250
Patent No. 5288275
GENERAL INFORMATION:
APPLICANT: Wu, Sheue-Mei
APPLICANT: Stafford, Darrel W.
TITLE OF INVENTION: Vitamin K-Dependent Carboxylase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
ADDRESSEE: Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5268275th Carolina
COUNTRY: U.S.A.
ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/756,250
FILING DATE: 19910909
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,427
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-756-250-3

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLVQ 18

DB 7 PLVQ 10
||||

RESULT 41
US-08-178-554-1
Sequence 1, Application US/08178554
Patent No. 5446019
GENERAL INFORMATION:
APPLICANT: ELY, SUSAN
APPLICANT: TIPPETT, JANET MARY
TITLE OF INVENTION: BACTERIAL STRAIN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9300124.6
FILING DATE: 06-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206082/SBE 37367/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-178-554-1

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
||||
DB 3 SLTL 6

RESULT 42
US-08-036-555B-164
Sequence 164, Application US/08036555B
Patent No. 5530109
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
PREPARATION AND USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York

```

; COUNTRY: USA
; ZIP: 10022
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
; US-08-036-555B-164

```

```

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 6 DVEK 9
Db 9 DVEK 12

```

```

RESULT 43
US-08-469-569-164
; Sequence 164, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:

```

```

; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
; US-08-469-569-164

```

```

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 6 DVEK 9
Db 9 DVEK 12

```

```

RESULT 44
US-08-249-322A-164
; Sequence 164, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/249,322A
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 250.4
TELEPHONE: (212) 688-3200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-249-322A-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 45
US-08-469-526A-164
Sequence 164, Application US/08469526A
Patent No. 5792849
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew
APPLICANT: Stroobant, Paul
APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Marchionni, Mark
APPLICANT: Chen, Malo Su
APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,526A
FILING DATE: 06 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
APPLICATION NUMBER: 07/907,138
FILING DATE: 03-JUN-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-526A-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 46
US-08-734-591A-164
Sequence 164, Application US/08734591A
Patent No. 5854220
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew
APPLICANT: Stroobant, Paul
APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Hiles, Ian
APPLICANT: Marchionni, Mark
APPLICANT: Chen, Mario
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
SOFTWARE: WordPerfect (Version 7.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,591A


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; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/307,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-591A-164

```

```

Query Match      22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      6 DVEK 9
        |||||
Db      9 DVEK 12

```

```

RESULT 47
US-08-469-660-164
; Sequence 164, Application US/08469660
; Patent No. 5876973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660

```

```

; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-660-164

```

```

Query Match      22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 DVEK 9
        |||||
Db      9 DVEK 12

```

```

RESULT 48
US-09-371-710-41
; Sequence 41, Application US/09371710A
; Patent No. 6146868
; GENERAL INFORMATION:
; APPLICANT: Kozel, Thomas R.
; APPLICANT: Bloomer, Sherri L.
; APPLICANT: Savoy, Anne C.
; TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of
; TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof
; FILE REFERENCE: D6245
; CURRENT APPLICATION NUMBER: US/09/371,710A
; CURRENT FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: associated amino acid sequence of PCR primer 45-mer
US-09-371-710-41

```

```

Query Match      22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      9 KLHL 12
        |||||
Db      3 KLHL 6

```

```

RESULT 49
US-08-470-335-164

```

; Sequence 164, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-470-335-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 50
US-08-602-999A-253
; Sequence 253, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; PREPARATION AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 863-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-253

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 12 LPLP 15
Db 6 LPLP 9

RESULT 51
US-08-735-021-164
; Sequence 164, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in 1 is unknown.
US-08-735-021-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 52
US-08-734-664A-164

; Sequence 164, Application US/08734664A
; Patent No. 6204241
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbling LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,664A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-664A-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9

Db 9 DVEK 12
RESULT 53
US-08-470-339-164
; Sequence 164, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; EARLIER FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-470-339-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9
Db 9 DVEK 12

RESULT 54
US-09-648-386-41
; Sequence 41, Application US/09648386
; Patent No. 6284508
; GENERAL INFORMATION:
; APPLICANT: Kozel, Thomas R.
; APPLICANT: Bloomer, Sherri L.
; APPLICANT: Savoy, Anne C.
; TITLE OF INVENTION: Glucuronoxylmannan (GXM)-O-Acetylhydrolase of
; TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof
; FILE REFERENCE: D6245D
; CURRENT APPLICATION NUMBER: US/09/648,386
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/371,710
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: associated amino acid sequence of PCR primer 45-mer
US-09-648-386-41

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KJHL 12
Db 3 KJHL 6

RESULT 55

US-09-500-124-253
; Sequence 253, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOMLKS, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-253

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLP 15
Db 6 LPLP 9

RESULT 56

US-08-467-602-164

; Sequence 164, Application US/08467602C
; Patent No. 6444642
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 04585/028003
; CURRENT APPLICATION NUMBER: US/08/467,602C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/209,204
; EARLIER FILING DATE: 1994-03-08
; EARLIER APPLICATION NUMBER: 08/059,022
; EARLIER FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.

US-08-467-602-164

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 57

PCR-US94-05083C-160
; Sequence 160, Application PC/TUS9405083C
; GENERAL INFORMATION:
; APPLICANT: Robert Sklar, Mark Marchionni,
; APPLICANT: David I. Gwynne
; TITLE OF INVENTION: METHODS FOR ALTERING
; TITLE OF INVENTION: MUSCLE CONDITION
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360
; MEDIUM TYPE: kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05083C
; FILING DATE: 06-MAY-94
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,204
; FILING DATE: 08-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/028WO1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: Xaa in position 1 is
OTHER INFORMATION: unknown.
PCT-US94-05083C-160

Query Match 22.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9
Db 9 DVEK 12

RESULT 58

PCT-US95-06846A-164
Sequence 164, Application PC/TUS9506846A
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew David; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06846A
FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,322
FILING DATE: 26-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5250.5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: Xaa in position 1 is unknown.
PCT-US95-06846A-164

Query Match 22.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9
Db 9 DVEK 12

RESULT 59

US-08-291-601-3
Sequence 3, Application US/08291601
Patent No. 5679527
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E.
TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: Maine
COUNTRY: US
ZIP: 03911

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,601
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9401M
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-291-601-3

Query Match 22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5
Db 8 LTLT 11

RESULT 60

US-08-602-999A-92
Sequence 92, Application US/08602999A

Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-92

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 5 PLPL 8

RESULT 61
US-09-177-249-248
; Sequence 248, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01

; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 248
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-248

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 9 SLTL 12

RESULT 62
US-08-278-865-92
; Sequence 92, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-278-865-92

Query Match 22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 5 PLPL 8

RESULT 63

US-09-500-124-92
; Sequence 92, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-92
Query Match 22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 PLPL 16
Db 5 PLPL 8
RESULT 64
US-07-956-700B-82
; Sequence 82, Application US/07956700B
; Patent No. 553992
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-07-956-700B-82
Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 LHLPL 13
Db 5 LHLPL 8
RESULT 65
US-08-258-851-6
; Sequence 6, Application US/08258851
; Patent No. 5583244
; GENERAL INFORMATION:
; APPLICANT: Elizabeth A. Allegretto
; APPLICANT: J. Wesley Pike
; TITLE OF INVENTION: DETECTION OF RETINOID
; TITLE OF INVENTION: RECEPTOR SUBTYPE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,851
; FILING DATE: 10 June 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

```
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
;
US-08-258-851-6

Query Match          22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PLVQ 18
Db      10 PLVQ 13

RESULT 66
US-08-440-391-11
; Sequence 11, Application US/08440391
; Patent No. 5656725
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; TITLE OF INVENTION: MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-440-391-11

Query Match          22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 LPLV 17
Db      11 LPLV 14

RESULT 67
US-08-476-537-82
; Sequence 82, Application US/08476537
```

```
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
;
US-08-476-537-82

Query Match          22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 LHLP 13
Db      5 LHLP 8

RESULT 68
US-08-485-607-82
; Sequence 82, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
```


;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/956,700
;; FILING DATE: 10/21/92
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Thomas E. No. 5792627thrup
;; REGISTRATION NUMBER: 33,268
;; REFERENCE/DOCKET NUMBER: ARCD:058
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 1-312-744-0090
;; TELEFAX: 1-312-755-4489
;; INFORMATION FOR SEQ ID NO: 82:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: Amino acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; MOLECULE TYPE: Peptide
;;
US-08-485-607-82

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 10 LHL P 13
|||
Db 5 LHL P 8

RESULT 69
US-08-908-597A-11
; Sequence 11, Application US/08908597A
; Patent No. 5863795
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; TITLE OF INVENTION: MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,597A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-908-597A-11

Query Match 22.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 14 LPLV 17
||||
Db 11 LPLV 14

RESULT 70
US-08-764-640-34
; Sequence 34, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Depince, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,640
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-34

Query Match 22.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 LTLT 5
||||
Db 5 LTLT 8

RESULT 71
US-08-475-879-82
; Sequence 82, Application US/08475879
; Patent No. 5972644

; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; CARBOXYLASE
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thchurp
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-475-879-82

Query Match 22.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LHLP 13
Db 5 LHLP 8

RESULT 72
US-08-973-225-34
; Sequence 34, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC

; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,225A
; FILING DATE: 04-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-973-225-34

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5
Db 5 LTLT 8

RESULT 73
US-09-244-298A-34
; Sequence 34, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprince, Randolph B.
; APPLICANT: Poddaturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,298A
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392

; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-244-298A-34

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5
Db 5 LTLT 8

RESULT 74

US-09-236-385A-11
; Sequence 11, Application US/09236385A
; Patent No. 6221615
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,385A
; FILING DATE: 25-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; (C) ATTORNEY DOCKET NO. 104322.147CIP

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; US-09-236-385A-11

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17
Db 11 LPLV 14

RESULT 75

US-09-516-704-34

; Sequence 34, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Gates, Christian
; Schatz, Peter J.
; Balasubramanian, Palaniappan
; Wagstrom, Christopher R.
; Hendren, Richard W.
; Deprience, Randolph B.
; Poddaturi, Surekha
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/516,704
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
; US-09-516-704-34

Query Match 22.2%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5
Db 5 LTLT 8

Search completed: November 25, 2003, 20:30:00
Job time : 15.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 4.80233 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWMHQPP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	7	S71299	ICL2 protein - Par
2	3	42.9	7	PT0283	Ig heavy chain CRD
3	3	42.9	10	PT0322	Ig heavy chain CRD
4	3	42.9	11	YHRT	morphogenetic neur
5	3	42.9	11	YHHU	morphogenetic neur
6	3	42.9	11	YHBO	morphogenetic neur
7	3	42.9	11	YHAE	morphogenetic neur
8	3	42.9	11	YHJPHY	morphogenetic neur
9	3	42.9	12	PN0046	ATP synthase D cha
10	3	42.9	13	G61458	Ig lambda chain V-
11	3	42.9	15	B39109	hypothetical 1.5K
12	3	42.9	15	A60221	apolipoprotein A-I
13	3	42.9	17	SI0786	enamelin, 26K - bo
14	3	42.9	19	PC1323	endopeptidase Clp
15	3	42.9	19	S59486	cell wall protein,
16	3	42.9	19	A37968	neural surface pro
17	3	42.9	20	S28779	octopamine recepto
18	2	28.6	4	PT0661	T-cell receptor be
19	2	28.6	5	A32516	cholecystokinin-5
20	2	28.6	5	B37988	acid proteinase li
21	2	28.6	5	PT0580	T-cell receptor be
22	2	28.6	6	A31263	dihydrofolate redu
23	2	28.6	6	A61068	locustakinin - mlg
24	2	28.6	6	S71349	beta-crystallin B2
25	2	28.6	7	A61081	tryptophyllin, bas
26	2	28.6	7	PC1316	large granule L3 c
27	2	28.6	7	I46868	alpha-myosin heavy
28	2	28.6	7	A39590	neural cell adhesi
29	2	28.6	7	A58718	carnocin UI49 - Ca

30	2	28.6	7	2	PN0649	pullulanase (EC 3.
31	2	28.6	8	2	SI0596	adipokinetic hormo
32	2	28.6	8	2	PQ0012	cholecystokinin -
33	2	28.6	8	2	A43001	cholecystokinin -
34	2	28.6	8	2	B24749	neuropeptide B - b
35	2	28.6	8	2	S43971	tumor-associated a
36	2	28.6	8	2	B39745	endoglycosylcerami
37	2	28.6	8	2	SI6324	hypothetical prote
38	2	28.6	8	2	S21288	lectin - potato (f
39	2	28.6	8	2	PT0030	inulinase (EC 3.2.
40	2	28.6	8	2	JS0315	leucokinin V - Mad
41	2	28.6	8	2	JS0316	leucokinin VI - Ma
42	2	28.6	8	2	JS0317	leucokinin VII - M
43	2	28.6	8	2	JS0318	leucokinin VIII -
44	2	28.6	8	2	E47393	neuropeptide calla
45	2	28.6	8	2	A14683	aspartate transami
46	2	28.6	8	2	PT0368	Ig gamma chain C r
47	2	28.6	8	2	SI0783	enamelin f - bovin
48	2	28.6	8	2	PT0559	T-cell receptor be
49	2	28.6	8	2	A38887	T-cell receptor ga
50	2	28.6	8	2	C39690	neural cell adhesi
51	2	28.6	9	2	A61102	parathyroid hormo
52	2	28.6	9	2	A24244	adipokinetic hormo
53	2	28.6	9	2	A61357	phylocaerulein -
54	2	28.6	9	2	A61358	bradykinin-like pe
55	2	28.6	9	2	A61057	Thr-6 bradykinin -
56	2	28.6	9	2	A26744	bradykinin-like pe
57	2	28.6	9	2	A61363	bradykinin - commo
58	2	28.6	9	2	A60579	bradykinin-like pe
59	2	28.6	9	2	B60246	ornitho-kinin - ch
60	2	28.6	9	2	B41983	orf downstream to b
61	2	28.6	9	2	S55696	phosphoenolpyruvat
62	2	28.6	9	2	D57444	neuropeptide Grb-A
63	2	28.6	9	2	A61620	locustamyotropin I
64	2	28.6	9	2	S65433	bradykinin - horn
65	2	28.6	9	2	S77984	cytochrome-c oxida
66	2	28.6	9	2	PT0299	Ig heavy chain CRD
67	2	28.6	9	2	S26508	collagen alpha 2(V
68	2	28.6	9	2	IS8350	gene C-mpl protein
69	2	28.6	9	2	B30572	T-cell receptor be
70	2	28.6	9	2	A43065	hydroxyproline-3-b
71	2	28.6	10	1	XAVI6B	angiotensin-conver
72	2	28.6	10	1	XASNPC	angiotensin-conver
73	2	28.6	10	1	RHAQ1	gonadoliberin I -
74	2	28.6	10	1	SFPGNK	neuromedin K - pig
75	2	28.6	10	2	JCI367	thryoliberin poten
76	2	28.6	10	2	A61337	caerulein - frog (
77	2	28.6	10	2	A13687	caerulein-like pep
78	2	28.6	10	2	PC2171	triacylglycerol li
79	2	28.6	10	2	S39030	lysyl-bradykinin -
80	2	28.6	10	2	SI8396	probable glucose-6
81	2	28.6	10	2	C35389	urease (EC 3.5.1.5
82	2	28.6	10	2	A59272	peptide-N4-(N-acet
83	2	28.6	10	2	B59272	peptide-N4-(N-acet
84	2	28.6	10	2	H28027	protein P11 - curl
85	2	28.6	10	2	A36454	trypsin-modulating
86	2	28.6	10	2	B37196	bradykinin-potenti
87	2	28.6	10	2	H37196	bradykinin-potenti
88	2	28.6	10	2	S26506	collagen alpha 1(V
89	2	28.6	10	2	SI0785	enamelin, 22K - bo
90	2	28.6	10	2	B38887	T-cell receptor ga
91	2	28.6	10	2	S65387	cytochrome-c oxida
92	2	28.6	10	2	C30572	T-cell receptor be
93	2	28.6	10	2	PH0923	T-cell receptor be
94	2	28.6	10	2	B61218	alpha-gliadin 6Ha
95	2	28.6	10	2	S33789	neuropeptide pec-H
96	2	28.6	11	1	XASVIB	bradykinin-potenti
97	2	28.6	11	1	XASNEA	bradykinin-potenti
98	2	28.6	11	1	EOOCC	eledoisin - curled
99	2	28.6	11	1	EOOCC	eledoisin - musky
100	2	28.6	11	2	D60409	kassinin-like pept

ALIGNMENTS

RESULT 1

S71299
 ICL2 protein - Paramecium tetraurelia (fragment)
 C;Species: Paramecium tetraurelia
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C;Accession: S71299
 R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A;Title: Characterization of centrin genes in Paramecium.
 A;Reference number: S71298; MUID:96248429; PMID:8665928
 A;Accession: S71299
 A;Molecule type: protein
 A;Residues: 1-7 <NAD>
 A;Experimental source: strain d4-2
 C;Genetics:
 A;Genetic code: SGC5

Query Match 42.9%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 2 QPP 4

RESULT 2

PT0283
 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0283
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and 3

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0283
 A;Molecule type: DNA
 A;Residues: 1-7 <YAM>

A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 5 QPP 7

RESULT 3

PT0322
 Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0322
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and 3

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0322
 A;Molecule type: DNA
 A;Residues: 1-10 <YAM>

A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
 |||
 Db 6 SWM 8

RESULT 4

YHRT
 morphogenetic neuropeptide - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: A01427
 R;Bodenmuller, H.; Schaller, H.C.
 Nature 293, 579-580, 1981
 A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427
 A;Molecule type: protein
 A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation: synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical stru
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called h
 C;Superfamily: unassigned animal peptides
 C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutar
 F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 1 QPP 3

RESULT 5

YHUU
 morphogenetic neuropeptide - human
 C;Species: Homo sapiens (man)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: B01427; A01427
 R;Bodenmuller, H.; Schaller, H.C.
 Nature 293, 579-580, 1981
 A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427
 A;Molecule type: protein
 A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation: synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical stru
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called h
 C;Superfamily: unassigned animal peptides
 C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuro
 F;1/Modified site: blocked amino end (Gln) (probably pyroglutamate carboxylic acid) #st

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 1 QPP 3

RESULT 6

YHBO
morphogenetic neuropeptide - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: C01427, A01427
R;Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele
A;Reference number: A93266; MUID:82035850; PMID:7290191
A;Accession: C01427
A;Molecule type: protein
A;Residues: 1-11 <BOD>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head
malian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropep
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 1 QPP 3

RESULT 7

YHAE
morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)
N;Alternate names: head activator
C;Species: Anthopleura elegantissima
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A93900, A01427
R;Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A;Reference number: A93900
A;Accession: A93900
A;Molecule type: protein
A;Residues: 1-11 <SCH>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head
n mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 1 QPP 3

RESULT 8

YHUFHY
morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: B93900; A01427
R;Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A;Reference number: A93900
A;Accession: B93900
A;Molecule type: protein
A;Residues: 1-11 <SCH>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure
C;Comment: This peptide was first isolated from nerve cells of hydra and was called h
n mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 1 QPP 3

RESULT 9

PN0046
ATP synthase D chain, mitochondrial - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C;Accession: PN0046
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne
A;Reference number: PN0041
A;Accession: PN0046
A;Molecule type: protein
A;Residues: 1-12 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blo
C;Keywords: brain; mitochondrion

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOP 6

Db 6 HOP 8

RESULT 10

G61458
Ig lambda chain V-II region (AZI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C;Accession: G61458; P0159
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, B.
J. Exp. Med. 170, 1551-1558, 1989
A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-a
A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: G61458
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glyco
C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 6 QPP 8

RESULT 11

B39109
 hypothetical 1.5K protein - hepatitis C virus
 N;Alternate names: hypothetical protein 2
 C;Species: hepatitis C virus
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
 C;Accession: B39109; JQ1585
 R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
 A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
 A;Reference number: A39109; MUID:91156678; PMID:1705704
 A;Accession: B39109
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-15 <HAN>
 A;Cross-references: GB:M58406
 R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A;Title: Cloning and sequencing of the structural region and expression of putative core
 A;Reference number: JQ1584; MUID:92300349; PMID:1318944
 A;Accession: JQ1585
 A;Molecule type: genomic RNA
 A;Residues: 1-15 <KUM>
 A;Experimental source: strain U.K.

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 5 QPP 7

RESULT 12

A60221
 apolipoprotein A-I - common carp (fragment)
 C;Species: Cyprinus carpio (common carp)
 C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
 C;Accession: A60221
 R;Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
 J. Neurochem. 55, 1237-1243, 1990
 A;Title: Fish apolipoprotein A-I has heparin binding activity: implication for nerve reg
 A;Reference number: A60221; MUID:90376100; PMID:2118944
 A;Accession: A60221
 A;Molecule type: protein
 A;Residues: 1-15 <HAR>
 A;Note: protein from plasma and from optic nerve yielded the same sequence
 C;Keywords: lipid binding; lipoprotein

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 2 QPP 4

RESULT 13

S10786
 enamelin, 26K - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C;Accession: S10786
 R;Strawich, E.; Glimcher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
 A;Reference number: S10780; MUID:90336641; PMID:2379503
 A;Accession: S10786
 A;Molecule type: protein
 A;Residues: 1-17 <STR>
 C;Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 3 QPP 5

RESULT 14

PC1323
 endopeptidase Clp (EC 3.4.21.92) chain P [similarity] - curled-leaved tobacco chlorop
 C;Species: chloroplast Nicotiana glauca [curled-leaved tobacco]
 C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-2000
 C;Accession: PC1323
 R;Fejes, E.; Engler, D.; Maliga, P.
 Theor. Appl. Genet. 79, 28-32, 1990
 A;Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana som
 A;Reference number: PC1321
 A;Accession: PC1323
 A;Molecule type: DNA
 A;Residues: 1-19 <FEU>
 C;Genetics:
 A;Genome: chloroplast
 C;Function:
 A;Description: ATP-driven cleavage of proteins to small peptides
 A;Note: magnesium required
 C;Superfamily: endopeptidase Clp chain P
 C;Keywords: ATP; chloroplast; hydrolase; serine proteinase
 F;3/Active site: His #status predicted

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
 |||
 Db 3 HQP 5

RESULT 15

S59486
 cell wall protein, 22K - kidney bean (fragment)
 C;Species: Phaseolus vulgaris (kidney bean)
 C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S59486
 R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A;Title: Specificity in the immobilisation of cell wall proteins in response to diffe
 A;Reference number: S59481; MUID:96011753; PMID:7548825
 A;Accession: S59486
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <WOJ>

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 |||
 Db 3 QPP 5

RESULT 16
 A37968
 neural surface protein Bravo - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Aug-1997
 C;Accession: A37968; A36345
 R;De la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
 J. Cell Biol. 112, 1049, 1991
 A;Reference number: A37968; MUID:91154309; PMID:1999455
 A;Contents: erratum
 A;Accession: A37968
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19
 R;De la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
 J. Cell Biol. 111, 3087-3096, 1990
 A;Title: Topologically restricted appearance in the developing chick retinotectal system
 A;Reference number: A36345; MUID:91100421; PMID:2269667
 A;Accession: A36345
 A;Molecule type: protein
 A;Residues: 1-7,9-19 <DE2>
 Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 Db 15 QPP 17
 RESULT 17
 S28779
 octopamine receptor - common eastern firefly (fragment)
 C;Species: Photinus pyralis (common eastern firefly)
 C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 23-Feb-1997
 C;Accession: S28779
 R;Nathanson, J.A.; Kantham, L.; Hunnicutt, E.J.
 FEBS Lett. 259, 117-120, 1989
 A;Title: Isolation and N-terminal amino acid sequence of an octopamine ligand binding pr
 A;Reference number: S28779; MUID:90092510; PMID:2513233
 A;Accession: S28779
 A;Molecule type: protein
 A;Residues: 1-20 <NAT>
 C;Keywords: G protein-coupled receptor; membrane protein; neurotransmitter receptor
 Query Match 42.9%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MHQ 5
 Db 18 MHQ 20
 RESULT 18
 PT0661
 T-cell receptor beta chain V-D-J region (121-1Bv) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0661
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0661
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FE>
 A;Experimental source: day 4 postnatal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SW 2
 Db 2 SW 3
 RESULT 19
 A32516
 cholecystokinin-5 - dog
 N;Alternate names: CCK-5
 C;Species: Canis lupus familiaris (dog)
 C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
 C;Accession: A32516
 R;Shively, J.; Reeve Jr., J.R.; Bysseselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.
 Am. J. Physiol. 252, G272-G275, 1987
 A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
 A;Reference number: A32516; MUID:87153871; PMID:3826354
 A;Accession: A32516
 A;Molecule type: protein
 A;Residues: 1-5 <SHI>
 C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholec
 C;Superfamily: gastrin
 C;Keywords: amidated carboxyl end; neuropeptide
 F;5/Modified site: amidated carboxyl end (Phe) #status experimental
 Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WM 3
 Db 2 WM 3
 RESULT 20
 B37988
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
 C;Species: Physarum polycephalum
 C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
 C;Accession: B37988
 R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki
 J. Biol. Chem. 265, 19898-19903, 1990
 A;Title: Purification and characterization of a novel intracellular acid proteinase f
 A;Reference number: A37988; MUID:91060608; PMID:2246266
 A;Accession: B37988
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <MUR>
 Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db 3 PP 4
 RESULT 21
 PT0580
 T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0580
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0580

A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
 ||
 Db 3 SW 4

RESULT 22

A31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f

C;Species: Plasmodium falciparum
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996

C;Accession: A31263

R;Peterson, D.S.; Walliker, D.; Welles, T.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988

A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase

A;Reference number: A94217; PMID:89057886; PMID:2904149

A;Accession: A31263

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-6 <P>

C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
 ||
 Db 2 SW 3

RESULT 23

A61068

locustakinin - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995

C;Accession: A61068

R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.

Regul. Pept. 37, 49-57, 1992

A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, pri

A;Reference number: A61068; PMID:92262851; PMID:1585017

A;Accession: A61068

A;Molecule type: protein

A;Residues: 1-6 <SCH>

C;Keywords: amidated carboxyl end; cephalomotropic peptide; neuropeptide

F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
 ||
 Db 4 SW 5

RESULT 24

S71349

beta-crystallin B2 - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 07-May-1999

C;Accession: S71349

R;Dirks, R.P.H.; Kraft, H.J.; van Genesen, S.T.; Klok, E.J.; Pfundt, R.; Schoenmakers, J

Eur. J. Biochem. 239, 23-32, 1996

A;Title: The cooperation between two silencers creates an enhancer element that contr

A;Reference number: S71349; PMID:96305362; PMID:8706714

A;Accession: S71349

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-6 <DIR>

A;Cross-references: EMBL:X83671

A;Experimental source: strain Wistar; lens epithelial cells

C;Genetics:

A;Gene: CRYBB2

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
 ||
 Db 5 HQ 6

RESULT 25

A61081

tryptophyllin, basic - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: A61081

R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.

Int. J. Pept. Protein Res. 33, 391-395, 1989

A;Title: Isolation, structure determination and synthesis of a novel tryptophan-conta

A;Reference number: A61081

A;Accession: A61081

A;Molecule type: protein

A;Residues: 1-7 <MON>

C;Comment: The biological activity of this peptide was not determined.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hydroxyproline; skin

F;3/Modified site: 4-hydroxyproline (Pro) #status experimental

F;7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
 ||
 Db 4 SW 5

RESULT 26

PC1316

large granule L3 chain - horseshoe crab (Tachypleus tridentatus) (fragment)

C;Species: Tachypleus tridentatus

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C;Accession: PC1316

R;Shigenaga, T.; Takavenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.;

J. Biochem. 114, 307-316, 1993

A;Title: Separation of large and small granules from horseshoe crab (Tachypleus tride

A;Reference number: PC1309; PMID:94110249; PMID:8282718

A;Accession: PC1316

A;Molecule type: protein

A;Residues: 1-7 <SHI>

C;Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
 ||
 Db 3 QP 4

RESULT 27

I46868
 alpha-myosin heavy chain - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 C:Accession: I46868
 R:Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
 A:Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular myosin heavy chain mRNAs
 A:Reference number: I46868; MUID:84221901; PMID:6328491
 A:Accession: I46868
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7 <ERI>
 A:Cross-references: GB:K01698; NID:gl65538; PIDN:AAA31415.1; PID:gl65539

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
 ||
 Db 3 MH 4

RESULT 28
 A39690
 neural cell adhesion molecule, cardiac splice form -, -, -, - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 C:Accession: A39690
 R:Reyes, A.A.; Small, S.J.; Akesson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
 A:Reference number: A39690; MUID:9141516; PMID:1996115
 A:Accession: A39690
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-7 <REV>
 A:Cross-references: GB:M63970
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 1 QP 2

RESULT 29
 A58718
 carnocin U149 - Carnobacterium sp. (fragment)
 C:Species: Carnobacterium sp.
 C:Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
 C:Accession: A58718
 R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Hollo, H.; Nes, I.F.
 Appl. Environ. Microbiol. 58, 1417-1422, 1992
 A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobacterium strain
 A:Reference number: A58718; MUID:92321768; PMID:1622206
 A:Accession: A58718
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <STO>
 C:Keywords: antibiotic; lanthionine

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 5 QP 6

RESULT 30
 PNO649
 pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
 C:Species: Bacillus sp.
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
 C:Accession: PNO649
 R:Kim, C.H.; Choi, H.I.; Lee, D.S.
 Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
 A:Title: Purification and biochemical properties of an alkaline pullulanase from alkaliphilic Bacillus sp.
 A:Reference number: PNO649; MUID:94080025; PMID:7764261
 A:Accession: PNO649
 A:Molecule type: protein
 A:Residues: 1-7 <KIM>
 C:Comment: This enzyme is used together with glucoamylase to improve the efficiency of starch liquefaction in high maltose syrups.
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 5 SW 6

RESULT 31
 S10596
 adipokinetic hormone - pond skimmer
 C:Species: Libellula auripennis
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
 C:Accession: S10596
 R:Gaede, G.
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
 A:Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone
 A:Reference number: S10596; MUID:90359055; PMID:2390213
 A:Accession: S10596
 A:Molecule type: protein
 A:Residues: 1-8 <BIO>
 C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamate; modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F1/Modified site: amidated carboxyl end (Trp) #status experimental
 F1/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 Db 7 SW 8

RESULT 32
 PQ0012
 cholecystokinin - southeastern quoll
 N:Alternate names: CCK
 C:Species: Dasyurus viverrinus (southeastern quoll)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
 C:Accession: PQ0012
 R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
 Peptides 9, 429-431, 1988
 A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
 A:Reference number: PQ0012; MUID:88234141; PMID:3375140
 A:Accession: PQ0012
 A:Molecule type: protein
 A:Residues: 1-8 <FAN>
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
 F2/Binding site: sulfate (Tyr) (covalent) #status predicted

F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WM 3
||
Db 5 WM 6

RESULT 33

A43001
cholecystokinin - tammar wallaby
N;Alternate names: CCK
C;Species: Macropus eugenii (tammar wallaby)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C;Accession: A43001; PQ0012
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; PMID:88234141; PMID:3375140
A;Accession: A43001
A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WM 3
||
Db 5 WM 6

RESULT 34

B24749
neuropeptide B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C;Accession: B24749
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two
A;Reference number: A94074; PMID:86067985; PMID:3865193
A;Accession: B24749
A;Molecule type: protein
A;Residues: 1-8 <YAN>
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
||
Db 4 QP 5

RESULT 35

S43971
tumor-associated antigen MUT1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C;Accession: S43971
R;Mandelblat, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine

A;Reference number: S43971; PMID:94217811; PMID:8164742

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAN>
C;Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
||
Db 7 QP 8

RESULT 36

B39745
endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)
C;Species: Rhodococcus sp.
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 31-Dec-1993
C;Accession: B39745
R;Ito, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases.
ble using these activator proteins.
A;Reference number: A39745; PMID:91210321; PMID:1850427
A;Accession: B39745
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <ITO>
C;Keywords: glycosidase; hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 2 PP 3

RESULT 37

S16324
hypothetical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely lin
A;Reference number: S16323; PMID:91266907; PMID:1675603
A;Accession: S16324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <RUB>
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 7 PP 8

RESULT 38

S21288
lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C;Accession: S21288

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
 A:Reference number: S21288; PMID:92272683; PMID:1590771
 A:Accession: S21288
 A:Molecule type: protein
 A:Residues: 1-8 <MIL>
 A:Experimental source: var. Ulster Sceptre
 C:Function:
 A:Description: may be involved in defence mechanism of the plant
 C:Keywords: hydroxyproline; lectin

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
 ||
 7 PP 8

Db

RESULT 39
 PT0030
 inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)
 N:Alternate names: inulase
 C:Species: Aspergillus ficuum
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
 C:Accession: PT0030
 R:Etalibi, M.; Barattini, J.C.
 Agric. Biol. Chem. 54, 61-68, 1990
 A:Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.
 A:Reference number: PT0030; PMID:90344234; PMID:1368526
 A:Accession: PT0030
 A:Molecule type: protein
 A:Residues: 1-8 <ERT>
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 5 QP 6

Db

RESULT 40
 JS0315
 leucokinin V - Madeira cockroach
 C:Species: Leucophaea maderae (Madeira cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: JS0315
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A:Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropin
 A:Reference number: JS0315
 A:Accession: JS0315
 A:Molecule type: protein
 A:Residues: 1-8 <HOL>
 C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 6 SW 7

Db

RESULT 41
 JS0316
 leucokinin VI - Madeira cockroach
 C:Species: Leucophaea maderae (Madeira cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: JS0316
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A:Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropin
 A:Reference number: JS0316
 A:Accession: JS0316
 A:Molecule type: protein
 A:Residues: 1-8 <HOL>
 C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 6 SW 7

Db

RESULT 42
 JS0317
 leucokinin VII - Madeira cockroach
 C:Species: Leucophaea maderae (Madeira cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: JS0317
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 31-34, 1987
 A:Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the
 A:Reference number: JS0317
 A:Accession: JS0317
 A:Molecule type: protein
 A:Residues: 1-8 <HOL>
 C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 6 SW 7

Db

RESULT 43
 JS0318
 leucokinin VIII - Madeira cockroach
 C:Species: Leucophaea maderae (Madeira cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: JS0318
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 31-34, 1987
 A:Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the
 A:Reference number: JS0318
 A:Accession: JS0318
 A:Molecule type: protein
 A:Residues: 1-8 <HOL>
 C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 6 SW 7

Db

QY 1 SW 2
||
6 SW 7

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 HQ 5
||
Db 2 HQ 3

RESULT 44

E47393
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: E47393
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A;Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequen
A;Reference number: A47393; MUID:93211980; PMID:8460157
A;Accession: E47393
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <DUV>
A;Experimental source: whole flies
A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 6 PP 7
||
Db 2 PP 3

RESULT 45

A14683
aspartate transaminase (BC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm
N;Alternate names: aspartate aminotransferase, mitochondrial
C;Species: Gallus gallus (chicken)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A14683
R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.
FEBS Lett. 108, 98-102, 1979
A;Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
A;Reference number: A14683; MUID:80092116; PMID:520566
A;Accession: A14683
A;Molecule type: protein
A;Residues: 1-8 <WIL>
C;Keywords: aminotransferase; mitochondrion

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 5 QP 6
||
Db 6 QP 7

RESULT 46

PT0368
Ig gamma chain C region (gamma-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
C;Accession: PT0368
R;Millili, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.
Mol. Immunol. 28, 753-761, 1991
A;Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.
A;Reference number: PT0368; MUID:91312348; PMID:1906981
A;Accession: PT0368
A;Molecule type: mRNA
A;Residues: 1-8 <MIL>
A;Experimental source: fetal liver
C;Keywords: immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 8;

QY 4 HQ 5
||
Db 2 HQ 3

RESULT 47

S10783
enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S10783
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tootch 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10783
A;Molecule type: protein
A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 6 PP 7
||
Db 4 PP 5

RESULT 48

PT0559
T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0559
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0559
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 6 PP 7
||
Db 4 PP 5

RESULT 49

A38887
T-cell receptor gamma chain (5t.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: A38887
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: A38887
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-8 <WHE>
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
Db 2 SW 3

RESULT 50
C39690
neural cell adhesion molecule, cardiac splice form -, -, + - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C;Accession: C39690
R;Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A;Reference number: A39690; MUID:91141516; PMID:1996115
A;Accession: C39690
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-8 <REV>
A;Cross-references: GB:M63970
A;Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
||
Db 1 QP 2

RESULT 51
A61102
parathyroid hormone-like protein, humoral hypercalcemia of malignancy - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
R;Weir, B.C.; Burtis, W.J.; Morris, C.A.; Brady, T.G.; Insogna, K.L.
Endocrinology 123, 2744-2751, 1988
A;Title: Isolation of 16,000-b Dalton parathyroid hormone-like proteins from two animal tissues
A;Reference number: A61102; MUID:89064600; PMID:3197642
A;Accession: A61102
A;Molecule type: protein
A;Residues: 1-9 <WEI>
A;Experimental source: apocrine cell adenocarcinoma
A;Superfamily: parathyroid hormone-related protein; parathyroid hormone homology
C;Keywords: hormone; humoral hypercalcemia

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
||
Db 6 HQ 7

RESULT 52
A24244
adipokine hormone - bollworm
N;Alternate names: Hez-AKH
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C;Date: 31-Mar-1998 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C;Accession: A24244
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Heliothis zea
A;Reference number: A24244; MUID:86186794; PMID:3964263

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 2 PP 3

RESULT 55

A;Accession: A24244
A;Molecule type: protein
A;Residues: 1-9 <JAF>
C;Superfamily: adipokine hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamate
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
Db 7 SW 8

RESULT 53
A61357
phyllocaerulein - Sauvage's leaf frog
C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C;Accession: A61357
R;Anastasi, A.; Bertaccini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.
Br J. Pharmacol. 37, 198-206, 1969
A;Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like neuropeptide
A;Reference number: A61357; MUID:70005484; PMID:5824931
A;Accession: A61357
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ANA>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Binding site: sulfate (Tyr) (covalent) #status experimental
F;9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WM 3
||
Db 6 WM 7

RESULT 54
A61358
bradykinin-like peptide I - Japanese pond frog
C;Species: Rana nigromaculata (Japanese pond frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C;Accession: A61358
R;Nakajima, T.
Chem. Pharm. Bull. 16, 769-770, 1968
A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin of Rana nigromaculata
A;Reference number: A61358; MUID:68412013; PMID:5677638
A;Accession: A61358
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <NAK>
C;Superfamily: unassigned animal peptides
C;Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 2 PP 3

RESULT 55

A61057

Thr-6 bradykinin - scoliid wasp (Colpa interrupta)
 C:Species: Colpa interrupta
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Aug-2000
 C:Accession: A61057
 R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
 Comp. Biochem. Physiol. C 96, 157-162, 1990
 A:Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap
 A:Reference number: A61057; MUID:91130217; PMID:1980872
 A:Accession: A61057
 A:Molecule type: protein
 A:Residues: 1-9 <R1E>
 C:Superfamily: unassigned animal peptides
 C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 ||
 Db 2 pp 3

RESULT 56

Az6744
 bradykinin-like peptide - garden dagger wasp
 N:Alternate names: Thr-6-bradykinin
 C:Species: Megascolia flavifrons (garden dagger wasp)
 C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000
 C:Accession: Az6744
 R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
 Toxicon 25, 527-535, 1987
 A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
 A:Reference number: A94322; MUID:87293024; PMID:3617088
 A:Accession: Az6744
 A:Molecule type: protein
 A:Residues: 1-9 <YAS>
 C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 ||
 Db 2 pp 3

RESULT 57

A61363
 bradykinin - common frog
 C:Species: Rana temporaria (common frog)
 C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
 C:Accession: A61363
 R:Anastasi, A.; Erspamer, V.; Bertaccini, G.
 Comp. Biochem. Physiol. A 14, 43-52, 1965
 A:Title: Occurrence of bradykinin in the skin of Rana temporaria.
 A:Reference number: A61363
 A:Accession: A61363
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <ANA>
 C:Superfamily: unassigned animal peptides
 C:Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 ||
 Db 2 pp 3

RESULT 58

A60579
 bradykinin-like peptide - slider turtle
 C:Species: Pseudemys scripta (slider)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: A60579
 R:Conlon, J.M.; Hicks, J.W.; Smith, D.D.
 Endocrinology 126, 985-991, 1990
 A:Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from
 A:Reference number: A60579; MUID:90126625; PMID:2298179
 A:Accession: A60579
 A:Molecule type: protein
 A:Residues: 1-9 <CON>
 C:Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammals
 C:Superfamily: unassigned animal peptides
 C:Keywords: plasma

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 ||
 Db 2 pp 3

RESULT 59

B60246
 ornitho-kinin - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Aug-2000
 C:Accession: B60246
 R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.
 Adv. Exp. Med. Biol. 247A, 359-367, 1989
 A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemica
 A:Reference number: A60246; MUID:90102072; PMID:2603803
 A:Accession: B60246
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <KIM>
 C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 ||
 Db 2 pp 3

RESULT 60

B41983
 orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
 C:Species: Azotobacter vinelandii
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: B41983
 R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
 A:Title: Unification of the ferritin family of proteins.
 A:Reference number: A41983; MUID:92196129; PMID:1549605
 A:Accession: B41983
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid; protein
 A:Residues: 1-9 <GRO>
 A:Cross-references: GS:M03692; NID:G142297; PIDN:AAA22122.1; PID:G142299
 A>Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 28.6%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 3 PP 4

RESULT 61

S55696 phosphoenolpyruvate carboxykinase - Trypanosoma brucei

C:Species: Trypanosoma brucei
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S55696
R:Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Trypanosoma brucei
A:Reference number: S55696; MUID:95284106; PMID:7766679
A:Accession: S55696
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <HUN>

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
||
Db 1 QP 2

RESULT 62

D57444

neuropeptide Grb-AST B4 - two-spotted cricket

C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: D57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket Gryllus bimaculatus
A:Reference number: A57444; MUID:95403341; PMID:7673141
A:Accession: D57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
Db 8 SW 9

RESULT 63

A61620

locustamytotropin III - migratory locust

C:Species: Locusta migratoria (migratory locust)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C:Accession: A61620
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A:Title: Isolation, identification and synthesis of locustamytotropin III and IV, two additional locustamytotropins
A:Reference number: A61620
A:Accession: A61620
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <SCH>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QP 6
||
Db 3 QP 4

RESULT 64

S65433

bradykinin - horn fly (fragment)

C:Species: Haematobia irritans (horn fly)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65433
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, E.
Eur. J. Biochem. 237, 414-423, 1996
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipterous insect Haematobia irritans
A:Reference number: S65431; MUID:96215437; PMID:8647080
A:Accession: S65433
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <Wij>

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
||
Db 2 PP 3

RESULT 65

S77984

cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)

C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C:Accession: S77984
R:Arnold, S.; Lee, J.; Kim, M.; Song, B.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77984
A:Molecule type: protein
A:Residues: 1-9 <ARN>

C:Genetics:
A:Experimental source: heart
A:Genome: nuclear
C:Function:
A:Pathway: oxidative phosphorylation; respiratory chain

C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
||
Db 3 QP 4

RESULT 66

P02999

Ig heavy chain CRD3 region (clone 5-103B) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: P02999
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and the role of the CDR3 region in the formation of the antigen binding site
A:Reference number: P02922; MUID:91108337; PMID:1899102
A:Accession: P02999
A:Molecule type: DNA
A:Residues: 1-9 <YAM>

A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
Db 3 SW 4

RESULT 67

S26508 collagen alpha 2(VI) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Dec-1998
C;Accession: S26508
R;Jander, R.; Rautenberg, J.; Glanville, R.W.
Eur. J. Biochem. 133, 39-46, 1983

A;Title: Further characterization of the three polypeptide chains of bovine and human sh
A;Reference number: S26506; MUID:83209648; PMID:6852033
A;Accession: S26508

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <JAN>
C;Keywords: hydroxyproline
F;7/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 6 PP 7

RESULT 68

I58350 gene c-mpl protein - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 28-Feb-1997
C;Accession: I58350
R;Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995

A;Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a recep
A;Reference number: I58350; MUID:95166571; PMID:7862460
A;Accession: I58350

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-9 <RES>

A;Cross-references: GB:S76841; NID:g912992

C;Genetics:

A;Gene: c-mpl

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
Db 3 SW 4

RESULT 69

B30572 T-cell receptor beta chain C region (CRTB29) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997

C;Accession: B30572

R;Williams, C.B.; Gutman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of uti
A;Reference number: A30563; MUID:89110038; PMID:2563271

A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-9 <WIL>

C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 8 PP 9

RESULT 70

A43065 hydroxyproline-3-bradykinin - frog (Haleophryne purcelli)

C;Species: Haleophryne purcelli

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: A43065

R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.

Experientia 35, 1133, 1979

A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the Sout
A;Reference number: A43065; MUID:80024576; PMID:488255

A;Accession: A43065

A;Molecule type: protein

A;Residues: 1-9 <NAK>

C;Keywords: bradykinin; hydroxyproline; skin

F;3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 2 PP 3

RESULT 71

XAV16B

angiotensin-converting enzyme inhibitor V-6-II - jararaca

C;Species: Bothrops jararaca (jararaca)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995

C;Accession: A01255

R;Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocy, O.

Biochemistry 10, 4033-4039, 1971

A;Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca
A;Reference number: A90356; MUID:72118526; PMID:4334402

A;Accession: A01255

A;Molecule type: protein

A;Residues: 1-10 <OND>

A;Note: the structure of the peptide was confirmed by synthesis

C;Comment: This peptide also potentiates bradykinin by inhibiting the kinases that ir
C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
||
Db 9 PP 10

RESULT 72

XASNPC

angiotensin-converting enzyme inhibitor - aspiv viper

C;Species: Vipera aspis (aspic viper)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
 C;Accession: A60377
 R;Komori, Y.; Sugihara, H.
 Int. J. Biochem. 22, 767-771, 1990
 A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the
 A;Reference number: A60377; MUID:90382616; PMID:2169439
 A;Accession: A60377

A;Molecule type: protein

A;Residues: 1-10 <KOM>

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7

|||

9 PP 10

Db

RESULT 73

RHAQ1

N;gonadoliberin I - American alligator

C;Alternate names: gonadotropin-releasing hormone I

C;Species: Alligator mississippiensis (American alligator)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997

C;Accession: A60066

R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson

Regul. Pept. 33, 105-116, 1991

A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of

A;Reference number: A60066; MUID:91352338; PMID:1882082

A;Accession: A60066

A;Molecule type: protein

A;Residues: 1-10 <LOV>

C;Superfamily: gonadoliberin

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

28.6%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

|||

8 QP 9

Db

RESULT 74

SPFGNK

Neuromedin K - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 23-Aug-1996

C;Accession: A01560

R;Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.

Biochem. Biophys. Res. Commun. 114, 533-540, 1983

A;Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.

A;Reference number: A01560; MUID:83282812; PMID:6576785

A;Accession: A01560

A;Molecule type: protein

A;Residues: 1-10 <KAN>

A;Note: the structure of the peptide was confirmed by synthesis

C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu

C;Superfamily: neurokinin B precursor

C;Keywords: amidated carboxyl end; hormone; spinal cord

F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

28.6%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4

|||

2 MH 3

Db

RESULT 75

JC1367

thyroliberin potentiating neuropeptide - bovine

N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiati

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1997

C;Accession: JC1367

R;Bulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.

Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992

A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovin

A;Reference number: JC1367; MUID:93111999; PMID:1472021

A;Accession: JC1367

A;Molecule type: protein

A;Residues: 1-10 <BUL>

A;Experimental source: hypothalamus

C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin precursor

C;Function:

A;Description: potentiates thyroliberin-induced thyrotropin secretion

C;Superfamily: thyroliberin precursor

C;Keywords: hypothalamus; neuropeptide

Query Match

28.6%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3

|||

4 WM 5

Db

Search completed: November 25, 2003, 19:36:09

Job time : 4.80233 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.48256 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWHQPP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	11	1	MORN HUMAN
2	3	42.9	20	1	OAR PHOPY
3	2	28.6	4	1	OCF3 OCTMI
4	2	28.6	6	1	ER01 LITRU
5	2	28.6	6	1	L0K1 L0CMI
6	2	28.6	7	1	LANC CARUI
7	2	28.6	7	1	TPFY PACDA
8	2	28.6	7	1	UF04 MOUSE
9	2	28.6	8	1	AKH LIBAU
10	2	28.6	8	1	ALL5 CALVO
11	2	28.6	8	1	CKN MACRU
12	2	28.6	8	1	LCK1 LEUMA
13	2	28.6	8	1	LCK2 LEUMA
14	2	28.6	8	1	LCK3 LEUMA
15	2	28.6	8	1	LCK4 LEUMA
16	2	28.6	8	1	LCK5 LEUMA
17	2	28.6	8	1	LCK6 LEUMA
18	2	28.6	8	1	LCK7 LEUMA
19	2	28.6	8	1	LCK8 LEUMA
20	2	28.6	8	1	NPB BOVIN
21	2	28.6	8	1	PK2 PERAM
22	2	28.6	9	1	AL10 CARMA
23	2	28.6	9	1	COKE THUOB
24	2	28.6	9	1	FAR3 PENMO
25	2	28.6	9	1	FAR4 PENMO
26	2	28.6	9	1	FRF1 SARBU
27	2	28.6	9	1	KNL3 BOMVA
28	2	28.6	9	1	LMT3 L0CMI
29	2	28.6	9	1	RT33 BOVIN
30	2	28.6	9	1	YBFR AZOVI
31	2	28.6	10	1	AH3 PRUSE
32	2	28.6	10	1	BPP2 BOTIN
33	2	28.6	10	1	BPP2 BOTJA

34	2	28.6	10	1	BPP8 BOTIN
35	2	28.6	10	1	BPP VIPAS
36	2	28.6	10	1	BRK ONCMY
37	2	28.6	10	1	CABR LITXA
38	2	28.6	10	1	COXM RAT
39	2	28.6	10	1	FAR6 PANRE
40	2	28.6	10	1	GONI ALLMI
41	2	28.6	10	1	TKNK PIG
42	2	28.6	10	1	TMOF AEDAE
43	2	28.6	10	1	UPA2 HUMAN
44	2	28.6	10	1	UPA5 HUMAN
45	2	28.6	10	1	URE3 MORMO
46	2	28.6	10	1	ASL1 BACSE
47	2	28.6	11	1	BPP3 BOTIN
48	2	28.6	11	1	BPP4 BOTIN
49	2	28.6	11	1	BPPB AGRHA
50	2	28.6	11	1	BPP AGRHP
51	2	28.6	11	1	BRK MEGFL
52	2	28.6	11	1	CA31 LITCI
53	2	28.6	11	1	CEP1 ACHFU
54	2	28.6	11	1	LADD ONCMY
55	2	28.6	11	1	TKN1 PSEGU
56	2	28.6	11	1	TKN1 UPERU
57	2	28.6	11	1	TKN2 PSEGU
58	2	28.6	11	1	TKN3 PSEGU
59	2	28.6	11	1	TKN4 PSEGU
60	2	28.6	11	1	TKN5 PSEGU
61	2	28.6	11	1	TKNA ONCMY
62	2	28.6	11	1	TKN ELENO
63	2	28.6	12	1	FAR7 PENMO
64	2	28.6	12	1	FARI CALVO
65	2	28.6	12	1	FIFI SARBU
66	2	28.6	12	1	HS9A RAT
67	2	28.6	12	1	TKN2 KASMA
68	2	28.6	13	1	ACT7 SOYBN
69	2	28.6	13	1	AH4 PRUSE
70	2	28.6	13	1	BPP1 BOTJA
71	2	28.6	13	1	BRK PARID
72	2	28.6	13	1	EX22 LITRU
73	2	28.6	13	1	EP65 HUMAN
74	2	28.6	13	1	LMT4 L0CMI
75	2	28.6	13	1	MP1 MICOC
76	2	28.6	13	1	TV13 PHYRO
77	2	28.6	14	1	MARI ALRSP
78	2	28.6	14	1	NAST VESBA
79	2	28.6	14	1	PH1 PRUSE
80	2	28.6	14	1	TAT HV1W2
81	2	28.6	14	1	TAT HV1Z8
82	2	28.6	15	1	AF1L MALPA
83	2	28.6	15	1	AH2 PRUSE
84	2	28.6	15	1	CH11 PEA
85	2	28.6	15	1	CKA2 CONAL
86	2	28.6	15	1	FKB7 PINPS
87	2	28.6	15	1	IRBP CRISP
88	2	28.6	15	1	MR1 PALPR
89	2	28.6	15	1	NUO8 SOLTU
90	2	28.6	15	1	PH3 PRUSE
91	2	28.6	15	1	PRP MYCBO
92	2	28.6	15	1	RBS PHYPA
93	2	28.6	15	1	SODM STRGR
94	2	28.6	15	1	UC06 MAIZE
95	2	28.6	15	1	UC19 MAIZE
96	2	28.6	15	1	UE15 HORVU
97	2	28.6	15	1	UN01 PINPS
98	2	28.6	15	1	UP01 METAN
99	2	28.6	15	1	URE2 MORMO
100	2	28.6	16	1	AF1S MALPA

ALIGNMENTS

RESULT 1

MORN HUMAN
 ID MORN HUMAN STANDARD; PRT; 11 AA.
 AC P01163;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Morphogenetic neuroptide (Head activator) (HA).
 OS Homo sapiens (Human),
 OS Rattus norvegicus (Rat),
 OS Bos taurus (Bovine),
 OS Anthopleura elegantissima (Sea anemone), and
 OS Hydra attenuata (Hydra vulgaris);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 RX MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuroptide, the head activator,
 RT from coelenterates to humans.";
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A. elegantissima, and H. attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from
 RT hydra.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
 RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuroptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
 RT in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
 CC -!- IN THE G2/MITOSIS TRANSITION.
 CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
 CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
 CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
 CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
 DR PIR; A01427; YHRT.
 DR PIR; A93900; YHXA.
 DR PIR; B01427; YHHU.
 DR PIR; B93900; YHJPHY.
 DR PIR; C01427; YHBO.
 DR GK; P01163; -.
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;
 Query Match 42.9%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 DB 1 QPP 3
 RESULT 2
 OAR_PHOPHY
 ID_OAR_PHOPHY STANDARD; PRT; 20 AA.
 AC P14803;
 DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Octopamine receptor (Octopamine binding protein) (Fragment).
 OS Photinus pyralis (North American firefly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia;
 OC Cantharoidea; Lampyridae; Photinus.
 NCBI_TaxID=7054;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Light organ;
 RX MEDLINE=90092510; PubMed=2513233;
 RA Nathanson J.A., Kantham L., Hunnicutt E.J.;
 RT "Isolation and N-terminal amino acid sequence of an octopamine ligand
 RT binding protein.";
 RL FEBS Lett. 259:117-120(1989).
 CC -!- FUNCTION: PUTATIVE RECEPTOR FOR OCTOPAMINE. OCTOPAMINE (OA) IS A
 CC NEUROTRANSMITTER, NEUROHORMONE, AND NEUROMODULATOR IN
 CC INVERTEBRATES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 CC PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR PIR; S28779; S28779.
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; PARTIAL.
 KW G-protein coupled receptor.
 FT UNSURE 2
 FT UNSURE 9 9
 FT UNSURE 19 19
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2500 MW; ACBC81A11BE8D4B CRC64;
 Query Match 42.9%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MHQ 5
 DB 18 MHQ 20
 RESULT 3
 OCP3_OCTMI
 ID_OCP3_OCTMI STANDARD; PRT; 4 AA.
 AC P58649;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-3/Ocp-4.
 OS Octopus minor (Octopus);
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor.";
 RL Peptides 21:623-630(2000).
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less
 CC active than Ocp-3.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD RES 2 2 D-SERINE (IN OCP-4).
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B81000000 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
Db 2 SW 3

RESULT 4

ID E101_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella";
RL Aust. J. Chem. 52:639-645 (1999).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
||
Db 5 WM 6

RESULT 5

ID LOK1_LOCMI STANDARD; PRT; 6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustakinin 1.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57 (1992).
CC -I- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC PIR; A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
||
Db 4 SW 5

RESULT 6

ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422 (1992).
CC -I- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON_TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
||
Db 5 QP 6

RESULT 7

ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P834E5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (Pdt-1).
OS Pachymedusa dactyloides (Giant Mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactyloides tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA".
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -I- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Skin.
CC -I- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.

DR GO: 0045986; P: negative regulation of smooth muscle contraction; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 FT MOD RES 3 3
 FT MOD RES 7 7
 FT MOD RES 7 7
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 Db 2 pp 3

RESULT 8
 UF04 MOUSE
 ID UF04 MOUSE STANDARD; PRT; 7 AA.
 AC P38642;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast; PubMed=7523108;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS; ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
 FT NON TER 7 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 Db 3 pp 4

RESULT 9
 AKH LIBAU
 ID AKH LIBAU STANDARD; PRT; 8 AA.
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipoketic hormone (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
 OX NCBI_TaxID=6966;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipoketic/red-pigment-
 concentrating hormone family isolated and sequenced from a
 dragonfly.";
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT

CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR, S10596; S10596.
 DR InterPro; IPR02047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 8 8
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
 Db 7 SW 8

RESULT 10
 ALL5 CALVO
 ID ALL5 CALVO STANDARD; PRT; 8 AA.
 AC P41841;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callistostatin 5 (Met-callistostatin 1) ([HYD3]Met-callistostatin).
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93211180; PubMed=8460157;
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
 RA Thorpe A.;
 RT "Callistostatin: neuropeptides from the blowfly Calliphora vomitoria
 with sequence homology to cockroach allatostatins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 DR PIR; E47393; E47393.
 KW Neuropeptide; Amidation; Hydroxylation.
 FT MOD RES 3 3
 FT MOD RES 8 8
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB47768 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
 Db 2 pp 3

RESULT 11
 CCKN MACEU
 ID CCKN MACEU STANDARD; PRT; 8 AA.

AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CKK).
GN
OS Macropus eugenii (Mammal wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RN SEQUENCE.
RC SPECIES=M. eugenii, and D. viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
DB 5 WM 6

AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CKK).
GN
OS Macropus eugenii (Mammal wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RN SEQUENCE.
RC SPECIES=M. eugenii, and D. viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
DB 5 WM 6

AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CKK).
GN
OS Macropus eugenii (Mammal wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RN SEQUENCE.
RC SPECIES=M. eugenii, and D. viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
DB 5 WM 6

AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CKK).
GN
OS Macropus eugenii (Mammal wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RN SEQUENCE.
RC SPECIES=M. eugenii, and D. viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
DB 5 WM 6

QY 1 SW 2
DB 6 SW 7

RESULT 13
LCK2 LEUMA
ID LCK2 LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
DB 6 SW 7

RESULT 14
LCK3 LEUMA
ID LCK3 LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
DB 6 SW 7

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
6 SW 7

Db

RESULT 15

LCK4_LEUMA
ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
6 SW 7

Db

RESULT 16

LCK5_LEUMA
ID LCK5_LEUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR; JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
6 SW 7

Db

RESULT 17

LCK6_LEUMA
ID LCK6_LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND PIR; JS0316; JS0316.
KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
FT MOD_RES 1
FT MOD_RES 8
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
6 SW 7

Db

RESULT 18

LCK7_LEUMA
ID LCK7_LEUMA STANDARD; PRT; 8 AA.
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.

DR PIR; JS0317; JS0317.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 866 MW; D66365A5B9CD76A CRC64;

AMIDATION.

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 6 SW 7

RESULT 19

LCK8_LEUMA STANDARD; PRT; 8 AA.

AC P19930;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Leucokinin VIII (L-VIII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.

DR PIR; JS0318; JS0318.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAAD98 CRC64;

AMIDATION.

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
 ||
 6 SW 7

RESULT 20

NPB_BOVIN STANDARD; PRT; 8 AA.

AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

AMIDATION.

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 4 QP 5

RESULT 21

PPK2_PERAM STANDARD; PRT; 8 AA.

AC P82692;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinnin-2 (Pea-PK-2) (FXPRIL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;

RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinnins from the
 RT retrocerebral complex of the American cockroach.";
 RL Peptides 18:473-478(1997).
 RN [2]

RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;

RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRILamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).

CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).

CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.

CC -1- MASS SPECTROMETRY: MW=883; METHOD=WALDI.

CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR InterPro; IPR001484; Pyrokinnin.

DR PROSITE; PS00539; PYROKININ; FALSE NEG.

KW Neuropeptide; Amidation; Pyrokinnin.

FT MOD_RES 8

SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
 ||
 2 PP 3

RESULT 22

AL10_CARMA STANDARD; PRT; 9 AA.

AC P81813;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 10.
 OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 9
 FT SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;
 SQ
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QP 6
 Db 3 QP 4

RESULT 23
 COXE_THUOB
 ID -COXE_THUOB STANDARD; PRT; 9 AA.
 AC P80975;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide via (EC 1.9.3.1) (Fragment).
 OS *Thunnus obesus* (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
 DR PIR; S77984.
 DR InterPro; IPR001349; COX6A.
 DR PROSITE; PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON TER 1
 FT NON TER 9
 FT SEQUENCE 9 AA; 1136 MW; 62E072C9CE0776DB CRC64;
 SQ
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QP 6
 Db 3 QP 4

RESULT 24
 FAR3_PENMO
 ID -FAR3_PENMO STANDARD; PRT; 9 AA.
 AC P83318;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
 OS *Penaeus monodon* (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk; PubMed=11959015;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn *Penaeus monodon*.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 FT SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;
 SQ
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QP 6
 Db 2 QP 3

RESULT 25
 FAR4_PENMO
 ID -FAR4_PENMO STANDARD; PRT; 9 AA.
 AC P83319;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
 OS *Penaeus monodon* (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn *Penaeus monodon*.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 FT SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;
 SQ
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 2 QP 3

RESULT 26

FFL1_SARBU
ID FFL1_SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meeusen T., Mertens I., Clynen B., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 1 QP 2

RESULT 27

KNL3_BOMVA
ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.

SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7

Db 2 PP 3

RESULT 28

LMT3_LOCMI
ID LMT3_LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin_3 (LOM-WT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 3 QP 4

RESULT 29

RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRP333.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";

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RL J. Biol. Chem. 276:19363-19374 (2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 9
FT NON_TER 1 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB0589 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 5 QP 6

RESULT 30
YBFR AZOVI
ID YBFR AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
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CC -----
DR EMBL; M83692; AAA22122.1; -.
DE PIR; B41983;
KW Hypothetical protein.
FT NON_TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 3 PP 4

RESULT 31
AH3_PRUSE
ID AH3_PRUSE STANDARD; PRT; 10 AA.
AC P29761;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COFYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
CC KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 3 PP 4

RESULT 32
BPP2_BOTIN
ID BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 9 PP 10

RESULT 33
BPP2_BOTJA
ID BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).
DE Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 9 PP 10

RESULT 34
BPP8 BOTIN STANDARD; PRT; 10 AA.
AC P30476;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5.1 (Angiotensin-converting enzyme inhibitor).
DE Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A.; Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; H37196; H37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2F835545761F6D8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7

Db 9 PP 10

RESULT 35
BPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).
DE Viperas aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Viperas.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE
RC TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Viperas aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 9 PP 10

RESULT 36
BRK ONCMY STANDARD; PRT; 10 AA.
AC Q3PR21;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma.";
RL FEBS Lett. 334:75-78(1993).
CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

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Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY      6 PP 7
      ||
Db      3 PP 4

RESULT 37
CAER_LITXA
ID CAER_LITXA STANDARD; PRT; 10 AA.
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caerulein.
OS Litoria xanthomera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
  Ramsay S.L.;
RT "New caerin antibacterial peptides from the skin glands of the
  Australian tree frog Litoria xanthomera.";
RL J. Pept. Sci. 3:181-185(1997).
CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1354; METHOD=Fab.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro: IPR001651; Gastrin.
DR PROSITE, PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1290 MW; 99DBF3837861BB5A CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY      2 WM 3
      ||
Db      7 WM 8

RESULT 38
COXM_RAT
ID COXM_RAT STANDARD; PRT; 10 AA.
AC P80431;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
  (fragment).
DE (fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;

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RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
  amino-terminal sequences suggest identity of the fetal heart and the
  adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
  CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
  MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
  c + 2 H(2)O.
CC PIR; S65387; S65387.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY      4 HQ 5
      ||
Db      2 HQ 3

RESULT 39
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P84860;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
  Maule A.G.;
RT "Isolation, characterization and pharmacology of FMRFamide-related
  peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FMRP (FMRFAMIDE RELATED PEPTIDE)
  FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY      5 QP 6
      ||
Db      5 QP 6

RESULT 40
GON1_ALLMI
ID GON1_ALLMI STANDARD; PRT; 10 AA.
AC P37041, P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)
  (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QP 6
DB 8 QP 9
RESULT 41
TKNK PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B (NKB) (Neuromedin K).
GN TAC3 OR NKNB.
OS Sus scrofa (Pig), and
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
RN [1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RP SEQUENCE.
RC SPECIES=R. ridibunda; TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NKT tachykinin receptor agonist isolated with
neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01560; SPPGNK.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CA1 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MH 4
DB 2 MH 3
RESULT 42
TMOF AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=71159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PP 7
DB 5 PP 6
RESULT 43
UPA2 HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;

RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON TER 1 1
FT UNSURE 6 6
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB7775B7 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PP 7
DB 5 PP 6
RESULT 44
UPA5 HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON TER 1 1
FT VARIANT 9 9 G -> Y.
FT NON TER 10 10 /FTID=VAR_000002.
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QP 6
DB 3 QP 4
RESULT 45
URE3 MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
DE amidohydrolase) (Fragment).

GN UREA.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
[1]
RP SEQUENCE
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR; C35389; C35389.
KW Hydrolase.
FT NON TER 10 10
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PP 7
DB 5 PP 6
RESULT 46
ASL1 BACSE STANDARD; PRT; 11 AA.
ID ASL1_BACSE
AC P83146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
[1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HQ 5
DB 10 HQ 11
RESULT 47


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BPP3 BOTIN
ID _BPP3 BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 4 PP 5

RESULT 48
BPP4 BOTIN
ID _BPP4 BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20B5B9F13C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 PP 7
Db 4 PP 5

RESULT 49
BPP5 AGKHA
ID _BPP5 AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydus blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad.; B. Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNEA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 4 PP 5

RESULT 50
BPP AGKHP
ID _BPP AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JCO002; XAVIEH.

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KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db 4 PP 5

RESULT 51
 BRK MEGFL STANDARD; PRT; 11 AA.
 AC P12797; 11 AA.
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Megascollakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 peptide ([Thr6]bradykinin)].
 OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hymenoptera; Apocrita; Aculeata; Scolioidea;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
 OC Scoliidae; Megascollia.
 NCBI_TaxID=7437;
 [1]
 RN SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp Megascollia flavifrons.";
 RL Toxicon 25:527-535 (1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;
 RT "Two kinins isolated from the venom of Megascollia flavifrons.";
 RL Toxicon 26:34-34 (1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
 CR PIR: B26744; B26744.
 KW Bradykinin; Vasodilator.
 FT PEPTIDE 1 11
 FT PEPTIDE 1 11
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db 2 PP 3

RESULT 52
 CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 NCBI_TaxID=94770;

RN SEQUENCE, AND MASS SPECTROMETRY.
 RP TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502 (1999).
 CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; FALSE NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 4 4 SULFATION.
 FT MOD RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WM 3
 Db 8 WM 9

RESULT 53
 CEPL_ACHFU STANDARD; PRT; 11 AA.
 AC P22790;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 NCBI_TaxID=6530;
 [1]
 RN SEQUENCE.
 RP STRAIN=Perusac; TISSUE=Heart atrium;
 RX MEDLINE=90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, Achatina fulica.";
 RL Biochem. Biophys. Res. Commun. 167:777-783 (1990).
 CC -!- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
 CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
 CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
 CC MOVEMENT OF ACHATINA.
 CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
 DR PIR: A34662; A34662.
 KW Hormone; Amidation.
 FT MOD RES 11 11
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SW 2
 Db 4 SW 5

RESULT 54

LADD ONCMY
ID LADD ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
RT "A rainbow trout lectin with multimeric structure."
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -!- FUNCTION: LECTIN THAT BINDS SEPHAROSE.
CC -!- COFACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.
CC -!- SUBUNIT: MULTIMERIC.
KW Lectin; Calcium.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7

Db 9 PP 10

RESULT 55

TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri."
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B60409; B60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 1 QP 2

RESULT 57

TKN2_PSEGU
ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Eudean R.;
RT "Structure of uperolein, a physalamin-like endecapeptide occurring
in the skin of Uperoleia rugosa and Uperoleia marmorata."
RL Experientia 31:394-395(1975).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1252 MW; 32867C3B59CDD457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 1 QP 2

FT MOD_RES 1 1
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 1 QP 2

RESULT 56

TKN1_UPERU
ID TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-SEP-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Eudean R.;
RT "Structure of uperolein, a physalamin-like endecapeptide occurring
in the skin of Uperoleia rugosa and Uperoleia marmorata."
RL Experientia 31:394-395(1975).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1252 MW; 32867C3B59CDD457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 1 QP 2

```

OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; C60409; C60409. Protachykinin.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 11
FT MOD RES 11 11
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 1 QP 2

RESULT 58
TKN3_PSEGU STANDARD; PRT; 11 AA.
AC P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-III (PG-KIII).
OS Pseudophryne guntheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B60409; E60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 11
FT MOD RES 11 11
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 1 QP 2

RESULT 59
TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guntheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B60409; E60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 11
FT MOD RES 11 11
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 1 QP 2

RESULT 60
TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).

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KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 11
FT MOD RES 11 11
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 1 QP 2

RESULT 59
TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guntheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B60409; E60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 11
FT MOD RES 11 11
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 1 QP 2

RESULT 60
TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).

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OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Skin.
 CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; F60409; F60409.
 DR InterPro; IPR003580; Protachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QP 6
 Db 1 QP 2

RESULT 61
 TKNA_ONCMY
 ID TKNA_ONCMY STANDARD; PRT; 11 AA.
 AC P28459;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; S23308; S23308.
 DR InterPro; IPR003580; Protachykinin.
 DR PIR; IPR002040; Tachykinin.
 PFam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;
 [1]
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 HQ 5
 Db 5 HQ 6

RESULT 62
 TKN_ELEMO STANDARD; PRT; 11 AA.
 ID TKN_ELEMO STANDARD; PRT; 11 AA.
 AC P01293;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musk octopus) (Ozaena moschata), and
 OS Eledone cirrhosa (Curled octopus) (Ozaena cirrhosa).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE
 RA Anastasi A., Erspamer V.;
 RT "The isolation and amino acid sequence of eledoisin, the active
 RT endecapeptide of the posterior salivary glands of Eledone.";
 RL Arch. Biochem. Biophys. 101:56-65(1963).
 CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Skin.
 CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; A01561; EOCC.
 DR PIR; B01561; EOCC.
 DR PDB; 1MXQ; 18-FEB-03.
 DR InterPro; IPR002040; Tachykinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
 KW 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QP 6
 Db 1 QP 2

RESULT 63
 FAR7_PENMO STANDARD; PRT; 12 AA.
 ID FAR7_PENMO STANDARD; PRT; 12 AA.
 AC P83322;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FWRamide-like neuropeptide FLP7 (GYRKPFGSIF-amide).
 OS Penaeus monodon (Pencid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.

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OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivitsuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RL of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 5 PP 6

RESULT 64
FARI CALVO
ID FARI CALVO STANDARD; PRT; 12 AA.
AC P41869;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliMIRFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; E44787.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914ABSA7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 4 QP 5

RESULT 65
FIF1 SARBU
ID FIF1 SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Neb-FIRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14ABSA7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 2 PP 3

RESULT 66
HS9A RAT
ID HS9A RAT STANDARD; PRT; 12 AA.
AC P82935;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver.";
RL Protoplasm 218:54-56(2001).
CC -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR InterPro; IPR001404; Hsp90.
DR PROSITE; PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD RES 4 4 PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT SIMILARITY).
FT MOD RES 6 6 PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT SIMILARITY).
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      6 PP 7
Db      3 PP 4

RESULT 70
BPPI_BOTJA
ID BPPI_BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]
RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72119526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A01253; XAV19B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PP 7
Db     12 PP 13

RESULT 71
BRK_PARID
ID BRK_PARID STANDARD; PRT; 13 AA.
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Waspkinin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T.; Yasuhara T., Nakajima T.;

"Isolation and sequential analysis of peptides on the venom sac of
Parapolybia indica.";
RL Eisei Dobutsu 39:105-111(1988).
CC -!- FUNCTION: Induces smooth muscle contraction.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3DB3ECC867 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PP 7
Db      5 PP 6

RESULT 72
E122_LITRU
ID E122_LITRU STANDARD; PRT; 13 AA.
AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1598 MW; C1808EF3B357322 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QP 6
Db      9 QP 10

RESULT 73
EP65_HUMAN
ID EP65_HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=90004678; PubMed=2507249;
RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins.";
RL Ciba Found. Symp. 145:102-118(1989).

```


CC -!- SURCELLULAR LOCATION: Cytoplasmic.
 DR GO: GO:0005737; C-cytoplasm; NAS.
 KW Glycoprotein.

FT NON TER 1 1
 FT CAROHYD 2 2 O-LINKED (GLCNAC).
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1300 MW; DOB873344C61A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
 ||
 Db 6 QP 7

RESULT 74

LMT4 LOCMT
 ID LMT4 LOCMT STANDARD; PRT; 13 AA.
 AC P41490;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamyotropin 4 (LOM-MT-4).
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamyotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE
 CC STIMULATOR THAN LOM-MT I, II AND III.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR PIR; B61620; B61620.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
 ||
 Db 3 HQ 4

RESULT 75

MPL MICOC
 ID MPL MICOC STANDARD; PRT; 13 AA.
 AC F81532;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE MPL protein (Fragments).
 OS Microplitis ocellatae (Braconid wasp).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
 CC Braconidae; Microgastrinae; Microplitis.
 OX NCBI_TaxID=99573;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Larva;
 RA Takahashi M., Quicke D.L.J.;
 RL Submitted (OCT-1998) to the SWISS-PROT data bank.
 CC -!- TISSUE SPECIFICITY: SALIVARY GLANDS.
 CC -!- DEVELOPMENTAL STAGE: LARVAL.
 FT NON CONS 10 11
 SQ SEQUENCE 13 AA; 1595 MW; OC0786C9DD82777B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
 ||
 Db 7 PP 8

Search completed: November 25, 2003, 19:28:23
 Job time : 3.55399 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 13.1453 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWMHQPP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

- SPTREMBL 23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	3	42.9	9	10	P82429	P82429	nicotiana t
2	3	42.9	9	16	Q935G1	Q935G1	salmonella
3	3	42.9	11	2	Q47569	Q47569	escherichia
4	3	42.9	11	13	Q8UUP1	Q8UUP1	xenopus lae
5	3	42.9	13	5	Q9U5J2	Q9U5J2	trypanosoma
6	3	42.9	13	12	Q67604	Q67604	squash leaf
7	3	42.9	15	10	Q9S8N8	Q9S8N8	hordeum vul
8	3	42.9	16	11	Q9JHB6	Q9JHB6	mus musculus
9	3	42.9	17	3	Q06800	Q06800	saccharomyc
10	3	42.9	17	4	Q14001	Q14001	homo sapien
11	3	42.9	18	11	Q9JIE9	Q9JIE9	mus musculus
12	3	42.9	19	13	Q9PRT0	Q9PRT0	gallus gall
13	3	42.9	19	13	Q9PRN4	Q9PRN4	petromyzon
14	3	42.9	20	16	Q8RGY4	Q8RGY4	fusobacteri
15	2	28.6	7	2	P72081	P72081	nocardia la
16	2	28.6	7	6	Q28742	Q28742	oryctolagus

17	2	28.6	7	8	P92214	P92214	amblyopyrum
18	2	28.6	7	8	P92393	P92393	hordeum vul
19	2	28.6	7	8	P92403	P92403	lophopyrum
20	2	28.6	7	8	P92427	P92427	peridictyon
21	2	28.6	7	8	P92430	P92430	aegilops ta
22	2	28.6	7	8	P92221	P92221	bromus iner
23	2	28.6	7	8	P92425	P92425	pseudoroegn
24	2	28.6	7	8	P92381	P92381	hordeum bra
25	2	28.6	7	8	P92387	P92387	henrardia p
26	2	28.6	7	8	P92210	P92210	agropyron c
27	2	28.6	7	8	P92440	P92440	thinopyrum
28	2	28.6	7	8	P92218	P92218	australopyr
29	2	28.6	7	8	P92390	P92390	heteranthel
30	2	28.6	7	8	P92372	P92372	haynaldia v
31	2	28.6	7	8	P92442	P92442	taeniathecu
32	2	28.6	7	8	P92226	P92226	crithopsis
33	2	28.6	7	8	P92235	P92235	hordeum mar
34	2	28.6	7	8	P92421	P92421	psathyrosta
35	2	28.6	8	4	Q16468	Q16468	homo sapien
36	2	28.6	8	5	P82685	P82685	periplaneta
37	2	28.6	8	5	P82686	P82686	periplaneta
38	2	28.6	8	5	P82687	P82687	periplaneta
39	2	28.6	8	5	P82688	P82688	periplaneta
40	2	28.6	8	5	P82689	P82689	periplaneta
41	2	28.6	8	6	Q9GMH3	Q9GMH3	lagenorhync
42	2	28.6	8	6	Q28666	Q28666	megaptera n
43	2	28.6	8	12	Q9J205	Q9J205	hepatitis c
44	2	28.6	8	12	Q64971	Q64971	alfalfa mos
45	2	28.6	9	2	Q53914	Q53914	streptomyce
46	2	28.6	9	2	Q43960	Q43960	azotobacter
47	2	28.6	9	2	Q91913	Q91913	pseudomonas
48	2	28.6	9	4	Q9UKJ6	Q9UKJ6	homo sapien
49	2	28.6	9	4	Q9UCS8	Q9UCS8	homo sapien
50	2	28.6	9	4	Q15891	Q15891	homo sapien
51	2	28.6	9	4	Q16386	Q16386	homo sapien
52	2	28.6	9	5	Q9TWV0	Q9TWV0	anthopleura
53	2	28.6	9	6	Q9GJV2	Q9GJV2	lagenorhync
54	2	28.6	9	6	Q9TT77	Q9TT77	bos taurus
55	2	28.6	9	6	Q9GJV3	Q9GJV3	lagenorhync
56	2	28.6	9	6	Q9GJV1	Q9GJV1	lagenorhync
57	2	28.6	9	6	Q8WFT4	Q8WFT4	diadema ant
58	2	28.6	9	10	P82440	P82440	nicotiana t
59	2	28.6	9	11	Q08979	Q08979	mus musculus
60	2	28.6	9	12	Q90350	Q90350	hepatitis g
61	2	28.6	9	12	Q71069	Q71069	canine dist
62	2	28.6	9	12	Q92766	Q92766	canine dist
63	2	28.6	9	12	Q71066	Q71066	canine dist
64	2	28.6	9	13	Q9PRJ4	Q9PRJ4	lepisosteus
65	2	28.6	9	13	Q8AYL5	Q8AYL5	carassius a
66	2	28.6	9	13	Q8AUM7	Q8AUM7	carassius a
67	2	28.6	10	2	Q9R5T2	Q9R5T2	acetobacter
68	2	28.6	10	2	P83062	P83062	bacillus ce
69	2	28.6	10	4	Q14096	Q14096	homo sapien
70	2	28.6	10	4	Q15342	Q15342	homo sapien
71	2	28.6	10	4	Q9UCR0	Q9UCR0	homo sapien
72	2	28.6	10	4	Q9UE86	Q9UE86	homo sapien
73	2	28.6	10	8	Q8WFT6	Q8WFT6	diadema ant
74	2	28.6	10	8	Q8WFT5	Q8WFT5	diadema ant
75	2	28.6	10	8	Q8SHA8	Q8SHA8	rhaphioleone
76	2	28.6	10	10	Q8LLJ0	Q8LLJ0	oryza sativ
77	2	28.6	10	10	Q92213	Q92213	aegilops sq
78	2	28.6	10	10	P81898	P81898	prunus dulc
79	2	28.6	10	10	P81899	P81899	prunus dulc
80	2	28.6	10	11	Q91WZ3	Q91WZ3	rattus sp.
81	2	28.6	10	11	Q9QVFO	Q9QVFO	mus sp. pro
82	2	28.6	10	11	Q9QVK7	Q9QVK7	mus sp. nep
83	2	28.6	10	11	Q8VHM9	Q8VHM9	mus musculus
84	2	28.6	10	11	Q9QV89	Q9QV89	mus sp. pro
85	2	28.6	10	11	Q8CJEO	Q8CJEO	rattus norv
86	2	28.6	10	12	Q9Q0W9	Q9Q0W9	polyomaviru
87	2	28.6	10	12	Q8JV70	Q8JV70	polyomaviru
88	2	28.6	10	12	Q9Q0W1	Q9Q0W1	polyomaviru
89	2	28.6	10	12	Q8JV68	Q8JV68	polyomaviru

90 2 28.6 10 12 090348 hepatitis g
 91 2 28.6 10 12 09QOV9
 92 2 28.6 10 12 08JW84
 93 2 28.6 10 12 08JW84
 94 2 28.6 10 12 08JW66
 95 2 28.6 10 12 08JW66
 96 2 28.6 10 12 08JW66
 97 2 28.6 10 12 08JW66
 98 2 28.6 10 12 08JW66
 99 2 28.6 10 12 08JW66
 100 2 28.6 10 12 08JW66

ALIGNMENTS

RESULT 1
 P82429 PRELIMINARY; PRT; 9 AA.
 ID P82429
 AC P82429
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DE 44 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PRTIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture";
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON TER
 SQ SEQUENCE 9 AA; 986 MW; C22CCACAC6C77776 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 DB 2 QPP 4

RESULT 2
 Q935G1 PRELIMINARY; PRT; 9 AA.
 ID Q935G1
 AC Q935G1
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Putative membrane protein (Fragment).
 GN HCM1.01C.
 OS Salmonella typhi.
 OG Plasmid pHCMI.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Comerton P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jageis K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar typhi CT18";
 RL Nature 413:848-852(2001).
 DR EMBL; AL513383; CAD09867.1; -.
 KW Plasmid; Complete proteome.
 FT NON TER
 SQ SEQUENCE 9 AA; 904 MW; 5FCDCC77776D86767 CRC64;

Query Match 42.9%; Score 3; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 DB 5 QPP 7

RESULT 3
 Q47569 PRELIMINARY; PRT; 11 AA.
 ID Q47569
 AC Q47569
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE Hypothetical 1.3 kDa protein (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=94162733; PubMed=7764507;
 RX Yamada M., Yanai S., Talkuder A.;
 RT "Analysis of products of the Escherichia coli genomic genes and
 RT regulation of their expressions: an applicable procedure for genomic
 RT analysis of other microorganisms";
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
 DR EMBL; D21156; BAA04692.1; -.
 KW Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 11 AA; 1322 MW; C088E40E37672732 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
 DB 1 MHQ 3

RESULT 4
 Q8UUP1 PRELIMINARY; PRT; 11 AA.
 ID Q8UUP1
 AC Q8UUP1
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Beta-Trip protein (Fragment).
 GN BETA-TRCP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Carnevali F.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ballarino M.;
 RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis";
 RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.
 DR EMBL; AJ28930; CAD21927.1; -.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 Db |||
 9 QPP 11

RESULT 5
 Q9U5J2 PRELIMINARY; PRT; 13 AA.
 AC Q9U5J2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE GPI-phospholipase C (Fragment).
 GN GPI-PLC.
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ILTar1;
 RA Webb H.D., Gaud A.F., Carrington M.;
 RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally related genes or to genes showing the same developmentally regulated expression";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ250727; CAB60093.1; -.
 DR InterPro: IPR003633; Varsurf_glyc_PPLC.
 DR Pfam: PF03490; Varsurf_PPLC; 1.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1541 MW; 535AA96B464CA373 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3
 Db |||
 11 SWM 13

RESULT 6
 Q67604 PRELIMINARY; PRT; 13 AA.
 AC Q67604
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Movement protein (Fragment).
 GN BCL1.
 OS Squash leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Los Mochis 1;
 RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;

RT "Diversity among geminiviruses associated with vegetables from Valle del Fuerte, Sinaloa, Mexico.";
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L27273; AAA47820.1; -.
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1376 MW; D471DB4D634E76C2 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 Db |||
 7 QPP 9

RESULT 7
 Q9S8N8 PRELIMINARY; PRT; 15 AA.
 AC Q9S8N8
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Protein E-22 (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94170739; PubMed=8125056;
 RA Flengsrud R.;
 RT "Separation of acidic barley endosperm proteins by two-dimensional electrophoresis";
 RL Electrophoresis 14:1060-1066(1993).
 SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
 Db |||
 4 QPP 6

RESULT 8
 Q9JHB6 PRELIMINARY; PRT; 16 AA.
 AC Q9JHB6
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Meprin 1 beta (Fragment).
 GN MEPIB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Dietrich J.M., Jiang W., Bond J.S.;
 RA Dietrich J.M., Jiang W., Bond J.S.;
 RT "A novel meprin beta' mRNA in mouse embryonal and human colon carcinoma cells";
 RL J. Biol. Chem. 271:2271-2278(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jiang W., Kumar J.M., Bond J.S.;
 RT "Structure of the mouse metalloprotease meprin beta gene (Mep1b): alternative splicing in cancer cells.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AF160982; AAF0401.1; --
 DR MGI; MGI:96964; Mep1b.
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1979 MW; EB9785A3F6189622 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
 Db 5 HQP 7

RESULT 9

Q06800 PRELIMINARY; PRT; 17 AA.

ID Q06800;
 AC Q06800;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE N1780.
 GN N1780.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 ON NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=96287653; PubMed=866380;
 RA Naar F., Becam A.M., Herbert C.J.;
 RT "The sequence of 36.8 kb from the left arm of chromosome XIV reveals
 RT 24 complete open reading frames: 18 correspond to new genes, one of
 RT which encodes a protein similar to the human myotonic dystrophy
 RT kinase."
 RL Yeast 12:169-175(1996).
 DR EMBL; X92517; CAA63292.1; --
 SQ SEQUENCE 17 AA; 2139 MW; BD7B9AFAFAD7F54AF CRC64;

Query Match 42.9%; Score 3; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
 Db 1 MHQ 3

RESULT 10

Q14001 PRELIMINARY; PRT; 17 AA.

ID Q14001;
 AC Q14001;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cyclic nucleotide phosphodiesterase (Fragment).
 GN CGPDE1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=97079687; PubMed=89213398;
 RA Loebner R.W., Winterpacht A., Seipel B., Zabel B.U.;
 RT "Molecular cloning and chromosomal assignment of the human homologue
 RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
 RT in fat metabolism located at 11p15.1."
 RL Genomics 37:211-218(1996).
 DR EMBL; X95522; CAA64776.1; --
 FT NON TER 17
 SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 Db 15 QPP 17

RESULT 11

Q0JIE9 PRELIMINARY; PRT; 18 AA.

AC Q0JIE9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Protein arginine N-methyltransferase 1 (Fragment).
 GN MSMT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20307889; PubMed=10848611;
 RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;
 RT "Arginine N-methyltransferase 1 is required for early postimplantation
 RT mouse development, but cells deficient in the enzyme are viable."
 RL Mol. Cell. Biol. 20:4859-4869(2000).
 DR EMBL; AF232718; AAF37294.1; --
 KW Methyltransferase; Transferase.
 FT NON TER 1
 FT NON TER 18
 SQ SEQUENCE 18 AA; 1931 MW; 392E2C312C4A8372 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
 Db 13 QPP 15

RESULT 12

Q0PRT0 PRELIMINARY; PRT; 19 AA.

AC Q0PRT0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE 23A7 antigen (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=95332492; PubMed=7608337;
 RA Denburg J.L., Caldwell R.T., Warner J.M.;
 RT "Developmental changes in epitope accessibility as an indicator of
 RT multiple states of an immunoglobulin-like neural cell adhesion
 RT molecule."
 RL J. Comp. Neurol. 354:533-550(1995).

SQ SEQUENCE 19 AA; 2051 MW; 83B67BEE484EBD03 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7

```
Db 15 QPP 17
||||
RESULT 13
Q9PRN4 PRELIMINARY; PRT; 19 AA.
ID Q9PRN4
AC Q9PRN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Melanotropin MSH-A.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 14 QPP 16
||||
RESULT 14
Q8RGY4 PRELIMINARY; PRT; 20 AA.
ID Q8RGY4
AC Q8RGY4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein FN0141.
GN FN0141.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21886394; PubMed=11889109;
RC STRAIN=ATCC 25586;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fongstein M., Kyriades N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010528; AAL94347.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 20 AA; 2542 MW; 15BD7516B34C2A14 CRC64;

Query Match 42.9%; Score 3; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 12 QPP 14
||||
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RESULT 15
P72081 PRELIMINARY; PRT; 7 AA.
ID P72081
AC P72081;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-FEB-2001 (TrEMBLrel. 19, Last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN CEFF.
OS Nocardia lactamurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411;
RA Coque J., Perez-Liarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactamurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
RL O-carbamoyltransferase for cephamycin biosynthesis.";
RL Gene 162:21-27(1995).
DR EMBL; Z21682; CAA79797.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 745 MW; 75A1B2CDD1E681C0 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
|||
Db 2 MH 3
||||
RESULT 16
Q28742 PRELIMINARY; PRT; 7 AA.
ID Q28742
AC Q28742;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hau H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
|||
Db 3 MH 4
||||
RESULT 17
P92214 PRELIMINARY; PRT; 7 AA.
ID P92214
AC P92214;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
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DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Amblyopyrum muticum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5572; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77756; CAB01346.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1
      SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match      28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

RESULT 18
P92393
ID P92393 PRELIMINARY; PRT; 7 AA.
AC P92393;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H3139; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77764; CAB01370.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1
      SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match      28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

RESULT 19
P92403
ID P92403 PRELIMINARY; PRT; 7 AA.
AC P92403;

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DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Lophopyrum.
OX NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6692; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77743; CAB01307.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1
      SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match      28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

RESULT 20
P92427
ID P92427 PRELIMINARY; PRT; 7 AA.
AC P92427;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein (Fragment).
GN RPS11.
OS Peridictyon sanctum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77749; CAB01325.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1
      SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match      28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

RESULT 21
P92430
ID P92430 PRELIMINARY; PRT; 7 AA.

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AC P92430;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01352.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 22
P92221
ID P92221 PRELIMINARY; PRT; 7 AA.
AC P92221;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromaeae; Bromus.
OX NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 23
P92425
ID P92425 PRELIMINARY; PRT; 7 AA.
AC P92425;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 24
P92381
ID P92381 PRELIMINARY; PRT; 7 AA.
AC P92381;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01361.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 25
P92425

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P92387
ID P92387 PRELIMINARY; PRT; 7 AA.
AC P92387;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
Db 1 pp 2

RESULT 26
P92210
ID P92210 PRELIMINARY; PRT; 7 AA.
AC P92210;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01391.1; -.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
Db 1 pp 2

P92440
ID P92440 PRELIMINARY; PRT; 7 AA.
AC P92440;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Thinopyrum bessarabicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6725; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77769; CAB01385.1; -.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
Db 1 pp 2

RESULT 28
P92218
ID P92218 PRELIMINARY; PRT; 7 AA.
AC P92218;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Australopyrum retrofractum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Australopyrum.
OX NCBI_TaxID=4597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6723; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77767; CAB01379.1; -.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7
Db 1 pp 2

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RESULT 29
P92390 PRELIMINARY; PRT; 7 AA.
ID P92390
AC P92390;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Heteranthelium pilliferum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Heteranthelium.
OX NCBI_TaxID=37679;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H5557; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RX Petersen G., Seberg O.;
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01328.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

RESULT 30
P92372 PRELIMINARY; PRT; 7 AA.
ID P92372
AC P92372;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Haynaldia villosa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD Clade; Panicoideae; Andropogoneae; Haynaldia.
OX NCBI_TaxID=40247;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H5561; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RX Petersen G., Seberg O.;
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01301.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

RESULT 31
P92442 PRELIMINARY; PRT; 7 AA.
ID P92442
AC P92442;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Taeniatherum caput-medusae (Medusahead).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Taeniatherum.
OX NCBI_TaxID=37687;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H10254; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RX Petersen G., Seberg O.;
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01358.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

RESULT 32
P92226 PRELIMINARY; PRT; 7 AA.
ID P92226
AC P92226;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Crithopsis delileana.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Crithopsis.
OX NCBI_TaxID=37674;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H5558; TISSUE=Leaf;
RC MEDLINE=97271648; PubMed=9126564;
RX Petersen G., Seberg O.;
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77751; CAB01331.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 1 PP 2

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Db          1 PP 2

RESULT 33
P92385
ID P92385 PRELIMINARY; PRT; 7 AA.
AC P92385; P92383;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum marinum (Seaside barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4519;
RN [1]_TaxID=4519;
SEQUENCE FROM N.A.
RP STRAIN=H299, and H801; TISSUE=Leaf;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77763; CAB01367.1; -
DR EMBL; Z77762; CAB01364.1; -
DR Chloroplast; Ribosomal protein.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 34
P92421
ID P92421 PRELIMINARY; PRT; 7 AA.
AC P92421; P92419;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Psathyrostachys fragilis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=37729;
RN [1]_TaxID=37729;
SEQUENCE FROM N.A.
RP STRAIN=H4372, and H917; TISSUE=Leaf;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77753; CAB01337.1; -
DR EMBL; Z77752; CAB01334.1; -
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 35
Q16468
ID Q16468 PRELIMINARY; PRT; 8 AA.
AC Q16468;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE DNA for cosmid cCl3-1134 PCR primer 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
SEQUENCE FROM N.A.
RP MEDLINE=96435920; PubMed=8938806;
RA James I.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
RA Anand R.;
RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
RT ESTs including 3 members of the Cystatin gene family and
RT identification of CpG islands.";
RL Genomics 32:425-430(1996).
DR EMBL; X88976; CAA61407.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 925 MW; FD5411A7376871E6 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
DB 1 MH 2

RESULT 36
P82685
ID P82685 PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Kinin-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_TaxID=6978;
SEQUENCE AND FUNCTION.
RP TISSUE=CORPORA CARDIACA;
RC MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
DB 6 SW 7

RESULT 37

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P82686
ID P82686 PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Kinin-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_TaxID=6978;
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db |||
6 SW 7

RESULT 38
P82687
ID P82687 PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Kinin-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_TaxID=6978;
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db |||
6 SW 7

P82688
ID P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Kinin-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_TaxID=6978;
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DDD8 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db |||
6 SW 7

RESULT 40
P82689
ID P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Kinin-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_TaxID=6978;
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 865 MW; C76365B449CDC775 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db |||
6 SW 7

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Qy 1 SW 2
Db 6 SW 7

RESULT 41
Q9GMH3 PRELIMINARY; PRT; 8 AA.
AC Q9GMH3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus obscurus (Dusky dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=27611;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140833; AAF98686.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 962 MW; 5BD1F417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 7 HQ 8

RESULT 42
Q28866 PRELIMINARY; PRT; 8 AA.
AC Q28866;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE Actin protein (Fragment).
GN ACTIN.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaeopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RA Palumbi S.R., Baker C.S.;
RX MEDLINE=94285813; PubMed=7912407;
RT "Contrasting population structure from nuclear intron sequences and
RT mtDNA of humpback whales.";
RL Mol. Biol. Evol. 11:426-435(1994).
DR EMBL; S73467; AAD14118.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 906 MW; 69C866D1F4177408 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 5 HQ 6

RESULT 43

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Q9J205 PRELIMINARY; PRT; 8 AA.
AC Q9J205;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Truncated polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Fan X., DiBisceglie A.M.;
RT "Identification of liver-specific quasiespecies of the hepatitis C
RT virus in chronically infected patients.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF211054; AAF30114.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; BID41AFAF7776DCA CRC64;

Query Match 28.6%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 3 PP 4

RESULT 44
Q64971 PRELIMINARY; PRT; 8 AA.
AC Q64971;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Putative ORF (Fragment).
OS Alfalfa mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Alfamovirus.
OX NCBI_TaxID=12321;
RN [1]
RP SEQUENCE FROM N.A.
RA Koper-Zwarthoff E.C., Brederode F.T.M., Veeneman G., van Boom J.H.,
RA Bol J.F.;
RT "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus
RT RNAs and the intercistronic function in RNA 3'.";
RL Nucleic Acids Res. 8:5635-5647(1980).
DR EMBL; V00047; CAA23416.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 69D40B0775A365B8 CRC64;

Query Match 28.6%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
Db 2 SW 3

RESULT 45
Q53914 PRELIMINARY; PRT; 9 AA.
AC Q53914;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Curd protein (Fragment).

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OS Streptomyces cyaneus (Streptomyces curacoi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1904;
RN [1]
RP SEQUENCE FROM N.A.
RA Bergh S.T., Uhlen M.;
RT "Cloning, analysis and heterologous expression of the polyketides
RT synthesis genes of Streptomyces curacoi.";
RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; M33704; AAA26724.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1027 MW; 995BDDDDC4140AB1 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 8 QP 9

RESULT 46
Q43960
ID Q43960 PRELIMINARY; PRT; 9 AA.
AC Q43960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hydrogenase-related protein (Fragment).
GN HUPA.
OS Azorobacter chroococcum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=353;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCD1;
RX MEDLINE=9505698; PubMed=7966281;
RA Du L., Tibelius K.H., Souza E.M., Garg R.P., Yates M.G.;
RT "Sequences, organization and analysis of the hupZMNQORV genes from
RT the Azorobacter chroococcum hydrogenase gene cluster.";
RL J. Mol. Biol. 243:549-557(1994).
DR EMBL; L25315; AAA64455.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1004 MW; EF421DD045B69B11 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
Db 1 MH 2

RESULT 47
Q99193
ID Q99193 PRELIMINARY; PRT; 9 AA.
AC Q99193;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RpoB beta-subunit of RNA polymerase (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RA Borodin A.M., Danilkevich A.V., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;

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RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of
RT RNA polymerase in Pseudomonas putida.";
RL Dokl. Biochem. 302:1261-1265(1988).
DR EMBL; X15849; CAA33847.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 852 MW; 5B4167776DC76727 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 6 PP 7

RESULT 48
Q9UKJ6
ID Q9UKJ6 PRELIMINARY; PRT; 9 AA.
AC Q9UKJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Androgen receptor (Fragment).
GN AR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Li X.Q., Wu Q.F.;
RT "A splice-site mutation in Androgen Receptor gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159087; AAF04001.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1272 MW; 6F2B8415B331B684 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
Db 3 MH 4

RESULT 49
Q9UCS8
ID Q9UCS8 PRELIMINARY; PRT; 9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075698; PubMed=1742316;
RA Enholm C., Bozas S.E., Tenkanen H., Kirszenbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I.";
RL Biochim. Biophys. Acta 1086:255-260(1991).
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

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Query Match 28.6%; Score 2; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
 Db 3 PP 4

RESULT 50
 ID Q15891 PRELIMINARY; PRT; 9 AA.
 AC Q15891
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE (Clone XP2E8) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN TISSUE=Placenta;
 RC SEQUENCE FROM N.A.
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-X.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32131; AAA73881.1; -.
 FT NON TER 1 1
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1030 MW; E56635A1A33686D1 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
 Db 2 HQ 3

RESULT 51
 ID Q16386 PRELIMINARY; PRT; 9 AA.
 AC Q16386;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mex40 protein (Fragment).
 GN MEX40.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95400293; PubMed=7670464;
 RA Budarf M.L., Collins J., Gong W., Roe B., Wang Z., Bailey L.C.,
 RA Sellinger B., Michaud D., Driscoll D.A., Emanuel B.S.;
 RT "Cloning a balanced translocation associated with DiGeorge syndrome
 RT and identification of a disrupted candidate gene."
 RL Nat. Genet. 10:269-278(1995).
 DR EMBL; S79485; AAD14301.1; -.
 FT NON TER 1 1
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1137 MW; 734911A69446837B CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WM 3
 Db 3 WM 4

RESULT 52
 ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
 AC Q9TWV0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Antho-RPAMIDE-NEUROPEPTIDE.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nyantheae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Gimmelikhuijzen C.J.;
 RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
 RT an N-terminally protected, biologically active neuropeptide from sea
 RT anemones."
 RL Peptides 13:851-857(1992).
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
 Db 2 PP 3

RESULT 53
 ID Q9GJV2 PRELIMINARY; PRT; 9 AA.
 AC Q9GJV2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Actin (Fragment).
 OS Lagenorhynchus obliquidens (Pacific white-sided dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Lagenorhynchus
 OX NCBI_TaxID=90247;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hare M.P., Cipriano F., Palumbi S.R.;
 RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
 RT Speciation, Systematics and Conservation."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF140831; AAF98684.1; -.
 DR EMBL; AF140826; AAF98679.1; -.
 DR EMBL; AF140827; AAF98680.1; -.
 DR EMBL; AF140828; AAF98681.1; -.
 DR EMBL; AF140829; AAF98682.1; -.
 DR EMBL; AF140830; AAF98683.1; -.
 FT NON TER 1 1
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
 Db 8 HQ 9

RESULT 54

Q9TT77

ID Q9TT77 PRELIMINARY; PRT; 9 AA.
 AC Q9TT77;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Wilm's tumor protein 1 (Fragment).
 GN WIL.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=21015404; PubMed=11130975;

RA Brouillette J.A., Andrew J.R., Venta P.J.;

RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence method";

RL Mamm. Genome 11:1079-1086(2000).

DR EMBL; AF202074; AAF20919.1; -.

FT NON_TER 1 1

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1231 MW; 58DDF41416D1F403 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 6; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5

Db 4 HQ 5

RESULT 55

Q9GJV3

ID Q9GJV3 PRELIMINARY; PRT; 9 AA.
 AC Q9GJV3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Actin (Fragment).
 OS Lagenorhynchus obscurus (Dusky dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Lagenorhynchus.
 OX NCBI_TaxID=27611;
 RN [1]

SEQUENCE FROM N.A.

RA Hare M.P., Cipriano F., Palumbi S.R.;

RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for Speciation, Systematics and Conservation";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF140834; AAF98687.1; -.

DR EMBL; AF140832; AAF98685.1; -.

FT NON_TER 1 1

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 6; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5

Db 8 HQ 9

RESULT 56

Q9GJV1

ID Q9GJV1 PRELIMINARY; PRT; 9 AA.
 AC Q9GJV1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Actin (Fragment).
 OS Lagenorhynchus acutus (Atlantic white-sided dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Lagenorhynchus.
 OX NCBI_TaxID=90246;
 RN [1]

SEQUENCE FROM N.A.

RA Hare M.P., Cipriano F., Palumbi S.R.;

RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for Speciation, Systematics and Conservation";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF140834; AAF98687.1; -.

DR EMBL; AF140832; AAF98685.1; -.

FT NON_TER 1 1

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 6; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5

Db 8 HQ 9

ID Q9GJV1 PRELIMINARY; PRT; 9 AA.
 AC Q9GJV1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Actin (Fragment).
 OS Lagenorhynchus acutus (Atlantic white-sided dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Lagenorhynchus.
 OX NCBI_TaxID=90246;
 RN [1]

SEQUENCE FROM N.A.

RA Hare M.P., Cipriano F., Palumbi S.R.;

RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for Speciation, Systematics and Conservation";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF140825; AAF98678.1; -.

DR EMBL; AF140822; AAF98675.1; -.

DR EMBL; AF140823; AAF98676.1; -.

DR EMBL; AF140824; AAF98677.1; -.

FT NON_TER 1 1

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 6; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5

Db 8 HQ 9

RESULT 57

Q8WFT4

ID Q8WFT4 PRELIMINARY; PRT; 9 AA.
 AC Q8WFT4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit II (Fragment).
 GN COII.
 OS Diadema antillarum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Diademataceae; Diadematoidea; Diadematiidae;
 OC Diadema.
 OX NCBI_TaxID=105358;
 RN [1]

SEQUENCE FROM N.A.

RA STRAIN=DCA3;

RX MEDLINE=21323357; PubMed=11430656;

RA Lessios H.A., Kessing B.D., Pearse J.S.;

RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema";

RL Evolution 55:955-975(2001).

RN [2]

SEQUENCE FROM N.A.

RA STRAIN=DCA3;

RX MEDLINE=21323357; PubMed=11430656;

RA Lessios H.A., Kessing B.D., Pearse J.S.;

RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema";

RL Evolution 55:955-975(2001).

RN [2]

SEQUENCE FROM N.A.

RA STRAIN=DCA3;

RX MEDLINE=21323357; PubMed=11430656;

RA Lessios H.A., Kessing B.D., Pearse J.S.;

RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema";

RL Evolution 55:955-975(2001).

RN [2]

SEQUENCE FROM N.A.

RA STRAIN=DCA3;

RX MEDLINE=21323357; PubMed=11430656;

RA Lessios H.A., Kessing B.D., Pearse J.S.;

RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema";

RL Evolution 55:955-975(2001).

RN [2]

SEQUENCE FROM N.A.

RA STRAIN=DCA3;

RX MEDLINE=21323357; PubMed=11430656;

RA Lessios H.A., Kessing B.D., Pearse J.S.;

RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema";

RL Evolution 55:955-975(2001).

RN [2]

SEQUENCE FROM N.A.

RA STRAIN=DCA3;

RX MEDLINE=21323357; PubMed=11430656;

RA Lessios H.A., Kessing B.D., Pearse J.S.;

RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema";

RL Evolution 55:955-975(2001).

RN [2]

Qy 5 QP 6
||
Db 8 QP 9

RESULT 58

ID P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (TREMBlrel. 14, Created)
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 42 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture."
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON TER 9
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5B81B07 CRC64;

Query Match 28.6%; Score 2; DB 10; Length 9;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
||
Db 1 QP 2

RESULT 59

ID O08979 PRELIMINARY; PRT; 9 AA.
AC O08979;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMU1 protein (Fragment).
GN AMU1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Tumor;
RX MEDLINE=97332339; PubMed=9188573;
RA Amtoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AMU1 (core) site enhancer mutations in T-lymphomas
RT induced by attenuated SL3-3 murine leukemia virus mutants."
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match 28.6%; Score 2; DB 11; Length 9;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
||
Db 3 QP 4

RESULT 60

ID O90350 PRELIMINARY; PRT; 9 AA.
AC O90350;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=45255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SG3419;
RX MEDLINE=99266893; PubMed=10335862;
RA Wong S.B.J., Chan S.H., Ren E.C.;
RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:
RT predominance of group 2a and the Asian group 3 variant."
RL J. Med. Virol. 58:145-153(1999).
DR EMBL; AF078065; AAC32371.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 989 MW; D95CA5A5BEB9CDDD CRC64;

Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2
||
Db 8 SW 9

RESULT 61

ID O71069 PRELIMINARY; PRT; 9 AA.
AC O71069;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog EPM;
RA Liermann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026238; AAC09168.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 984 MW; F29CB32760587331 CRC64;

Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MH 4
||
Db 1 MH 2

RESULT 62

O92766
ID O92766 PRELIMINARY; PRT; 9 AA.
AC O92766
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #5526/89;
RA Liermann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026237; AAC09167.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;
Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MH 4
Db 1 MH 2
RESULT 63
O71066
ID O71066 PRELIMINARY; PRT; 9 AA.
AC O71066
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liermann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;
Query Match 28.6%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MH 4
Db 1 MH 2
RESULT 64
Q9PRJ4
ID Q9PRJ4 PRELIMINARY; PRT; 9 AA.
AC Q9PRJ4
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Bradykinin.
OS Lepisosteus osseus (long-nosed gar), and
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus.
OX NCBI_TaxID=34771, 7924;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [TrpS]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar."
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;
Query Match 28.6%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PP 7
Db 2 PP 3
RESULT 65
Q8AYL5
ID Q8AYL5 PRELIMINARY; PRT; 9 AA.
AC Q8AYL5
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT "Promoter characteristics of two Cyp19 genes differentially expressed
RT in the brain and ovary of teleost fish."
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR EMBL; AF324897; AAN32618.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;
Query Match 28.6%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QP 6
Db 7 QP 8
RESULT 66
Q8AUM7
ID Q8AUM7 PRELIMINARY; PRT; 9 AA.
AC Q8AUM7
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Cytochrome P450 aromatase (Fragment).
GN CYP19A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.

OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 in the brain and ovary of teleost fish.";
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324895; AAN32616.1; -.
 DR EMBL; AF324896; AAN32617.1; -.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;
 Query Match 28.6%; Score 2; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QP 6
 Db |||
 7 QP 8
 RESULT 67
 Q9R5T2 PRELIMINARY; PRT; 10 AA.
 ID Q9R5T2
 AC Q9R5T2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
 OS Acetobacter hansenii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Gluconacetobacter.
 OX NCBI_TaxID=436;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92027789; PubMed=1929428;
 RA Levy H.R., Cook C.;
 RT "Purification and properties of NADP-linked glucose-6-phosphate
 dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
 RL Arch. Biochem. Biophys. 291:161-167(1991).
 FT NON TER 1
 FT NON TER 10
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;
 Query Match 28.6%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db |||
 4 PP 5
 RESULT 68
 P83062 PRELIMINARY; PRT; 10 AA.
 ID P83062
 AC P83062
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE 92 kDa protein (fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dows B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON TER 10
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1044 MW; 36E840B73AEB0777 CRC64;
 Query Match 28.6%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db |||
 3 PP 4
 RESULT 69
 Q14096 PRELIMINARY; PRT; 10 AA.
 ID Q14096
 AC Q14096;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CYP2B6 gene cryptic exon 3A of cytochrome P450IIB6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90174922; PubMed=2308828;
 RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
 RT "Alternative splicing in the human cytochrome P450IIB6 gene: use of a
 cryptic exon within intron 3 and splice acceptor site within exon 4.";
 RL Nucleic Acids Res. 18:189-189(1990).
 DR EMBL; X16864; CAA34754.1; -.
 SQ SEQUENCE 10 AA; 885 MW; 4181B9D87DC77767 CRC64;
 Query Match 28.6%; Score 2; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PP 7
 Db |||
 4 PP 5
 RESULT 70
 Q15342 PRELIMINARY; PRT; 10 AA.
 ID Q15342
 AC Q15342;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Aml1 protein (fragment).
 GN AML1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9626397; PubMed=8634147;
 RA Levanon D., Bernstein Y., Negraru V., Ghozi M.C., Bar-Am I.,
 RA Aloya R., Goldenberg D., Lotem J., Groner Y.;
 RT "A large variety of alternatively spliced and differentially expressed
 mRNAs are encoded by the human acute myeloid leukemia gene AML1.";
 RL DNA Cell Biol. 15:175-185(1996).
 DR EMBL; X90978; CAA62465.1; -.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1254 MW; 8D99287B441AF365 CRC64;
 Query Match 28.6%; Score 2; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SW 2
 Db |||
 3 SW 4

RESULT 71

Q9UCR0 PRELIMINARY; PRT; 10 AA.
 AC Q9UCR0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE AUTOTAXIN (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE 10 AA; 1193 MW; 3E01FB40544B19D7 CRC64;
 RX MEDLINE=92129337; PubMed=1733949;
 RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
 RA Schiffmann B., Liotta L.A.;
 RT "Identification, purification, and partial sequence analysis of
 RT autotaxin, a novel motility-stimulating protein.";
 RL J. Biol. Chem. 267:2524-2529(1992).
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1193 MW; 3E01FB40544B19D7 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7

Db 2 PP 3

RESULT 72

Q9UE86 PRELIMINARY; PRT; 10 AA.
 AC Q9UE86;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Collagen alpha 1(I) chain (Fragment).
 GN COL1A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92042176; PubMed=1939261;
 RA Hawkins J.R., Supertti-Furga A., Steinmann B., Dalgleish R.;
 RT "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis
 RT imperfecta.";
 RL J. Biol. Chem. 266:22370-22374(1991).
 DR EMBL; S66556; AAB20361.1; --
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 777 MW; 2D20F6D867DD867 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7

Db 2 PP 3

RESULT 73

Q8WFT6 PRELIMINARY; PRT; 10 AA.
 AC Q8WFT6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit II (Fragment).
 GN COII.
 OS Diadema antillarum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
 OC Diadema.
 OX NCBI_TaxID=105358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DCA1;
 RX MEDLINE=21323357; PubMed=11430656;
 RA Lessios H.A., Kessing B.D., Pearse J.S.;
 RT "Population structure and speciation in tropical seas: global
 RT phylogeography of the sea urchin *Diadema*.";
 RL Evolution 55:955-975(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DCA1;
 RX MEDLINE=21561594; PubMed=11703875;
 RA Lessios H.A., Garrido M.J., Kessing B.D.;
 RT "Demographic history of *Diadema antillarum*, a keystone herbivore on
 RT Caribbean reefs.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
 DR EMBL; AY012856; AAL33830.2; --
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1301 MW; EDBB101B173B46CA CRC64;

Query Match 28.6%; Score 2; DB 8; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6

Db 9 QP 10

RESULT 74

Q8WFT5 PRELIMINARY; PRT; 10 AA.
 AC Q8WFT5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit II (Fragment).
 GN COII.
 OS Diadema antillarum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
 OC Diadema.
 OX NCBI_TaxID=105358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DCA2;
 RX MEDLINE=21323357; PubMed=11430656;
 RA Lessios H.A., Kessing B.D., Pearse J.S.;
 RT "Population structure and speciation in tropical seas: global
 RT phylogeography of the sea urchin *Diadema*.";
 RL Evolution 55:955-975(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DCA2;
 RX MEDLINE=21561594; PubMed=11703875;
 RA Lessios H.A., Garrido M.J., Kessing B.D.;
 RT "Demographic history of *Diadema antillarum*, a keystone herbivore on
 RT Caribbean reefs.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
 DR EMBL; AY012857; AAL33831.2; --
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 1

SQ SEQUENCE 10 AA; 1262 MW; COBB101B173B46DD CRC64;
Query Match 28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 9 QP 10

RESULT 75
Q8SHA8
ID O8SHA8 PRELIMINARY; PRT; 10 AA.
AC O8SHA8;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Rhampholeon spectrum.
OS Rhampholeon.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaleonidae;
OC Rhampholeon.
OX NCBI_TaxID=179929;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448772; AAL90598.1; -
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1279 MW; 35BF8E27336409D7 CRC64;
Query Match 28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 2 QP 3

Search completed: November 25, 2003, 19:34:03
Job time : 14.1453 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 17.8663 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWMHQPP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :			
A Genesecp 19Jun03:*			
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2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*		
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*		
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*		
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7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*		
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*		
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*		
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*		
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*		
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*		
13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*		
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*		
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*		
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18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*		
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*		
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*		
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*		
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*		
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*		
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SUMMARIES			
Result No.	Score	Query Match Length	ID Description
1	7	100.0	7 22 AAB72269 Colostrinin derive
2	7	100.0	7 22 AAB72522 Colostrinin peptid
3	7	100.0	7 22 AAB72554 Colostrinin peptid
4	7	100.0	7 22 AAB59332 Ewe colostrinin pe
5	7	100.0	7 23 AAE20251 Colostrinin consti
6	7	100.0	7 23 AAM51058 Colostrinin consti
7	7	100.0	7 23 AA014600 Neural cell regula
8	6	85.7	19 19 AAM40310 Human ITAK protein
9	5	71.4	15 22 AAB72279 Colostrinin derive

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10	5	71.4	15	22	AAB72531	Colostrinin peptid
11	5	71.4	15	22	AAB72563	Colostrinin peptid
12	5	71.4	15	22	AAB59334	Ewe colostrinin pe
13	5	71.4	15	23	AAB20261	Colostrinin consti
14	5	71.4	15	23	AAM51066	Colostrinin consti
15	5	71.4	15	23	AAO14610	Neural cell regula
16	4	57.1	10	22	AAG78781	Stachybotrys echin
17	4	57.1	11	23	ABG95549	Human novel secret
18	4	57.1	11	23	AAU93631	Granulocyte-colony
19	4	57.1	11	24	ABR00957	Human gene 11-enco
20	4	57.1	11	24	ABP99483	Human secreted pro
21	4	57.1	12	21	AAB28056	Human secreted pro
22	4	57.1	14	21	AAI92771	Oligopeptide mimot
23	4	57.1	17	23	AAU88216	Insulin/insulin-li
24	4	57.1	17	23	AAU90013	Insulin/insulin-li
25	4	57.1	20	22	ABBS0820	Human secreted pro
26	3	42.9	5	12	ABR12685	Pentapeptide paral
27	3	42.9	5	13	AAR27038	Consensus heavy ch
28	3	42.9	5	15	AAR51549	Mimotope peptide #
29	3	42.9	5	16	AAR69917	Pentameric mimotop
30	3	42.9	5	16	AAR74929	H-CDR-1 of anti-id
31	3	42.9	5	17	AAR98663	Peptide 43 from 88
32	3	42.9	5	19	AAW39866	Heavy chain CDR1 o
33	3	42.9	5	19	AAW44181	Monoclonal antibod
34	3	42.9	5	20	AAI48891	Membrane dipeptida
35	3	42.9	5	21	AAB21923	Human prostate-rec
36	3	42.9	5	21	AAB19754	Erythropoietin rec
37	3	42.9	5	21	AAB12174	Human CDR1 for II-
38	3	42.9	5	21	AAI92158	Murine 15B8 heavy
39	3	42.9	5	21	AAV80139	Chimeric anti-CD25
40	3	42.9	5	22	AAO14422	CD25 binding prote
41	3	42.9	5	22	AAG63123	Amino acid sequenc
42	3	42.9	5	22	AAE06499	Mouse prostate hom
43	3	42.9	5	23	AAB71236	Murine IgG1 catabo
44	3	42.9	5	23	AAU6924	Immunoglobulin cat
45	3	42.9	5	23	AAU11183	Mouse antibody Act
46	3	42.9	5	24	ABB82654	CDR1 fragment of a
47	3	42.9	6	12	AAI11738	Peptide epitope de
48	3	42.9	6	13	AAR24983	Arg-Arg contg. ant
49	3	42.9	6	15	AAR62181	U1 snRNP 70K prote
50	3	42.9	6	16	AAR73901	Neisseria meningit
51	3	42.9	6	17	AAW08657	Met-enkephalin ana
52	3	42.9	6	20	AAI296333	Phosphoenolpyruvat
53	3	42.9	6	20	AAI36355	Fragment of human
54	3	42.9	6	21	AAB28300	Human secreted pep
55	3	42.9	6	22	AAB72258	Colostrinin derive
56	3	42.9	6	22	AAB72511	Colostrinin peptid
57	3	42.9	6	22	AAB72543	Colostrinin peptid
58	3	42.9	6	22	ABBS9319	Colostrinin peptid
59	3	42.9	6	22	ABBS5512	Ewe colostrinin pe
60	3	42.9	6	23	AAE20240	Human elastase var
61	3	42.9	6	23	AAI51047	Colostrinin consti
62	3	42.9	6	23	AAO14589	Colostrinin consti
63	3	42.9	7	16	AAR77269	Neural cell regula
64	3	42.9	7	16	AAR73902	MRAA-230 tryptic p
65	3	42.9	7	16	AAR73883	Streptococcus pneu
66	3	42.9	7	16	AAR73897	Rubella virus glyco
67	3	42.9	7	16	AAR73879	Rubella virus glyco
68	3	42.9	7	19	AAV20876	Rubella virus stra
69	3	42.9	7	19	AAW61049	Human prenenilin I
70	3	42.9	7	20	AAI16906	Peptide from mouse
71	3	42.9	7	21	AAI16495	Heat shock protein
72	3	42.9	7	21	AAI17249	Linear peptide tha
73	3	42.9	7	21	AAI92768	SH3 antagonist pep
74	3	42.9	7	22	AAU72048	Heptapeptide mimot
75	3	42.9	7	22	AAW43873	Melanoma antigen
76	3	42.9	7	22	AAW43878	H11 binding site c
77	3	42.9	7	22	AAW44029	H11 binding site c
78	3	42.9	7	22	AAW44034	H11 binding site c
79	3	42.9	7	22	AAW44039	H11 binding site c
80	3	42.9	7	22	AAW44044	H11 binding site c
81	3	42.9	7	22	AAW44054	H11 binding site c
82	3	42.9	7	22	AAW44324	H11 binding site c

83 3 42.9 7 22 AAM44329 H11 binding site c
84 3 42.9 7 22 AAM45562 H11 binding site c
85 3 42.9 7 22 AAM45567 H11 binding site c
86 3 42.9 7 22 AAM45582 H11 binding site c
87 3 42.9 7 22 AAM45587 H11 binding site c
88 3 42.9 7 22 AAM46619 H11 binding site c
89 3 42.9 7 22 AAM46624 H11 binding site c
90 3 42.9 7 22 AAM46639 H11 binding site c
91 3 42.9 7 22 AAM46644 H11 binding site c
92 3 42.9 7 22 AAM46649 H11 binding site c
93 3 42.9 7 22 AAM46654 H11 binding site c
94 3 42.9 7 22 AAM46659 H11 binding site c
95 3 42.9 7 22 AAM46664 H11 binding site c
96 3 42.9 7 22 AAM46669 H11 binding site c
97 3 42.9 7 22 AAM46674 H11 binding site c
98 3 42.9 7 22 AAM46679 H11 binding site c
99 3 42.9 7 22 AAM46684 H11 binding site c
100 3 42.9 7 22 AAM46689 H11 binding site c

ALIGNMENTS

RESULT 1

AAB72269
ID AAB72269 standard; peptide; 7 AA.

XX
AC AAB72269;

XX
DT 14-MAY-2001 (first entry)

XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 24.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX
OS Synthetic.

XX
FN WO20011937-A2.

XX
PD 22-FEB-2001.

XX
PF 17-AUG-2000; 200WO-US22818.

XX
PR 17-AUG-1999; 99US-0149311.

XX
PA (TEXA) UNIV TEXAS SYSTEM.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.

XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX
DR WPI; 2001-202804/20.

XX
PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -

XX
PS Claim 1; Page 34; 50pp; English.

XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWMHQPP 7
|||||

Db 1 SWMHQPP 7
|||||

RESULT 2

AAB72522
ID AAB72522 standard; Peptide; 7 AA.

XX
AC AAB72522;

XX
DT 09-MAY-2001 (first entry)

XX
DE Colostrinin peptide #23.

XX
KW Dermatological; oxidative stress regulator; colostrinin.

XX
OS Unidentified.

XX
FN WO200112650-A2.

XX
PD 22-FEB-2001.

XX
PF 17-AUG-2000; 200WO-US22665.

XX
PR 17-AUG-1999; 99US-0149310.

XX
PA (TEXA) UNIV TEXAS SYSTEM.

XX
PI Stanton GJ, Hughes TK, Boldogh I;

XX
DR WPI; 2001-218342/22.

XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -

XX
PS Claim 6; Page 26; 48pp; English.

XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWMHQPP 7
|||||

Db 1 SWMHQPP 7
|||||

RESULT 3

AAB72554
ID AAB72554 standard; Peptide; 7 AA.

XX
AC AAB72554;

XX
DT 09-MAY-2001 (first entry)

XX

```

DE Colostrinin peptide #23.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW Colostrum.
XX Unidentified.
OS
XX WO200112651-A2.
PN
XX 22-FEB-2001.
PD
XX 17-AUG-2000; 2000WO-US22774.
PF
XX 17-AUG-1999; 99US-0149633.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Boldogh I;
PI
XX WPI; 2001-226545/23.
DR
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
PT
XX Claim 6; Page 21; 35pp; English.
PS
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7
DB |||||
1 SWMHQPP 7

RESULT 4
ARB59332
ID AAB59332 standard; Peptide; 7 AA.
XX
AC AAB59332;
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment C-7.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
OS
XX WO200075173-A2.
PN
XX 14-DEC-2000.
PD
XX 02-JUN-2000; 2000WO-GB02128.
PF
XX 02-JUN-1999; 99GB-0012852.
PR
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
PI
XX WPI; 2001-071058/08.
DR
XX Peptides having an N-terminal amino acid sequence isolated from
PT

PT Colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7
DB |||||
1 SWMHQPP 7

RESULT 5
AAE20251
ID AAE20251 standard; peptide; 7 AA.
XX
AC AAE20251;
XX
DT 18-JUN-2002 (first entry)
XX
XX Colostrinin constituent peptide #23.
DE
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FT Modified-site 7
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
PN
XX 21-FEB-2002.
PD
XX 17-AUG-2000; 2000WO-US22776.
PF
XX 17-AUG-2000; 2000WO-US22776.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Stanton GJ, Hughes TK, Boldogh I;
PI
XX WPI; 2002-269151/31.
PD
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
PS
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

```


CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7
 |||||
 Db 1 SWMHQPP 7

RESULT 6

AA051058
 ID AAM51058 standard; Peptide; 7 AA.

AC AAM51058;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide (casein amino acids 157-163).

DE Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 157-163. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7
 |||||
 Db 1 SWMHQPP 7

RESULT 7

AA014600

ID AAO14600 standard; peptide; 7 AA.

AC AAO14600;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 23.

DE Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

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CC the method of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7
   |||||
Db 1 SWMHQPP 7

RESULT 8
AAW40310
ID AAW40310 standard; Protein; 19 AA.
XX
AC AAW40310;
XX
DT 23-JUN-1998 (first entry)
XX
DE Human ITAK protein peptide substrate.
XX
KW Interleukin-1/tumour necrosis factor activated kinase; ITAK; inhibitor;
KW cytokine mediated inflammation; antagonist; disorder; therapy.
XX
OS Synthetic.
XX
PN WO9747750-A1.
XX
PD 18-DEC-1997.
XX
PF 09-JUN-1997; 97WO-US08516.
XX
PR 10-JUN-1996; 96US-0633414.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Anderson DM, Bird TA, Sims JE, Virca G;
XX
DR WPI; 1998-052314/05.
XX
PT Nucleic acid encoding interleukin-1/tumour necrosis factor activated
PT kinase - used to identify specific antagonists for treatment of
PT cytokine-mediated inflammation
XX
PS Claim 20; Page 33; 80pp; English.
XX
CC This sequence represents a peptide substrate used to assay a novel
CC interleukin-1/tumour necrosis factor alpha activated kinase (ITAK).
CC Antagonists of ITAK are used to treat IL-1 or TNF alpha-mediated
CC inflammatory disorders e.g. rheumatoid arthritis, inflammatory bowel
CC disease, type I diabetes, psoriasis, Alzheimer's disease, reperfusion
CC injury, malignancy, transplant rejection, neuropathy associated with
CC human immunodeficiency virus etc. Cells containing ITAK can be used to
CC raise antibodies for assay of ITAK or to inhibit IL-1 and TNF alpha
CC activity. Gene products that associate with ITAK are potential inhibitors
CC and can be used to detect ITAK genes. Antisense sequences inhibit
CC expression of ITAK. Inhibition of ITAK selectively blocks cell responses
CC to IL-1 and TNF alpha, but not responses to other cytokines.
XX
SQ Sequence 19 AA;

Query Match 85.7%; Score 6; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQP 6
   |||||
Db 12 SWMHQP 17

RESULT 9

AAB72279
ID AAB72279 standard; peptide; 15 AA.
XX
AC AAB72279;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 34.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (REGC-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2001-202804/20.
XX
PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.
XX
SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQPP 7
   |||||
Db 1 MHQPP 5

RESULT 10
AAB72531
ID AAB72531 standard; Peptide; 15 AA.
XX
AC AAB72531;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #32.
XX
KW Dermatological; oxidative stress regulator; colostrinin.

```


RESULT 13
AAE20261
ID AAE20261 standard; peptide; 15 AA.
XX AC AAE20261;
XX AC AAE20261;
XX DT 18-JUN-2002 (first entry)
XX DE Colostrin constituent peptide #32.
XX DE Blood cell regulator; colostrin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnary.
XX OS Unidentified.
XX OS
XX FH Key Location/Qualifiers
FT Modified-site 15 /note= "Optionally C-terminal amide"
XX PN WO200213850-A1.
XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22776.
XX PR 17-AUG-2000; 2000WO-US22776.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX DR WPI; 2002-269151/31.
XX PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrin, its
PT constituent peptide and/or analog -
XX Claim 6; Page 26; 5lpp; English.
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrin constituent peptide.
XX Sequence 15 AA;
SQ

Query Match 71.4%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MHQPP 7
DB 1 MHQPP 5

RESULT 14
AAW51066
ID AAW51066 standard; Peptide; 15 AA.
XX AC AAW51066;
XX DT 30-MAY-2002 (first entry)
XX DE Colostrin constituent peptide (casein amino acids 159-173).
XX DE Colostrin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX OS Homo sapiens.
XX OS
XX FH Key Location/Qualifiers
FT Modified-site 15 /note= "optional C-terminal amidation"
XX PN WO200213849-A1.
XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22775.
XX PR 17-AUG-2000; 2000WO-US22775.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX DR WPI; 2002-269150/31.
XX PT Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrin, its constituent peptide
PT and/or analogue -
XX Claim 1; Page 34; 54pp; English.
XX The present sequence is that of a colostrin constituent peptide
CC that is used as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified
CC as having a beta-casein homologue precursor, and corresponds to
CC casein amino acids 159-173. Methods are claimed for: inducing a
CC cytokine in a cell by contact with an immunological regulator,
CC where the cell is present in a cell culture, a tissue, an organ
CC or an organism, and the cell is mammalian, including human;
CC modulating an immune response in a cell by contact with the
CC immunological regulator under conditions effective to induce a
CC cytokine; modulating an immune response in a patient by administering
CC an immunological regulator under conditions effective to induce a
CC cytokine, where the immunological regulator is administered topically
CC or as part of a dietary supplement, and where the immune response is
CC specific or non specific, an interferon response or an antibody
CC response; modulating blood cell proliferation by contacting blood
CC cells with a blood cell regulator, where the blood cells are present
CC in a cell culture or an organism, are mammalian or human, and where
CC the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patient. A
CC claimed cytokine-inducing composition comprises a pharmaceutical
CC carrier and an active agent such as the present peptide.
XX Sequence 15 AA;
SQ

Query Match 71.4%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MHQPP 7
DB 1 MHQPP 5

RESULT 15
AAO14610
ID AAO14610 standard; peptide; 15 AA.
XX
AC AAO14610;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 32.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 15 /note= "Optional C-terminal amide"
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22777.
XX
PR 17-AUG-2000; 2000WO-US22777.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
FT analog -
XX
PS Claim 7; Page 22; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX
SQ Sequence 15 AA;
Query Match 71.4%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
Qy 3 MHQPP 7
Db 1 MHQPP 5
RESULT 16
AAG78781
ID AAG78781 standard; peptide; 10 AA.
XX
AC AAG78781;
XX
DT 10-JAN-2002 (first entry)
XX
DE Stachybotrys echinata derived peptide.
XX
KW Isoindole derivative; cardiant; antidiabetic; antimicrobial;

KW antibiotic; SERCA2 inhibitor; heart insufficiency; circulatory system;
KW diabetes; infection.
XX
OS Stachybotrys echinata.
XX
PN EP1130027-A1.
XX
PD 05-SEP-2001.
XX
PF 29-FEB-2000; 2000EP-0104114.
XX
PR 29-FEB-2000; 2000EP-0104114.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Vertesy L, Kogler H, Markus A, Schiell M;
XX
DR WPI; 2001-627636/73.
XX
PT New isoindole derivatives prepared by microbial fermentation, useful
PT for the treatment and prevention of heart insufficiency, diabetes
PT mellitus and microbial infection -
XX
PS Claim 6; Page 18; 21pp; German.
XX
CC The present invention relates to isoindole derivatives capable of acting
CC as SERCA2 inhibitors. These can be used in the prevention and treatment
CC of heart insufficiency, weakness in the heart and circulatory system,
CC diabetes and microbial infection. The present sequence is a peptide which
CC may form part of the compound of the invention.
XX
SQ Sequence 10 AA;
Query Match 57.1%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 MHQP 6
Db 1 MHQP 4
RESULT 17
ABG95549
ID ABG95549 standard; Peptide; 11 AA.
XX
AC ABG95549;
XX
DT 15-JAN-2003 (first entry)
XX
DE Human novel secreted protein gene 86 polypeptide #1.
XX
KW Human; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasia;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
OS Homo sapiens.
XX
FN US6420526-B1.
XX
PD 16-JUL-2002.
XX
PF 08-SEP-1998; 98US-0149476.
XX
PR 07-MAR-1997; 97US-038621P.
PR 07-MAR-1997; 97US-040161P.
PR 07-MAR-1997; 97US-040162P.
PR 07-MAR-1997; 97US-040163P.

PR	07-MAR-1997;	97US-040333P.	PR	22-AUG-1997;	97US-056878P.	
PR	07-MAR-1997;	97US-040334P.	PR	22-AUG-1997;	97US-056879P.	
PR	07-MAR-1997;	97US-040336P.	PR	22-AUG-1997;	97US-056880P.	
PR	07-MAR-1997;	97US-040626P.	PR	22-AUG-1997;	97US-056881P.	
PR	11-APR-1997;	97US-043311P.	PR	22-AUG-1997;	97US-056882P.	
PR	11-APR-1997;	97US-043312P.	PR	22-AUG-1997;	97US-056884P.	
PR	11-APR-1997;	97US-043313P.	PR	22-AUG-1997;	97US-056886P.	
PR	11-APR-1997;	97US-043314P.	PR	22-AUG-1997;	97US-056887P.	
PR	11-APR-1997;	97US-043315P.	PR	22-AUG-1997;	97US-056888P.	
PR	11-APR-1997;	97US-043356P.	PR	22-AUG-1997;	97US-056889P.	
PR	11-APR-1997;	97US-043576P.	PR	22-AUG-1997;	97US-056892P.	
PR	11-APR-1997;	97US-043578P.	PR	22-AUG-1997;	97US-056893P.	
PR	11-APR-1997;	97US-043580P.	PR	22-AUG-1997;	97US-056894P.	
PR	11-APR-1997;	97US-043669P.	PR	22-AUG-1997;	97US-056903P.	
PR	11-APR-1997;	97US-043670P.	PR	22-AUG-1997;	97US-056908P.	
PR	11-APR-1997;	97US-043671P.	PR	22-AUG-1997;	97US-056909P.	
PR	11-APR-1997;	97US-043672P.	PR	22-AUG-1997;	97US-056910P.	
PR	11-APR-1997;	97US-043674P.	PR	22-AUG-1997;	97US-056911P.	
PR	23-MAY-1997;	97US-047492P.	PR	05-SEP-1997;	97US-057761P.	
PR	23-MAY-1997;	97US-047500P.	PR	05-SEP-1997;	97US-057650P.	
PR	23-MAY-1997;	97US-047501P.	PR	12-SEP-1997;	97US-057669P.	
PR	23-MAY-1997;	97US-047502P.	PR	12-SEP-1997;	97US-058785P.	
PR	23-MAY-1997;	97US-047503P.	PR	06-OCT-1997;	97US-061060P.	
PR	23-MAY-1997;	97US-047581P.	XX	06-MAR-1998;	98WO-US04493.	
PR	23-MAY-1997;	97US-047582P.	PA	(HUMA-) HUMAN GENOME SCI INC.		
PR	23-MAY-1997;	97US-047583P.	XX			
PR	23-MAY-1997;	97US-047584P.	PI	Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;		
PR	23-MAY-1997;	97US-047585P.	PI	Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;		
PR	23-MAY-1997;	97US-047586P.	PI	Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;		
PR	23-MAY-1997;	97US-047587P.	PI	Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;		
PR	23-MAY-1997;	97US-047588P.	XX			
PR	23-MAY-1997;	97US-047589P.	DR	WPI; 2002-634796/68.		
PR	23-MAY-1997;	97US-047590P.	XX			
PR	23-MAY-1997;	97US-047592P.	XX			
PR	23-MAY-1997;	97US-047593P.	PT	New isolated human secreted protein for diagnosing, preventing,		
PR	23-MAY-1997;	97US-047594P.	PT	treating or ameliorating medical conditions and used as a food additive		
PR	23-MAY-1997;	97US-047595P.	PT	or preservative -		
PR	23-MAY-1997;	97US-047596P.	XX			
PR	23-MAY-1997;	97US-047597P.	PS	Disclosure; Column 78; 129pp; English.		
PR	23-MAY-1997;	97US-047598P.	XX			
PR	23-MAY-1997;	97US-047599P.	CC	The invention relates to an isolated protein that is one of 186 human		
PR	23-MAY-1997;	97US-047599P.	CC	secreted proteins, given in the specification, encoded by one of		
PR	23-MAY-1997;	97US-047599P.	CC	109 cDNA sequences also given in the specification. The protein is used		
PR	23-MAY-1997;	97US-047600P.	CC	in a pharmaceutical composition used to prevent, treat or ameliorate a		
PR	23-MAY-1997;	97US-047601P.	CC	medical condition in e.g. humans, mice, rabbits, goats, horses, cats,		
PR	23-MAY-1997;	97US-047612P.	CC	dogs, chickens or sheep. Disorders which are diagnosed or treated include		
PR	23-MAY-1997;	97US-047613P.	CC	autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative		
PR	23-MAY-1997;	97US-047614P.	CC	disorders e.g. neoplasms of the breast or liver, cardiovascular disorders		
PR	23-MAY-1997;	97US-047615P.	CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,		
PR	23-MAY-1997;	97US-047617P.	CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease,		
PR	23-MAY-1997;	97US-047618P.	CC	infections caused by bacteria, viruses and fungi and ocular disorders		
PR	23-MAY-1997;	97US-047632P.	CC	e.g. corneal infection. The polypeptides can also be used to aid wound		
PR	06-JUN-1997;	97US-047633P.	CC	healing and epithelial cell proliferation, to prevent skin aging due to		
PR	06-JUN-1997;	97US-048964P.	CC	culture, to maintain organs before transplantation, for supporting cell		
PR	13-JUN-1997;	97US-048974P.	CC	growth of primary tissues, to regenerate tissues and in chemotaxis. The		
PR	08-JUL-1997;	97US-051926P.	CC	polypeptides can also be used as a food additive or preservative to		
PR	16-JUL-1997;	97US-052874P.	CC	increase or decrease storage capabilities, fat content, lipid, protein,		
PR	18-AUG-1997;	97US-055724P.	CC	carbohydrate, vitamins, minerals, cofactors and other nutritional		
PR	22-AUG-1997;	97US-056630P.	CC	components. The present sequence represents one of the novel human		
PR	22-AUG-1997;	97US-056631P.	CC	secreted proteins of the invention.		
PR	22-AUG-1997;	97US-056632P.	XX			
PR	22-AUG-1997;	97US-056636P.	SQ	Sequence 11 AA;		
PR	22-AUG-1997;	97US-056637P.				
PR	22-AUG-1997;	97US-056662P.				
PR	22-AUG-1997;	97US-056664P.				
PR	22-AUG-1997;	97US-056845P.				
PR	22-AUG-1997;	97US-056862P.				
PR	22-AUG-1997;	97US-056864P.				
PR	22-AUG-1997;	97US-056872P.				
PR	22-AUG-1997;	97US-056874P.				
PR	22-AUG-1997;	97US-056875P.				
PR	22-AUG-1997;	97US-056876P.				
PR	22-AUG-1997;	97US-056877P.				

Query Match 57.1%; Score 4; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 85;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQPP 7

DB 1 HQPP 4

RESULT 18

AAU93631
ID AAU93631 standard; Peptide; 11 AA.
XX
AC AAU93631;
XX
XX 02-JUL-2002 (first entry)
XX
XX Granulocyte-colony stimulating factor receptor binding peptide #437.
XX
XX G-CSFR; granulocyte-colony stimulating factor receptor; cytokine;
KW haematopoietic growth factor; neutrophil proliferation; AIDS;
KW neutrophil differentiation; acquired immunodeficiency syndrome;
KW chemotherapy-induced neutropenia; community acquired pneumonia;
XX depressed neutrophil count; immunostimulant.
XX
OS Synthetic.
XX
XX WO200207676-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US23046.
XX
XX 20-JUL-2000; 2000US-0620091.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Cwirla SE, Balu P, Duffin DJ, Piplani S, McEwen-Merrill B;
PI Schatz PJ;
XX
XX WPI; 2002-329382/36.
XX
XX Novel compounds, useful for treating depressed neutrophil count,
PT comprise peptide chains of approximately 6 to 40 amino acids in length
PT that bind to granulocyte-colony stimulating factor receptor -
XX
XX Claim 41; Page 66; 90pp; English.
XX
XX The invention relates to compounds comprising a peptide chain
CC approximately 6 to 40 amino acids in length that binds to granulocyte-
CC colony stimulating factor receptor (G-CSFR). The compounds contain
CC specific sequences of the generic peptides appearing as AAU79402-AAU79406
CC and the generic sequences XV.1XV.2XV.3XV.4XV.5XV.6XV.7XV.8 (where
CC XV.1 = E, C, Q, V or Y; XV.2 = E, A, L, M, S, W or Q; XV.3 = K, R or T;
CC XV.4 = L, A or V; XV.5 = R, A, M, H, E, V, L, G, D, Q or S; XV.6 = E or
CC V; XV.7 = A or G; and XV.8 = R, H, G or L) and XVI.1XVI.2XVI.3XVI.4XVI.5
CC XVI.6XVI.7XVI.8XVI.9 (where XVI.1 = A, E or G; XVI.2 = E, H or D;
CC XVI.3 = R or G; XVI.4 = K, Y, M, N, O, R, D, I, S or E; XVI.5 = A, S or
CC P; XVI.6 = E, D, T, Q, K or A; XVI.7 = R, W, K, L, S, A or Q; XVI.8 = R
CC or E; and XVI.9 = W, G or P). The compounds are used for treating
CC conditions associated with depressed neutrophil count e.g. chemotherapy-
CC induced neutropenia, AIDS-induced neutropenia or community-acquired
CC pneumonia-induced pneumonia. The compounds are useful as in vitro as
CC tools for understanding the biological role of granulocyte-colony
CC stimulating factor (G-CSF) a haematopoietic growth factor and
CC cytokine that stimulates neutrophil proliferation and differentiation),
CC including evaluation of many factors thought to influence, and be
CC influenced by, production of white blood cells, in the development of
CC compounds that bind to G-CSFR, as reagents for detecting G-CSF receptor
CC or related receptor on living cells, fixed cells, in biological fluid, in
CC tissue homogenates or in purified natural biological materials, in situ
CC staining, fluorescence-activated cell sorting (FACS), Western blotting or
CC enzyme-linked immunosorbent assay (ELISA), in receptor purification or
CC in purifying cells expressing G-CSFR on the cell surface (or inside
CC permeabilised cells) as a commercial research reagent for various medical
CC and diagnostic uses or to treat a disease that would benefit from the
CC ability to of a compound to mimic the effects of G-CSF in vivo.
CC The compounds bind specifically to G-CSFR and allow for studies of
CC biological activities mediated by the receptor and for the treatment of
CC diseases, disorders and conditions that would benefit from activating or
CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of
CC the invention.
XX

SQ Sequence 11 AA;
Query Match 57.1%; Score 4; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SWMH 4
Db 5 SWMH 8
RESULT 19
ABR00957
ID ABR00957 standard; peptide; 11 AA.
XX
AC ABR00957;
XX
XX 12-MAY-2003 (first entry)
XX
XX Human gene 11-encoded secreted protein HAGEQ79, SEQ ID NO:438.
XX
XX Human; secreted protein; cancer; tumour; hyperproliferative disorder;
KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;
KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;
KW drug screening; chromosome identification; chromosome mapping;
KW cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;
KW antianaemic; vulnerary.
XX
XX Homo sapiens.
XX
XX WO200277013-A2.
XX
XX 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US09370.
XX
XX 27-MAR-2001; 2001US-278650P.
XX
XX 12-SEP-2001; 2001US-0950082.
XX
XX 12-SEP-2001; 2001US-0950083.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2003-040578/03.
XX
XX N-PSDB; ABZ73291.
XX
XX New human secreted proteins and nucleic acids, useful for detecting or
XX treating cancer or other hyperproliferative disorders, autoimmune
XX disorders, inflammatory disorders, HIV disease, hepatitis or anemia -
XX
XX Claim 13; Page 1384; 2474pp; English.
XX
XX ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted
XX protein genes, and ABP00947-ABP01363 represent the proteins they encode.
XX ABZ73698-ABZ74687 represent human secreted protein genomic fragments. The
XX invention also encompasses antibodies specific for the secreted proteins,
XX the use of the secreted proteins in drug screening and recombinant
XX vectors and host cells comprising a nucleic acid of the invention. The
XX secreted proteins are thought to be involved in biological activities
XX associated with cellular signalling, cellular differentiation, cell
XX migration, prohormone activation and neurotransmitter activity. The
XX secreted proteins, nucleic acids encoding them, antibodies or antibody
XX fragments specific for the secreted proteins, and modulators of protein
XX activity are useful for diagnosing or treating cancers or other
XX hyperproliferative disorders. Additionally, the secreted proteins and
XX their nucleic acids may also be used in the treatment of autoimmune
XX disorders, inflammatory disorders, diseases involving angiogenesis, AIDS
XX (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote
XX wound healing. Nucleic acids of the invention may be used for chromosome
XX identification, chromosome mapping, in gene therapy, for identifying
XX individuals from minute biological samples, as hybridisation probes, and
XX as molecular weight markers. The present sequence represents a human

CC	secreted protein of the invention.	
XX		
SQ	Sequence 11 AA;	
	Query Match 57.1%; Score 4; DB 24; Length 11;	
	Best Local Similarity 100.0%; Pred. No. 85;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	3 MHQP 6	
Db	1 MHQP 4	
RESULT 20		
ABP99483		
ID	ABP99483 standard; Protein; 11 AA.	
XX		
AC	ABP99483;	
XX		
DT	26-MAR-2003 (first entry)	
XX		
DE	Human secreted protein SEQ ID NO 427.	
XX		
KW	Human; secreted protein; nootropic; neuroprotective; cytostatic;	
KW	viricide; dermatological; immunosuppressive; antiinflammatory; anti-HIV;	
KW	vulnerary; antibacterial; antiparkinsonian; antisickling; antianaemic;	
KW	antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective;	
KW	antiinflammatory; antiallergic; antidiabetic; antitumor; anticonvulsant;	
KW	antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine;	
KW	cardiovascular disorder; neurological disease; nephrotropic;	
KW	gene therapy.	
OS	Homo sapiens.	
XX		
PN	WO200277186-A2.	
XX		
PD	03-OCT-2002.	
XX		
PF	26-MAR-2002; 2002WO-US09188.	
XX		
PR	27-MAR-2001; 2001US-278650P.	
PR	12-SEP-2001; 2001US-0950082.	
PR	12-SEP-2001; 2001US-0950083.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM;	
XX		
DR	WPI; 2003-040583/03.	
DR	N-PSDB; ABZ66904.	
XX		
PS	Claim 1; Page 1393; 2423pp; English.	
XX		
CC	The invention relates to novel human genes (ABZ66891-ABZ68209) and the	
CC	encoded secreted proteins (ABP9470-ABP99872) useful for preventing,	
CC	treating or ameliorating medical conditions e.g. by protein or gene	
CC	therapy The genes are isolated from a range of human tissues disclosed	
CC	in the specification. The nucleic acids, proteins, antibodies and	
CC	(ant)agonists are useful in the diagnosis, treatment and prevention of:	
CC	(a) cancer, e.g. breast and ovarian cancer and other cancers of the	
CC	adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,	
CC	lung or urogenital; (b) immune disorders e.g. Addison's disease,	
CC	allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,	
CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid	
CC	arthritis and ulcerative colitis; (c) cardiovascular disorders such as	
CC	myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.	
CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,	
CC	bacterial, fungal and parasitic infections.	
XX		
SQ	Sequence 11 AA;	
	Query Match 57.1%; Score 4; DB 24; Length 11;	
	Best Local Similarity 100.0%; Pred. No. 85;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	3 MHQP 6	
Db	1 MHQP 4	
RESULT 21		
AAB28056		
ID	AAB28056 standard; peptide; 12 AA.	
XX		
AC	AAB28056;	
XX		
DT	02-FEB-2001 (first entry)	
XX		
DE	Human secreted protein SEQ ID NO: 104.	
XX		
KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;	
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;	
KW	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;	
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;	
KW	neurological disease; infection; human; secreted protein.	
OS	Homo sapiens.	
XX		
PN	WO200055177-A2.	
XX		
PD	21-SEP-2000.	
XX		
PF	09-MAR-2000; 2000WO-US06058.	
XX		
PR	12-MAR-1999; 99US-0124145.	
PR	03-DEC-1999; 99US-0168654.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM, Komatsoulis G;	
XX		
DR	WPI; 2000-638177/61.	
DR	N-PSDB; AAC59152.	
XX		
PT	Novel nucleic acids encoding 49 human secreted proteins useful for	
PT	treating cancers, hyperproliferative disorders, inflammatory disorders,	
PT	neurological disorders and cardiovascular disorders -	
XX		
PS	Claim 11; Page 363; 389pp; English.	
XX		
CC	Sequences AAB28012-B28060 represent the amino acid sequences of 49	
CC	human secreted proteins encoded by the genes AAC59108-C59156. The genes	
CC	and proteins are useful for preventing, ameliorating or treating medical	
CC	conditions, e.g. by protein or gene therapy. The genes are isolated from	
CC	a range of human tissues disclosed in the specification. The nucleic	
CC	acids, proteins, antibodies and (ant)agonists are useful in the	
CC	diagnosis, treatment and prevention of: (a) cancer, e.g. breast and	
CC	ovarian cancer, and other cancers of the adrenal gland, bone, bone	
CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;	
CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune	
CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,	
CC	Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative	
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;	
CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and	
CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal	
CC	and parasitic infections.	
XX		
SQ	Sequence 12 AA;	
	Query Match 57.1%; Score 4; DB 21; Length 12;	
	Best Local Similarity 100.0%; Pred. No. 91;	

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
 DB 1 MHQP 4

RESULT 22
 AAU92771
 ID AAU92771 standard; peptide; 14 AA.
 XX
 AC AAU92771;
 XX
 XX 29-AUG-2000 (first entry)
 XX
 DE Oligopeptide mimotope C19 of surface LOS of serogroup B meningococcus.
 XX
 XX Heptapeptide; epitope; mimotope; surface lipo-oligosaccharide; LOS;
 KW meningitis; anti-bacterial; anti-inflammatory; vaccine.
 XX
 OS Neisseria meningitidis.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 2..10
 FT
 XX WO200025814-A2.
 XX
 XX 11-MAY-2000.
 XX
 XX 27-OCT-1999; 99WO-GB03559.
 XX
 XX 30-OCT-1998; 98GB-0023835.
 XX
 XX (UNLO) UNIV COLLEGE LONDON.
 XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 XX
 XX Charalambous BM, Feavers IM;
 XX
 XX WPI; 2000-365403/31.
 DR
 XX
 XX Use of a mimotope of a surface lipooligosaccharide of a serogroup B
 PT meningococcus for a vaccine against serogroup B meningococci
 XX
 XX Example 2; Page 19; 39pp; English.
 XX
 XX Mimotopes of a surface lipooligosaccharide (LOS) of a serogroup B
 CC meningococcus comprise an oligopeptide which is structurally more
 CC constrained than an unsubstituted linear form of the oligopeptide. The
 CC oligopeptide is cyclic and contains a heptapeptide, such as the generic
 CC sequence of AAU92767. The mimotopes are useful in vaccines against
 CC serogroup B meningococci, especially Neisseria meningitidis, which
 CC causes meningitis. The LOS is a surface glycolipid that forms a major
 CC outer membrane component and possesses a terminal galactose acceptor
 CC sites for sialic acid. Sialylation of the LOS in immunotype B
 CC meningococci may enhance the ability of the organism to evade the human
 CC immune response. Therefore alternative target antigens on the surface of
 CC serogroup B meningococci are important.
 XX
 SQ Sequence 14 AA;

Query Match 57.1%; Score 4; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMH 4
 DB 3 SWMH 6

RESULT 23
 AAU88216
 ID AAU88216 standard; Peptide; 17 AA.
 XX

AC AAU88216;
 XX
 XX 19-JUN-2002 (first entry)
 XX
 DE Insulin/insulin-like growth factor receptor-binding peptide #180.
 XX
 XX Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke;
 KW diabetic neuropathy.
 XX
 XX Synthetic.
 OS
 XX WO200172771-A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 29-MAR-2000; 2000WO-US08528.
 XX
 XX 29-MAR-2000; 2000WO-US08528.
 XX
 XX (DGIB-) DGI BIOTECHNOLOGIES LLC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandacki WS;
 PI Hansen PH, Ravera M, Hsiao K;
 XX
 XX WPI; 2002-025774/03.
 DR
 XX
 XX Modulating insulin activity in mammalian cells, for treating e.g.
 PT diabetes and tumours, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors -
 XX
 XX Disclosure; Page 44; 390pp; English.
 XX
 XX The invention relates to a method of modulating insulin activity in
 CC mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR
 CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
 CC of the invention.
 XX
 SQ Sequence 17 AA;

Query Match 57.1%; Score 4; DB 23; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
 DB 12 MHQP 15

RESULT 24
 AAU90013
 ID AAU90013 standard; Peptide; 17 AA.
 XX
 XX AAU90013;
 AC
 XX
 XX 18-JUN-2002 (first entry)
 XX
 XX Insulin/insulin-like growth factor receptor-binding peptide #1969.
 DE
 XX

KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW ophthalmological; insulin; receptor; gene therapy; diabetes;
KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW diabetic retinopathy; neurological diseases; stroke;
KW diabetic neuropathy.
XX
OS Synthetic.
XX
PN WO200172771-A2.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2000; 2000WO-US08528.
XX
PR 29-MAR-2000; 2000WO-US08528.
XX
XX (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO) NOVO NORDISK AS.
XX
XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Ravera M, Hsiao K;
XX
XX WPI; 2002-025774/03.
XX
XX Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumours, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors -
XX
XX Disclosure; Figure 3C; 390pp; English.
XX
XX The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU8034-AAU90957 represent IR
CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
CC of the invention.
XX
SQ Sequence 17 AA;
Query Match 57.1%; Score 4; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MHQP 6
Db 12 MHQP 15
RESULT 25
ABB50820
ID ABB50820 standard; Protein; 20 AA.
XX
AC ABB50820;
XX
XX 07-FEB-2002 (first entry)
DT
XX Human secreted protein encoded by gene 75 SEQ ID NO:773.
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
KW cytostatic; cardiant; anti-angiogenic; ophthalmological;
KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;
KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
KW

KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
KW Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
KW Chaga's cardiomyopathy; coronary arteriosclerosis; angogenic disorder;
KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
KW neurological disorder; Huntington's chorea; Alzheimer's disease;
KW Parkinson's disease; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200162891-A2.
XX
XX 30-AUG-2001.
XX
XX 21-FEB-2001; 2001WO-US05614.
XX
XX 24-FEB-2000; 2000US-184836P.
PR 29-MAR-2000; 2000US-193170P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
PI Ruben SW, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
PI Zeng Z, Greene JW;
XX
XX WPI; 2001-625724/72.
XX
XX Nucleic acids encoding 207 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
PT disease and diabetic retinopathy -
XX
XX Disclosure; Page 178; 1533pp; English.
XX
XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
CC activities based on the tissues and cells the genes are expressed in.
CC Example of these activities include: immunomodulatory; antisclerotic;
CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
CC in gene therapy and vaccine production. (I) and (II) can be used in the
CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Chaga's disease), cardiovascular diseases (e.g. Scimitar syndrome,
CC Chaga's cardiomyopathy and coronary arteriosclerosis), angogenic
CC disorders (e.g. corneal graft neovascularisation and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
CC ABA83193 and ABB50300 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 20 AA;
Query Match 57.1%; Score 4; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HQPP 7
Db 1 HQPP 4
RESULT 26
AAR12685
ID AAR12685 standard; Protein; 5 AA.
XX
XX AAR12685;
XX
XX 31-JUL-1991 (first entry)
DT

XX Pentapeptide paralogue for use as chromatographic affinity ligand.
DE HPLC.
XX
KW Synthetic.
OS
XX WO9106356-A.
XX
XX 16-MAY-1991.
XX
XX 31-OCT-1990; 90WO-EP06333.
XX
XX 31-OCT-1989; 89US-0429721.
XX
XX (TERR-) TERRAPIN TECHN INC.
XX
XX Kauvar LM;
XX
XX WPI; 1991-163985/22.
XX
XX Identifying paralog with specific affinity for analyte - using
PT candidate paralog with systematically varied values of at least
PT 2 parameters.
XX
XX Claim 41; Fig 8; 95pp; English.
XX
XX Peptide is one of a panel, each of which have systemically varied
CC values of at least two parameters. A test protein is matched against
CC the panel, and the paralogues with highest binding affinity are
CC selected. Selected paralogues are bound to a matrix which is
CC incorporated into the HPLC gel and used as affinity ligands.
CC Technique is useful in chromatographic separation, purification
CC and binding assay.
XX
XX Sequence 5 AA;
SQ
Query Match 42.9%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 WMH 4
Db 1 WMH 3
RESULT 27
ID AAR27038 standard; peptide; 5 AA.
XX
XX AAR27038;
XX
XX 25-MAR-2003 (updated)
DT 01-MAR-1993 (first entry)
XX
XX Consensus heavy chain CDR1 used in humanised Mab.
DE Monoclonal antibody; complementarity determining region; framework;
XX antigens; tumour; melanoma; carcinoma; glioma.
KW
KW Non human.
OS
XX WO9215683-A1.
XX
XX 17-SEP-1992.
PD
XX 04-MAR-1992; 92WO-EF00480.
XX
XX 06-MAR-1991; 91EP-0103389.
XX
XX (MERE) MERCK PATENT GMBH.
PA Bendig MM, Kettleborough CA, Saldanha J;
PI

XX WPI; 1992-331729/40.
XX
XX Human monoclonal antibodies binding to human receptors - for
PT treatment and diagnosis of tumours, e.g. melanoma and carcinoma
XX
XX Claim 4; Page 62; 89pp; English.
XX
XX The CDR1 sequence was that of a consensus sequence of CDR1 deduced
CC from antigen binding sites of non-human origin. The sequence is
CC from the heavy chain hypervariable region. The sequence may be used
CC to produce humanised monoclonal antibodies comprising CDRs of non
CC human origin and frameworks of variable and constant regions of
CC human heavy and light chains. The humanised antibodies or their
CC chimeric variants may be used as therapeutic or diagnostic agents in
CC order to combat e.g. glioma, melanoma or carcinoma.
CC See also AAR27299-300 and AAR27037-51.
XX
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 5 AA;
SQ
Query Match 42.9%; Score 3; DB 13; Length 5;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 WMH 4
Db 3 WMH 5
RESULT 28
ID AAR51549 standard; peptide; 5 AA.
XX
XX AAR51549;
XX
XX 25-MAR-2003 (updated)
DT 19-OCT-1994 (first entry)
XX
XX Minotope peptide #43 from panel of maximally diverse minotopes.
DE
XX minotope panel; rational drug design; candidate drug;
KW screening assay; hydrophobicity; antibody repertoire.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "acetylated"
XX
XX US5300425-A.
XX
XX 05-APR-1994.
PD
XX 06-DEC-1989; 89US-0447009.
XX
XX 13-OCT-1987; 87US-0108130.
PR 11-OCT-1988; 88US-0255906.
XX
XX 06-DEC-1989; 89US-0447009.
XX
XX (TERR-) TERRAPIN TECHNOLOGIES INC.
XX
XX Kauvar LM;
XX
XX WPI; 1994-109390/13.
XX
XX Screening of candidate drugs for binding to receptor - by
PT comparing inverse image antibody profile of drug with
PT minotype-binding profile of receptor
XX
XX Example 3; Fig 3; 29pp; English.
XX
XX A panel of 88 pentapeptides was designed on the basis of decreasing

CC hydrophobicity and periodic variation of hydrophobic moment. The
 CC peptides were labelled with iodine-125 and tested with individual
 CC members of a basal antibody repertoire. (Spleen cells were
 CC harvested from mice and used to provide a panel of
 CC antibody-secreting hybridoma cells as a subset of the complete
 CC B-cell repertoire). Nearly uniform binding to all antibody members
 CC of the repertoire was observed. The test was then repeated with the
 CC addition of a defined amount of analyte to the mixture. A small
 CC number of wells showed greatly decreased labelling and these
 CC antibodies represented the successful result of an initial screen
 CC for those which preferentially bind analyte.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WMH 4
 ||||
 Db 1 WMH 3
 RESULT 29
 AAR69917
 ID AAR69917 standard; peptide; 5 AA.
 AC AAR69917;
 XX
 DT 25-MAR-2003 (updated)
 DT 18-OCT-1995 (first entry)
 XX
 DE Pentameric mimotope 43 used to obtain highly specific antibodies.
 XX
 KW mimotope; antibody; production; high specificity; detection;
 KW immunoassay; high performance liquid chromatography.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Acetyl-Trp"
 XX
 PN US5384263-A.
 XX
 PD 24-JAN-1995.
 XX
 PF 04-JUN-1993; 93US-0072190.
 XX
 PR 11-OCT-1988; 88US-0255906.
 PR 13-OCT-1987; 87US-0108130.
 PR 04-JUN-1993; 93US-0072190.
 XX
 XX (TERR-) TERRAPIN TECHNOLOGIES INC.
 PA
 XX
 PI Kauvar LM;
 XX
 DR WPI; 1995-105497/14.
 XX
 PT Producing antibodies with high specificity and affinity for an
 PT analyte - by immunisation with selected mimotope, also analyte
 PT detection kits; useful for immunoassay of materials usually
 PT analysed by HPLC
 XX
 XX Example 3; Fig 3; 25pp; English.
 PS
 XX AAR69875-969 are pentameric mimotopes designed on the basis of
 CC decreasing hydrophobicity and periodic variation of hydrophobic
 CC moment. All the pentapeptides are acetylated at the N-terminus except
 CC E12 (for FITC) (sic). E12 is not identified in the specification.
 CC The mimotopes are used in the method of the invention to obtain
 CC antibodies specifically and strongly reactive with a desired

CC analyte. The mimotope is obtd. by reacting a panel of starting
 CC antibodies (Abs) representative of the resting B cell repertoire of a
 CC mammal with an analyte (so as to identify analyte-reacting Abs) and
 CC then reacting each of a panel of candidate mimotopes representative
 CC of a random set of 3D contours with the analyte-reacting Abs. A
 CC subject is immunised with one or more mimotopes identified and the
 CC product Abs are recovered from the serum of the subject.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WMH 4
 ||||
 Db 1 WMH 3
 RESULT 30
 AAR74929
 ID AAR74929 standard; peptide; 5 AA.
 XX
 AC AAR74929;
 XX
 DT 19-JAN-1996 (first entry)
 XX
 DE H-CDR-1 of anti-idiotypic antibody against human anticancer antibody.
 XX
 KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN JP07101999-A.
 XX
 PD 18-APR-1995.
 XX
 PF 06-OCT-1993; 93JP-0272950.
 XX
 PR 06-OCT-1993; 93JP-0272950.
 XX
 PA (HAGI/) HAGIWARA Y.
 XX
 DR WPI; 1995-182987/24.
 XX
 PT Novel anti-idiotypic antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 XX
 PS Claim 1; Page 2; 28pp; Japanese.
 XX
 CC A new anti-idiotypic antibody against a human anticancer monoclonal
 CC antibody is claimed. This antibody contains in its heavy chain 3
 CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2
 CC (AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the
 CC light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
 CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
 CC encoding it are useful in pharmacological, medical and biochemical
 CC fields.
 XX
 SQ Sequence 5 AA;
 Query Match 42.9%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WMH 4
 ||||
 Db 3 WMH 5

RESULT 31
 AAR98663
 ID AAR98663 standard; peptide; 5 AA.
 AC
 XX AAR98663;
 AC

25-MAR-2003 (updated)
 DT 11-MAR-1997 (first entry)
 DT

Peptide 43 from 88 member diverse mimotope panel.

Panel; mimotope; decreasing hydrophobicity; periodic variation;
 KW hydrophobic moment; antibody; repertoire; identification; drug;
 KW candidate; receptor; binding; ligand; rational; design; selection;
 KW treatment; tumour; production; immunological reagent; analyte;
 KW detection; trace contaminant; mimotope.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Modified-site 1 /note= "acylated"
 FT

US5541070-A.

30-JUL-1996.

08-SEP-1993; 93US-0118133.

06-DEC-1989; 89US-0447009.

13-OCT-1987; 87US-0108130.

11-OCT-1988; 88US-0255906.

08-SEP-1993; 93US-0118133.

(KAUV/) KAUVAR L M.

Kauvar LM;

WPI; 1996-361955/36.

Identifying candidate drugs that bind a specific receptor by

competitive reaction with panel of mimotope(s) - useful in rational

drug design

Example 3; Fig 3; 27pp; English.

The present peptide is a member of a panel of 88 pentapeptide
 CC mimotopes designed on the basis of decreasing hydrophobicity, and
 CC periodic variation of hydrophobic moment. The panel was synthesised
 CC using the method of Geysen, H. M., et al, Proc. Natl. Acad. Sci.
 CC USA (1984), which uses lots of 96 pins; the remaining 8
 CC polyethylene pins being controls. The mimotopes were then mixed,
 CC 125-I labelled and tested with individual members of a basal
 CC antibody (Ab) repertoire. Nearly uniform binding to all members was
 CC found. The test was then repeated with the addition of a defined
 CC ant. of analyte. A small number showed greatly increased labelling,
 CC these Ab representing the successful result of an initial screen
 CC for those that pref. bind analyte.
 CC The above is an example of a claimed method for identifying members
 CC of a panel of candidate drugs, that bind to a receptor having a
 CC known ligand. It is useful in rational drug design, e.g. selection
 CC of monoclonal Ab for treating individual tumours, and for the prodn.
 CC of immunological reagents for any analyte, including those not
 CC normally detectable by immunoassay, e.g trace contaminants in soil,
 CC air or water.
 CC (Updated on 25-MAR-2003 to correct PF field.)

Sequence 5 AA;

Query Match 42.9%; Score 3; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 WMH 4
 Db 1 WMH 3

RESULT 32

AAW39866

ID AAW39866 standard; peptide; 5 AA.

AC AAW39866;

16-JUN-1998 (first entry)

Heavy chain CDRI of catalytic antibody 8G4E.

Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

Mus sp.

WO9749800-A1.

31-DEC-1997.

25-JUN-1997; 97WO-US10965.

25-JUN-1996; 96US-0672345.

(UYCO) UNIV COLUMBIA NEW YORK.

Landry DW;

WPI; 1998-077166/07.

New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding

Claim 19; Page 94; 147pp; English.

AAW39866-68 represent the sequences of the heavy chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 8G4E, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 8G4E antibody was
 CC identified using TSA3, and has a per minute Kcat of 0.12. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved).

Sequence 5 AA;

Query Match 42.9%; Score 3; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 WMH 4

Db 3 WMH 5

RESULT 33

AAW44181

ID AAW44181 standard; peptide; 5 AA.

AC AAW44181;

16-JUN-1998 (first entry)

XX Monoclonal antibody 12H5 heavy chain CDR SEQ ID NO:25.
 DE
 XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
 KW amelioration; kidney disorder; nephrotoxicity; anticancer.
 XX
 XX Unidentified.
 OS
 XX WO9749427-A1.
 FN
 XX 31-DEC-1997.
 PD
 XX 27-JUN-1997; 97WO-JP02241.
 XX
 XX 19-SEP-1996; 96JP-0247635.
 PR 27-JUN-1996; 96JP-0167286.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 PA
 XX Hayashi K, Kawachi Y, Masuho Y, Takasaki J;
 PI WPI; 1998-076914/07.
 XX
 XX Amelioration of kidney disorders caused by cisplatin administration
 PT - by treatment with an antibody inhibiting type II phospholipase A2
 PT activity
 PT
 XX Disclosure; Page 50; 74pp; Japanese.
 PS
 XX The present sequence represents a complementary determining region
 CC (CDR) from monoclonal antibody 12H5 heavy chain against type II
 CC phospholipase A2, from the present invention. The present invention
 CC describes a novel method for the amelioration of kidney disorders
 CC (such as acute renal failure) associated with the administration of
 CC cisplatin for the treatment of cancer. The method comprises treatment
 CC with a monoclonal antibody which inhibits the activity of type II
 CC phospholipase A2 (particularly of type II phospholipase A2 of human
 CC origin), or with a protein or peptide possessing the same inhibitory
 CC activity and containing a part of the antibody sequence. Preferably the
 CC antibody also inhibits the activity of ape and/or mouse type II
 CC phospholipase A2, and has the ability to release type II phospholipase
 CC A2 bound to a cell membrane. Three specific monoclonal antibodies
 CC having these properties which can be used are 12H5, 10.1 and 1.4,
 CC derived from hybridomas FERM BP-5300, FERM BP-5298 and FERM BP-5297
 CC respectively. The method can be used for suppressing the nephrotoxicity
 CC which is a characteristic feature of cisplatin administration, and
 CC therefore allowing more efficient use of this drug as an anticancer
 CC agent, e.g. by allowing an increased dosage to be used.
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 42.9%; Score 3; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WMH 4
 DB 3 WMH 5
 RESULT 34
 AAY48891
 ID AAY48891 standard; Peptide; 5 AA.
 XX
 XX AAY48891;
 AC
 XX 20-MAR-2003 (updated)
 DT 10-DEC-1999 (first entry)
 XX
 XX Membrane dipeptidase-binding prostate homing peptide #7.
 DE
 XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;

KW membrane dipeptidase.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9946284-A2.
 PN
 XX 16-SEP-1999.
 XX
 XX 10-MAR-1999; 99WO-US05284.
 XX
 XX 13-MAR-1998; 98US-0042107.
 PR 26-FEB-1999; 99US-0258754.
 XX
 XX (BURN-) BURNHAM INST.
 PA
 XX Rajotte D, Pasqualini R, Ruoslahti EI;
 PI WPI; 1999-571717/48.
 XX
 XX New peptides which selectively home to organs or tissues, used for,
 PT e.g. identifying target ligands and for therapy of pathological
 PT conditions -
 PT
 XX Example 6; Page 151; 193pp; English.
 PS
 XX The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC or tissue, for identifying a target molecule expressed by an organ or
 CC tissue or for treating an organ or tissue pathology, where the organ or
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences
 CC which are used in the exemplification of the present invention.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 42.9%; Score 3; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 HQP 6
 DB 2 HQP 4
 RESULT 35
 AAB21923
 ID AAB21923 standard; Peptide; 5 AA.
 XX
 XX AAB21923;
 AC
 XX 22-MAR-2001 (first entry)
 DT
 XX Human prostate-homing peptide #16.
 DE
 XX Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
 KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
 KW
 XX Homo sapiens.
 OS
 XX WO200042973-A2.
 FN
 XX 27-JUL-2000.
 PD
 XX 21-JAN-2000; 2000WO-US01602.
 PF
 XX 22-JAN-1999; 99US-0235902.
 PR
 XX (BURN-) BURNHAM INST.
 PA
 XX Ellerby HM, Bredezen DE, Pasqualini R, Ruoslahti EI;

XX WPI; 2000-499174/44.
XX Homing pro-apoptotic conjugate comprising a tumor homing molecule that
PT selectively homes to a mammalian cell type or tissue linked to an
PT antimicrobial peptide, useful for the treatment of prostate cancer -
XX
XX Example 9; Page 99; 118pp; English.
XX
XX The present invention relates to homing pro-apoptotic conjugates,
CC comprising of a tumour homing molecule that selectively homes to a
CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
CC homing pro-apoptotic conjugates are selectively internalised by the
CC mammalian cell type or tissue and exhibits high toxicity, especially to
CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
CC toxicity when not linked to the tumor homing molecule. The conjugates are
CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
CC prostate cancer or melanoma. The present sequence is a homing peptide
CC isolated in the present invention, which can be conjugated to an
CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
XX present invention.
XX
XX Sequence 5 AA;
XX
XX Query Match 42.9%; Score 3; DB 21; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 HQP 6
XX 2 HQP 4
XX
XX
XX RESULT 36
XX AAB19754
XX ID AAB19754 standard; Peptide; 5 AA.
XX AC AAB19754;
XX
XX 19-FEB-2001 (first entry)
XX
XX Erythropoietin receptor agonist MAB 3G9 VH region CDR1.
XX
XX Erythropoietin receptor; agonist; monoclonal antibody; MAb; mouse;
XX heavy chain variable region; antibody engineering; erythropoiesis;
XX anaemia; cytopenia; acute renal failure; antianaemic; therapy;
XX complementarity determining region; CDR.
XX
XX Mus sp.
XX
XX WO2000061637-A1.
XX
XX 19-OCT-2000.
XX
XX 14-APR-2000; 2000WO-US10284.
XX
XX 14-APR-1999; 99US-0129263.
XX
XX (SMTK) SMITHKLINE BEECHAM CORP.
XX
XX Erickson-Miller CL, Holmes SD, Taylor AH, Young PR;
XX
XX WPI; 2000-679469/66.
XX
XX Novel erythropoietin receptor agonist antibody useful for enhancing
PT erythropoiesis in the treatment of anemia, cytopenia or acute renal
PT failure -
XX
XX Claim 28; Page 50; 70pp; English.
XX
XX The present sequence is that of complementarity determining region
CC 1 (CDR1) of the heavy chain variable region (VH) (see AAB19745) of
CC 3G9, a murine erythropoietin receptor (EpoR) agonist monoclonal

CC antibody. Claimed EpoR agonist antibodies comprise a VH region
CC that includes the 3G9 VH CDRs. These include humanised agonist
CC antibodies in which the 3G9 VH CDRs are incorporated into a human
CC framework. The EpoR agonist antibodies are used in a claimed
CC method for enhancing erythropoiesis, for the treatment of anaemia,
CC cytopenia, acute renal failure, and other conditions with depressed
CC erythrocyte production. Agonist antibodies of EpoR have the same
CC therapeutic utility as the natural ligand, but with the advantages
XX of easier purification and longer half-life in vivo.
XX
XX Sequence 5 AA;
XX
XX Query Match 42.9%; Score 3; DB 21; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 WMH 4
XX 3 WMH 5
XX
XX
XX RESULT 37
XX AAB12174
XX ID AAB12174 standard; peptide; 5 AA.
XX AC AAB12174;
XX
XX 10-NOV-2000 (first entry)
XX
XX Human CDR1 for IL-2R monoclonal antibody.
XX
XX Human; CDR; humanised antibody; complementarity determining region;
XX IL-2Ralpha; interleukin-2 receptor; transplant rejection; CD25;
XX immunosuppression.
XX
XX Homo sapiens.
XX
XX WO2000030679-A1.
XX
XX 02-JUN-2000.
XX
XX 22-NOV-1999; 99WO-EP08988.
XX
XX 23-NOV-1998; 98GB-0025632.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MEH.
XX
XX Feutren G, Howell RK, Marbach P, Roberts A, Schreier MH, Schulz M;
XX WPI; 2000-399934/34.
XX
XX Preventing or treating transplant rejection in a recipient comprises
XX administering a monoclonal antibody specific for interleukin-2 receptor
XX beyond the very early phase following transplantation -
XX
XX Disclosure; Page 2; 17pp; English.
XX
XX The present sequence is a human complementarity determining region (CDR).
XX This sequence was used to generate a humanised antibody specific for the
XX alpha subunit of interleukin-2 receptor (IL-2Ralpha). The humanised
XX IL-2Ralpha antibody would be useful for preventing or treating transplant
XX rejection in a recipient of organ, tissue or modified or unmodified cell
XX transplant. The use of a monoclonal antibody specific for IL-2R decreases
XX transplant rejection in an immunosuppression-intolerant or non-compliant
XX recipient compared with available therapies. Also, undesirable side
XX effects associated with current treatments e.g. renal dysfunction,
XX hirsutism, gingival hyperplasia and hypertension are avoided.
XX
XX Sequence 5 AA;
XX
XX Query Match 42.9%; Score 3; DB 21; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|
|
|
Db 3 WMH 5

RESULT 38
AA92158
ID AAY92158 standard; Peptide; 5 AA.
XX AC
XX AAY92158;
XX DT 01-AUG-2000 (first entry)
XX DE
XX DE Murine 15B8 heavy chain variable region CDR 1.
XX KW Heavy chain; variable region; complementarity determining region; CDR 1;
KW anti-Tie2 kinase receptor; monoclonal antibody; 15B8; angiogenetic;
KW vascular-general; proliferative; antiischemic; cerebroprotective;
KW cardiant; agonist; antibody inhibition.
XX OS
XX Mus musculus.
XX PN WO200018804-A1.
XX PD 06-APR-2000.
XX PF 28-SEP-1999; 99WO-US22428.
XX PR 28-SEP-1998; 98US-0102098.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.
XX PI Holmes SD, Erickson-millier CL, Winkler JD;
XX WPI; 2000-293114/25.
XX Tie2 receptor agonist antibodies useful for promoting angiogenesis in
PT patients suffering from strokes and myocardial infarctions
XX
XX Claim 12; Page 40; 50pp; English.
XX AAY92158-60 are heavy chain CDR (complementarity determining regions)
CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal
CC antibody 15B8. Tie2 is a single-transmembrane, tyrosine kinase receptor
CC ('Tie' stands for tyrosine kinase receptor with immunoglobulin and
CC endothelial growth factor (EGF) homology domain(s)). Anti-Tie2
CC antibodies may be administered to enhance angiogenesis in mammals
CC suffering from ischemic disease, myocardial infarction or cerebral stroke
CC or other vascular diseases such as diabetes. It may also be used to
CC enhance endothelial cell survival and to promote haematopoietic or
CC megakaryocyte cell proliferation (claimed).
XX
XX Sequence 5 AA;

Query Match 42.9%; Score 3; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|
|
|
Db 3 WMH 5

RESULT 39
AAY80139
ID AAY80139 standard; peptide; 5 AA.
XX AC
XX AAY80139;
XX DT 19-MAY-2000 (first entry)

XX Chimeric anti-CD25 antibody Ig heavy chain hypervariable region CDR1.
XX Chimeric anti-CD25 antibody; CD25 binding molecule; immunoglobulin;
KW hypervariable region; complementary determining region; CDR1; CDR2; CDR3;
KW inflammation; rheumatoid arthritis; hyperproliferative skin disease.
XX OS
XX Homo sapiens.
XX PN WO200006604-A2.
XX PD 10-FEB-2000.
XX PF 26-JUL-1999; 99WO-EP05316.
XX PR 27-JUL-1998; 98GB-0016281.
XX PR 27-MAY-1999; 99GB-0012460.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (UNLO) UNIV COLLEGE LONDON.
XX Amlot PL, Schreier MH;
XX WPI; 2000-183090/16.
XX Use of CD25 binding molecules in the treatment of rheumatoid arthritis
XX and inflammatory or hyperproliferative skin diseases -
XX Claim 1; Page 11; 14pp; English.
XX The present invention describes CD25 binding molecules, which are used
CC to treat rheumatoid arthritis and inflammatory or hyperproliferative
CC skin diseases. The CD25 binding molecule comprises at least one
CC antigen binding site comprising at least one domain which comprises in
CC sequence, the hypervariable regions CDR1 (having the sequence RYMH),
CC CDR2 (having the sequence AYPGNSDTSYNQFEG) and CDR3 (having the
CC sequence DYGVRDF), or their direct equivalents. The CD25 binding
CC molecules are used in the treatment of rheumatoid arthritis and
CC inflammatory or hyperproliferative skin diseases, such as psoriasis,
CC atypical dermatitis, contact dermatitis and further eczematous
CC dermatitises, seborrheic dermatitis, Lichen planus, Pemphigus,
CC bullous Pemphigoid, Epidermolysis bullosa, urticaria, angiodemas,
CC vasculitides, erythemas, cutaneous eosinophilias, Lupus erythematosus
CC and acne. A more preferred CD25 binding molecule for use in accordance
CC with the present invention is selected from a chimeric anti-CD25 antibody
CC which comprises at least: (1) one immunoglobulin heavy chain, or
CC fragment, which comprises (i) a variable domain comprising in sequence
CC the hypervariable regions CDR1, CDR2 and CDR3 (as above) and (ii) the
CC constant part, or fragment, of a human heavy chain; and (2) one
CC immunoglobulin light chain, or fragment, which comprises (i) a variable
CC domain comprising in sequence the hypervariable regions CDR1', CDR2',
CC and CDR3' (SASSISIMQ, DTSKLAS and HQRSSYT, respectively) and (ii) the
CC constant part, or fragment, of a human light chain.
XX
XX Sequence 5 AA;

Query Match 42.9%; Score 3; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|
|
|
Db 3 WMH 5

RESULT 40
AAO14422
ID AAO14422 standard; peptide; 5 AA.
XX AC
XX AAO14422;
XX DT 03-MAY-2002 (first entry)

PA (BURN-) BURNHAM INST.
 XX Ruoslahi EI, Pasqualini R, Arap W, Bredesen DE, Ellerby HM;
 XX WPI; 2001-451901/48.
 XX
 XX Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
 PT prostate cancer, comprises a prostate-homing peptide linked to an
 PT antimicrobial peptide -
 XX
 XX Example 9; Page 98; 176pp; English.
 PS
 XX The patent discloses novel chimeric prostate-homing pro-apoptotic
 CC peptide which comprises a prostate-homing peptide linked to an
 CC antimicrobial peptide, where the chimeric peptide is selectively
 CC internalised by and exhibits high toxicity to prostate tissue and
 CC where the antimicrobial peptide has low mammalian cell toxicity when
 CC not linked to prostate-homing peptide. The chimeric peptide is used
 CC to direct an antimicrobial peptide in vivo to a prostate cancer, to
 CC induce selective toxicity in vivo in a prostate cancer, and to treat
 CC a patient with prostate cancer. The present sequence is mouse prostate
 CC homing peptide. This sequence is useful in the homing of pro-apoptotic
 CC conjugates of the invention.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 42.9%; Score 3; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 HQP 6
 DB 2 HQP 4

RESULT 43
 AAB71236
 ID AAB71236 standard; peptide; 5 AA.
 XX
 AC AAB71236;
 XX
 DT 26-NOV-2002 (first entry)
 XX
 DE Murine IgG1 catabolic site fragment SEQ ID 26.
 XX
 KW IgG; 9E10; immunoglobulin G; Fc receptor; FcRn; drug; murine;
 KW T-cell receptor binding ligand.
 XX
 OS Mus musculus.
 XX
 FN US2002098193-A1.
 XX
 PD 25-JUL-2002.
 XX
 XX 20-AUG-2001; 2001US-0933497.
 PF
 PR 03-MAR-1997; 97US-0811463.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Ward ES;
 PI
 XX WPI; 2002-681920/73.
 DR
 XX Composition for increasing serum half-life of agent, comprises mutant
 PT immunoglobulin G molecule or IgG Fc-hinge fragment and having increased
 PT serum half-life relative to IgG or relative to serum half-life of IgG -
 XX
 XX Disclosure; Page 10; 68pp; English.
 PS
 XX This invention describes a novel composition comprising a mutant
 CC immunoglobulin G (IgG) molecule or IgG Fc-hinge fragment. The mutant IgG
 CC molecule has an increased serum half-life relative to IgG and has one

CC amino acid substitution in the Fc-hinge region. The mutant IgG Fc-hinge
 CC fragment has an increased serum half-life relative to serum half-life of
 CC IgG, where the fragment has increased binding affinity for Fc receptor
 CC (FcRn) or has same or slightly lower affinity than IgG for binding to
 CC FcRn. The composition is useful for increasing the serum half-life of an
 CC agent, by conjugating the agent to a mutant IgG or IgG Fc hinge fragment
 CC having an increased serum half life, where the agent is a therapeutic
 CC drug, antigen binding polypeptide, antigen or receptor binding ligand.
 CC The receptor binding ligand is a T-cell receptor binding ligand. The
 CC composition is broadly applicable to an unlimited number of the
 CC therapeutic uses for the treatment of diseases or disorders as it can be
 CC used to reduce costs and discomfort to the patient by reducing the number
 CC of therapeutic doses needed. This sequence represents a fragment of
 CC murine IgG1 corresponding to the catabolic site described in the
 CC disclosure of the invention.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 42.9%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MHQ 5
 DB 2 MHQ 4

RESULT 44
 AAU86924
 ID AAU86924 standard; Peptide; 5 AA.
 XX
 AC AAU86924;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Immunoglobulin catalytic domain associated peptide #1.
 XX
 KW Immunoglobulin; IgG; fragment of crystallisation; Fc; Fc receptor;
 KW FcRn; Immunotherapeutic; vaccination.
 XX
 OS Synthetic.
 XX
 PN US6277375-B1.
 XX
 PD 21-AUG-2001.
 XX
 PF 03-MAR-1997; 97US-0811463.
 XX
 PR 03-MAR-1997; 97US-0811463.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Ward ES;
 PI
 XX WPI; 2002-214477/27.
 DR
 XX Composition comprising mutant immunoglobulin (Ig)G molecule having
 PT increased half-life relative to IgG, decreasing endogenous serum IgG in
 PT a subject, comprises amino acid substitutions in Fc-hinge fragment -
 XX
 XX Disclosure; Column 83; 62pp; English.
 PS
 XX The invention describes a composition comprising mutant immunoglobulin
 CC (Ig)G and IgG domains such as crystallisation fragment (Fc)-hinge
 CC fragments having an increased serum half-life allowing extended
 CC interaction with the Fc receptor, FcRn. The mutant IgG has amino acid
 CC substitutions (in CH2 domain of the Fc-hinge) of Thr to Leu at position
 CC 252, Thr to Ser at position 254, and Thr to Phe at position 256, or has
 CC amino acid substitutions (in CH3 domain of Fc-hinge) of His to Lys at
 CC position 433, His to Tyr at position 435, and His to Tyr at position 436.
 CC The composition has immunotherapeutic uses e.g. in vaccination, and is
 CC useful for decreasing endogenous serum IgG in a subject. The composition
 CC reduces the cost and discomfort to the patient by reducing the number of

CC therapeutic doses since the mutant immunoglobulin has increased serum
 CC half-life and persistence. This sequence represents a peptide associated
 CC with catalytic domains of the immunoglobulin and mutant immunoglobulin
 CC discussed in the invention.

XX SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
 |||
 Db 2 MHQ 4

RESULT 45

AAU11183
 ID AAU11183 standard; Peptide; 5 AA.

XX AC AAU11183;

DT 25-FEB-2002 (first entry)

XX DE Mouse antibody Act-1/LDP-02, heavy chain variable region CDR1.

XX KW Mouse; antibody; Act-1; alpha4beta7 integrin; anti-inflammatory;
 KW anti-asthmatic; immunosuppressive; heavy chain variable region;
 KW humanised antibody; LDP-02; leukocyte infiltration; mucosal tissue;
 KW quiescent inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; ileitis; Crohn's disease; nontropical sprue;
 KW enteropathy; seronegative arthropathy; collagenous colitis;
 KW eosinophilic gastroenteritis; pouchitis; ileocolic anastomosis;
 KW pancreatitis; insulin-dependent diabetes mellitus; mastitis;
 KW cholecystitis; cholangitis; pericholangitis; chronic bronchitis;
 KW chronic sinusitis; asthma; graft versus host disease; CDR1;
 KW complementarity determining region.

XX OS Mus musculus.

XX PN WO200178779-A2.

XX PD 25-OCT-2001.

XX PF 13-APR-2001; 2001WO-US12234.

XX PR 14-APR-2000; 2000US-0550082.

XX PR 27-DEC-2000; 2000US-0748960.

XX PA (MILL-) MILLENNIUM PHARM INC.
 (GETH) GENENTECH INC.

XX PI Brettman LR, Fox JA, Allison DE;

XX DR WPI; 2002-055233/07.

XX PT Treating a human with a disease associated with leukocyte infiltration
 PT of mucosal tissues, e.g. inflammatory bowel disease, asthma or graft
 PT versus host disease, by administering an anti-alpha4 beta 7 integrin
 PT antibody -

XX PS Claim 8; Fig 5; 81pp; English.

XX CC The invention relates to treating a human having a disease associated
 CC with leukocyte infiltration of mucosal tissues, comprising administering
 CC a humanised immunoglobulin (e.g. the humanised version of mouse
 CC antibody Act-1, LDP-02) or its antigen-binding fragment, which has
 CC binding specificity for alpha4beta7 integrin. The immunoglobulin or its
 CC fragment comprises an antigen binding region of non-human origin and at
 CC least a portion of an antibody of human origin. Also included is a method
 CC for inhibiting relapse and/or recurrence of quiescent inflammatory bowel
 CC disease in a human by administering the humanised immunoglobulin or its
 CC antigen-binding fragment, which has binding specificity for alpha4beta7

CC integrin. The treatment is used for treating a human having a disease
 CC associated with leukocyte infiltration of mucosal tissues, e.g.
 CC inflammatory bowel disease (e.g. ulcerative colitis, Crohn's disease,
 CC ileitis, Coeliac disease, nontropical sprue, enteropathy associated with
 CC seronegative arthropathies, microscopic or collagenous colitis,
 CC eosinophilic gastroenteritis, pouchitis and ileocolic anastomosis),
 CC pancreatitis, insulin-dependent diabetes mellitus, mastitis,
 CC cholecystitis, cholangitis, pericholangitis, chronic bronchitis,
 CC chronic sinusitis, asthma or graft versus host disease. The method is
 CC also useful for inhibiting relapse and/or recurrence of quiescent
 CC inflammatory bowel disease in a human, where quiescence has been induced
 CC by medical or surgical therapy. The present sequence is a mouse
 CC Act-1/LDP-02 antibody heavy chain variable region complementarity
 CC determining region as incorporated into the humanised antibody of the
 CC invention.

XX SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
 |||

Db 3 WMH 5

RESULT 46

ABB82654
 ID ABB82654 standard; peptide; 5 AA.

XX AC ABB82654;

XX DT 19-FEB-2003 (first entry)

XX DE CDR1 fragment of a chimeric anti-CD25 antibody.

XX KW CD25; immunosuppressive; hepatotropic; antiasthmatic; dermatological;
 KW antiarthritic; cytostatic; nephrotropic; neuroprotective; antitumor;
 KW antiinflammatory; vasotropic; complementarity determining region;
 KW steroid; CDR; anti-CD25 antibody.

XX OS Unidentified.

XX PN WO200281508-A2.

XX PD 17-OCT-2002.

XX PF 05-APR-2002; 2002WO-EP03808.

XX PR 06-APR-2001; 2001GB-0008816.

XX PR 06-APR-2001; 2001GB-0008817.

XX PR 06-APR-2001; 2001GB-0008821.

XX PA (UYBR-) UNIV BRISTOL.

XX PI Hearing SD, Dayan CM, Norman MR;

XX DR WPI; 2003-067514/06.

XX PT CD25 binding molecules useful for prevention and treatment of
 PT autoimmune hepatitis, asthma, eczema, vasculitis, temporal arthritis,
 PT leukemia, multiple sclerosis and Crohn's disease in steroid-resistant
 PT patients -

XX PS Claim 1; Page 20; 22pp; English.

XX CC The invention relates to a CD25 binding molecule (I) comprising at least
 CC one antigen binding site having at least one domain which comprises in
 CC sequence, the hypervariable regions CDR1, CDR2 and CDR3 (complementarity
 CC determining region), for use in prevention or treatment of diseases such
 CC as autoimmune hepatitis, asthma, eczema, vasculitis, temporal arthritis,
 CC leukemia, glomerulonephritis, multiple sclerosis and Crohn's disease in a

CC steroid-resistant patient. (I) is useful in the manufacture of a
 CC medicament for use in the prevention and treatment of autoimmune
 CC hepatitis, asthma, eczema, vasculitis, temporal arthritis, systemic lupus
 CC erythematosus, leukemia, glomerulonephritis, multiple sclerosis,
 CC ulcerative colitis, sarcoid and Crohn's disease in a steroid-sensitive or
 CC steroid-resistant patient. (I) is coadministered with a further drug
 CC substance. The use of CD25 binding molecules make the steroid-sensitive
 CC patients respond quicker and allow a lower dose of steroids to be used,
 CC thus significantly reducing the side effects of steroid treatments. The
 CC present sequence represents a hypervariable CDR1 fragment of a chimeric
 CC anti-CD25 antibody, a CD25 binding molecule.

SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 24; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
 ||||
 Db 3 WMH 5

RESULT 47

AAR11738
 ID AAR11738 standard; Protein; 6 AA.

XX AC AAR11738;

XX DT 25-MAR-2003 (updated)

DT 02-JUL-1991 (first entry)

XX DE Peptide epitope derived from P69 gene.

XX KW Yeast; Bordetella pertussis; P69; fusion protein; vaccine;
 KW whooping cough.

XX OS Synthetic.

XX PN EP425082-A.

XX PD 02-MAY-1991.

XX PF 03-SEP-1990; 90EP-0309614.

XX PR 04-SEP-1989; 89GB-0019940.

XX PR 21-MAY-1990; 90GB-0011358.

XX PA (WELL) WELLCOME FOUND LTD.

XX PI Charles IG, Fairweather NF;

XX DR WPI; 1991-126587/18.

XX PT Polypeptide for vaccine against eg Bordetella pertussis -

PT comprises amino acid sequence encoded by P 69 gene of B. pertussis

PT CN2992, or another strasin of B. pertussis or B. parapertussis.

XX PS Claim 6; Page 12; 24pp; English.

XX CC The peptide is composed of the amino acids encoded by nucleotides
 CC 1885-1902 of the P.69 gene of Bordetella pertussis CN 2992. It is
 CC an epitope and can be used to prepare a vaccine against whooping
 CC cough. The peptide may be synthesised by std. methods or produced
 CC as a recombinant fusion protein with the N-terminal of the HBV core
 CC antigen, pref. under control of the GAL7 promoter.

CC See also AAR11737 and AAR11739.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 ||||
 Db 4 QPP 6

RESULT 48

AAR24983
 ID AAR24983 standard; Protein; 6 AA.

XX AC AAR24983;

XX DT 25-MAR-2003 (updated)

DT 04-DEC-1992 (first entry)

XX DE Arg-Arg contg. antimicrobial peptide.

XX KW Binding assays; acceptor; antibody; diagnosis; therapeutic agents;

XX KW multiple oligomer mixture; antimicrobial.

XX OS Synthetic.

XX PN WO9209300-A1.

XX PD 11-JUN-1992.

XX PF 20-NOV-1991; 91WO-US08694.

XX PR 21-NOV-1990; 90US-0617023.

XX PR 16-MAY-1991; 91US-0701658.

XX PR 19-NOV-1991; 91US-0797551.

XX PA (ITER-) ITEREX PHARM LP.

XX PI Appel JR, Blondelle S, Cuervo JH, Houghten RA, Pinilla C;

XX DR WPI; 1992-216794/26.

XX CC Synthesis of multiple oligomer mixts., esp. oligopeptide mixts. - by
 PT coupling solid support particles with monomeric repeating unit
 PT cpds., used in binding assays for acceptors or antibodies and
 PT diagnosis
 XX Example; Page 142; 198pp; English.

XX CC The sequence is that of an oligopeptide which forms part of an
 CC equimolar mixture of monomeric repeating unit oligopeptides. The
 CC oligomer mixture can be used in binding assays for acceptors or
 CC antibodies, in diagnosis and for identifying therapeutic agents.

CC The peptide inhibits growth of E.coli (IC-50 24ug/ml).

CC See also AAR2498-R24510, AAR24960-R25016 and AAR25018-R25035.

CC (Updated on 25-MAR-2003 to correct PN field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4

||||

Db 4 WMH 6

RESULT 49

AAR62181

ID AAR62181 standard; Protein; 6 AA.

XX AC AAR62181;

XX DT 25-MAR-2003 (updated)

PA (FOUG-) HOUGHTEN PHARM INC.
 XX Appel JR, Houghten RA, Pinilla C;
 DR WPI; 1996-432985/43.
 XX Identifying oligopeptide ligands for an acceptor - by scanning
 PT synthetic peptide combinatorial libraries comprising
 XX self-solubilising, unsupported mixed oligopeptide(s)
 PS Example 5; Column 52; 75pp; English.
 XX The invention relates to a method of identifying oligopeptide ligands to
 CC a protein by scanning synthetic combinatorial peptide libraries (SCPL).
 CC The SCPL comprise sets of hexamers which contain either one of 6
 CC predetermined amino acids at one predetermined position in the hexamer
 CC and each set may have one predetermined amino acid at 1 of 6
 CC predetermined pos. in the hexamer. The method is useful for identifying
 CC biologically active sequences of e.g. pharmaceutical use. The peptides
 CC esp. inhibit the binding of e.g. an antibody to its antigen, a ligand to
 CC its receptor, etc.
 CC met-enkephalin
 CC The peptides AAW08641-66 and AAW09226-35 are N-terminally acylated and
 CC C-terminally amidated peptides, isolated from a SCPL, which inhibit the
 CC Met-enkephalin analogue (D-Ala,Mephe,Gly-O)-enkephalin (DAGO) from
 CC binding to the mu opioid receptor. This peptide inhibits binding with
 CC an IC50 of about 21 nM.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 17; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
 ||||
 Db 4 WMH 6

RESULT 52
 AAY29633
 ID AAY29633 standard; peptide; 6 AA.
 AC AAY29633;
 XX 19-OCT-1999 (first entry)
 XX Phosphoenolpyruvate carboxylase peptide #2.
 DE Phosphoenolpyruvate carboxylase peptide #2.
 XX Phosphoenolpyruvate carboxylase; PEPC; organic acid; succinic acid;
 KW aerobic Coryneform microbe; Brevibacterium flavum MJ-233.
 XX Brevibacterium flavum.
 OS JP11196887-A.
 XX JP11196887-A.
 FN 27-JUL-1999.
 XX 16-JAN-1998; 98JP-0020360.
 XX 16-JAN-1998; 98JP-0020360.
 XX (MITU) MITSUBISHI CHEM CORP.
 PA WPI; 1999-496658/42.
 DR Preparation of organic acid e.g. succinic acid - comprises reacting
 XX phosphoenol-pyruvate carboxylase gene recombinant microbe
 PT anaerobically with substrate
 XX Example 1; Page 13; 18pp; Japanese.

CC The present invention describes the preparation of an organic acid
 CC comprising reacting an aerobic Coryneform microbe recombined by
 CC phosphoenolpyruvate carboxylase (PEPC) gene anaerobically with an
 CC organic raw material in a reaction liquid containing carbonate ion,
 CC bicarbonate ion or carbon dioxide gas. The method can prepare an
 CC organic acid such as succinic acid efficiently in a high yield. The
 CC present sequence represents a peptide from Brevibacterium flavum MJ-233
 CC PEPC, used in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3
 ||||
 Db 1 SWM 3

RESULT 53
 AAY36355
 ID AAY36355 standard; Protein; 6 AA.
 XX AAY36355;
 AC AAY36355;

XX 17-SEP-1999 (first entry)
 XX Fragment of human secreted protein encoded by gene 3.
 DE Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS.

XX Homo sapiens.

XX WO9931117-A1.

XX 24-JUN-1999.

XX 17-DEC-1998; 98WO-US27059.

XX 19-DEC-1997; 97US-0068369.

XX 18-DEC-1997; 97US-0068006.

XX 18-DEC-1997; 97US-0068007.

XX 18-DEC-1997; 97US-0068008.

XX 18-DEC-1997; 97US-0068053.

XX 18-DEC-1997; 97US-0068054.

XX 18-DEC-1997; 97US-0068057.

XX 18-DEC-1997; 97US-0068064.

XX 18-DEC-1997; 97US-0070923.

XX 19-DEC-1997; 97US-0068169.

XX 19-DEC-1997; 97US-0068365.

XX 19-DEC-1997; 97US-0068367.

XX 19-DEC-1997; 97US-0068368.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Carter KC, Duan RD, Feng P, Ferrie AM, Florence C;
 PI Florence K, Greene JM, Janat F, Kyaw H, Moore PA;
 PI Ni J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y;
 PI Yu G;

XX WPI; 1999-418749/35.

XX New isolated human genes encoding secreted polypeptides
 PT Disclosure; Page 419; 537pp; English.

XX AAX97916 to AAX98029 represent 110 isolated human secreted protein

CC genes. AAY36224 to AAY36727 represent the secreted proteins encoded by
 CC the 110 human genes. The genes and their corresponding secreted
 CC polypeptides are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new genes.
 CC Specific uses are described for each of the 110 genes, based on which
 CC tissues they are most highly expressed in, and include developing
 CC products for the diagnosis or treatment of cancer, tumours, developmental
 CC abnormalities and foetal deficiencies, blood disorders, diseases of the
 CC immune system, autoimmune diseases, inflammation, allergies, Alzheimer's
 CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,
 CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular
 CC disorders, kidney disorders, digestive/endocrine disorders, infections
 CC and AIDS. The polypeptides are also useful for identifying their binding
 CC partners. The sequences given in AAX97907 to AAX97915 and AAY36223 are
 CC used in the exemplification of the present invention.

XX SQ Sequence 6 AA;
 Query Match 42.9%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
 Db 4 HQP 6

RESULT 54

AAB28300
 ID AAB28300 standard; Peptide; 6 AA.

AC AAB28300;

DT 14-FEB-2001 (first entry)

XX Human secreted peptide #17 encoded by cDNA#23.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200058355-A1.

XX 05-OCT-2000.

XX 22-MAR-2000; 2000WO-US07527.

XX 26-MAR-1999; 93US-0126501.

XX 22-DEC-1999; 93US-0171551.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-602358/57.

XX N-PSDB; AAC67653.

XX Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -

XX Claim 11; Page 346; 367pp; English.

XX Sequences AAB28278-B28326 represent the amino acid sequences of 50
 CC human secreted proteins encoded by the genes AAC67631-C67680. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from

CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

XX SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
 Db 1 WMH 3

RESULT 55

AAB72258
 ID AAB72258 standard; peptide; 6 AA.

AC AAB72258;

DT 14-MAY-2001 (first entry)

XX Colostrin derived cytokine inducing peptide SEQ ID 13.

XX Colostrin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrin as an immunological
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and

CC acquired immunological deficiencies.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 3 QPP 5

RESULT 56

AAB72511
ID AAB72511 standard; Peptide; 6 AA.

XX AC AAB72511;

DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #12.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22865.

XX 17-AUG-1999; 99US-0149310.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

DR WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations -

PS Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidizing species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 3 QPP 5

RESULT 57

AAB72543
ID AAB72543 standard; Peptide; 6 AA.

XX AC AAB72543;

DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #12.

XX Neuroprotective; neural cell differentiation regulator; colostrinin; colostrum.

XX Unidentified.

XX WO200112651-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22774.

XX 17-AUG-1999; 99US-0149633.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I;

XX WPI; 2001-226545/23.

XX Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient -

PS Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 3 QPP 5

RESULT 58

AAB59319

ID AAB59319 standard; Peptide; 6 AA.

XX AC AAB59319;

DT 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment B-4.

XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX
SQ Sequence 6 AA;
Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QPP 7
Db 3 QPP 5
RESULT 59
AAB55512
ID AAB55512 standard; Peptide; 6 AA.
XX
AC AAB55512;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human elastase variant segment peptide SEQ ID NO:82.
XX
KW Human; elastase; variant; substrate; mutant; mutagenesis; histidine;
KW human neutrophil elastase; H43A; cytosolic; proteolysis; ADEPT;
KW antibody-directed enzyme activated prodrug therapy.
XX
XX Homo sapiens.
XX
FN WO200068363-A2.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-US06692.
XX
PR 05-MAY-1999; 99US-0132640.
XX
PA (GETH) GENENTECH INC.
XX
PI Carter PJ, Dall'Acqua W, Rodrigues M;
XX
DR WPI; 2001-007389/01.
XX
PT Elastase variant (H43A) having altered substrate specificity useful for
PT antibody-directed enzyme activated prodrug therapy -
XX
PS Example 4; Fig 3; 79pp; English.
XX
CC The present invention describes a purified elastase variant (I) with
CC an amino acid sequence different from that of a precursor elastase,
CC the difference comprising a substitution of an active site histidine
CC residue corresponding to residue 43 in human neutrophil elastase with
CC a different amino acid residue so that (I) has substrate specificity
CC substantially different from the precursor elastase. (I) has cytostatic
CC activity, and can be used in antibody-directed enzyme activated prodrug
CC therapy. The elastase variant can be used to cleave a particular
CC substrate, especially those containing histidine residues at the
CC substrate site. Site-specific proteolysis is useful in therapeutic
CC applications, e.g. for antibody-directed enzyme activated prodrug

CC therapy (ADEPT). AAC88022, AAC88023 and AAB55432 to AAB55526 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 6 AA;
Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 MHQ 5
Db 2 MHQ 4
RESULT 60
AAE20240
ID AAE20240 standard; peptide; 6 AA.
XX
AC AAE20240;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #12.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnary.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "Optionally C-terminal amide"
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22776.
XX
PR 17-AUG-2000; 2000WO-US22776.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2002-269151/31.
XX
PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
PS Claim 6; Page 25; 51pp; English.
XX
CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidizing species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.

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XX Sequence 6 AA;
SQ
Query Match 42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
   |||
Db 3 QPP 5

RESULT 61
AAMS1047
ID AAMS1047 standard; Peptide; 6 AA.
XX
AC AAMS1047;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide.
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "Optional C-terminal amidation"
XX
PN WO200213849-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22775.
XX
PR 17-AUG-2000; 2000WO-US22775.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
XX WPI; 2002-369150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue -
XX
PS Claim 1; Page 34; 54pp; English.
XX
CC The present sequence is that of a colostrinin constituent peptide
CC that is used as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. The peptide is
CC classified as having a beta-casein homologue precursor. Methods
CC are claimed for: inducing a cytokine in a cell by contact with an
CC immunological regulator, where the cell is present in a cell
CC culture, a tissue, an organ or an organism, and the cell is
CC mammalian, including human; modulating an immune response in a cell
CC by contact with the immunological regulator under conditions
CC effective to induce a cytokine; modulating an immune response in a
CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator
CC is administered topically or as part of a dietary supplement, and
CC where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation
CC by contacting blood cells with a blood cell regulator, where the
CC blood cells are present in a cell culture or an organism, are
CC mammalian or human, and where the blood cells are increased in
CC number or differentiated; and a method for modulating blood cell
CC proliferation in a patent. A claimed cytokine-inducing composition
CC comprises a pharmaceutical carrier and an active agent such as the

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CC present peptide.
XX
SQ Sequence 6 AA;
Query Match 42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
   |||
Db 3 QPP 5

RESULT 62
AAO14589
ID AAO14589 standard; peptide; 6 AA.
XX
AC AAO14589;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 12.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "Optional C-terminal amide"
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22777.
XX
PR 17-AUG-2000; 2000WO-US22777.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
XX WPI; 2002-369152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog -
XX
XX Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX
SQ Sequence 6 AA;
Query Match 42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
   |||
Db 3 QPP 5

```

RESULT 63
 AAR77269
 ID AAR77269 standard; peptide; 7 AA.
 XX AC
 XX AAR77269;
 XX AC
 DT 06-FEB-1996 (first entry)
 XX AC
 DE MRSA-230 tryptic peptide fragment #3.
 XX AC
 XX Tryptic peptide; Staphylococcus aureus; methicillin-resistant; antibody;
 KW detection; vaccine; slide agglutination assay; lysostaphin digestion.
 KW Staphylococcus aureus.
 XX OS
 XX Staphylococcus aureus.
 XX PN WO9516915-A1.
 XX XX
 PD 22-JUN-1995.
 XX XX
 XX 14-DEC-1994; 94WO-FI00564.
 PF XX
 XX 17-DEC-1993; 93US-0169524.
 PR XX
 XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 PA XX
 XX Hilden P, Kuusela P;
 PI XX
 XX WPI; 1995-231663/30.
 DR XX
 XX Detection of Staphylococcus aureus esp. methicillin-resistant
 PT strains - using anti-MRSA-230 antibodies which may be used in
 PT vaccine compositions to promote an immune response against S. aureus
 XX
 XX Example 3; Page 14; 30pp; English.
 PS XX
 XX The sequences represented by AAR77267-72 are tryptic peptide fragments
 CC for MRSA-230. These fragments could be used to generate a set of probes
 CC for MRSA-230. MRSA-230 is a 230kD protein that was isolated from
 CC lysostaphin digests of methicillin-resistant Staphylococcus aureus. The
 CC S. aureus used test negative in standard S. aureus agglutination assays.
 CC Anti-MRSA-230 antibodies can be constructed by immunising rabbits with
 CC heat killed S. aureus that are agglutination negative. The S. aureus used
 CC to create these antibodies contain the MRSA-230 protein and this protein
 CC was the principle target of the antibodies. The antibodies can then be
 CC used in a method of detection of methicillin-resistant S. aureus that are
 CC not detected in slide agglutination assays. MRSA-230, and its active
 CC fragments, can be used in vaccine compositions which promote an immune
 CC response to MRSA-230 and S. aureus.
 XX
 SQ Sequence 7 AA;
 Query Match 42.9%; Score 3; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 Qpp 7
 Db 1 Qpp 3
 RESULT 64
 AAR73902
 ID AAR73902 standard; peptide; 7 AA.
 XX AC
 XX AAR73902;
 XX AC
 DT 25-MAR-2003 (updated)
 DT 05-DEC-1995 (first entry)
 XX XX
 DE Streptococcus pneumoniae surface protein A peptide 423-429.
 XX Streptococcus pneumoniae; surface protein A; vaccine;
 KW

KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
 XX viral; peptide 423-429.
 XX OS
 XX Streptococcus pneumoniae.
 XX PN WO9509232-A2.
 XX PD
 XX 06-APR-1995.
 XX XX
 XX 28-SEP-1994; 94WO-CA00516.
 PP XX
 XX 28-SEP-1993; 93US-0127499.
 PR XX
 XX (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX XX
 XX Sharma LR, Van Alstyne D;
 PI WPI; 1995-147431/19.
 XX XX
 XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 XX Claim 35; Page 76; 98pp; English.
 XX XX
 CC AAR73912 is the Streptococcus pneumoniae surface protein A. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in AAR73890 and AAR73902, which are recognised by a monoclonal
 CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
 CC peptides may be used in immunoassays to diagnose the presence of
 CC bacterial and/or viral meningitis agents in a sample, or in
 CC prophylactic and therapeutic meningitis treatments. The peptides may
 CC also be used as vaccines against meningitis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 7 AA;
 Query Match 42.9%; Score 3; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 Qpp 7
 Db 3 Qpp 5
 RESULT 65
 AAR73883
 ID AAR73883 standard; peptide; 7 AA.
 XX AC
 XX AAR73883;
 XX DT
 DT 25-MAR-2003 (updated)
 DT 05-DEC-1995 (first entry)
 XX XX
 DE Rubella virus glycosylated membrane-associated protein E2 313-319.
 XX XX
 KW Rubella virus; glycosylated membrane associated protein E2; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS;
 KW RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KW viral; peptide 313-319; Therien strain.
 XX
 XX Rubella virus.
 OS XX
 XX WO9509232-A2.
 PN XX
 XX 06-APR-1995.
 PD XX
 XX 28-SEP-1994; 94WO-CA00516.
 PF XX
 XX

PR 28-SEP-1993; 93US-0127499.
 XX (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 XX Sharma LR, Van Alstyne D;
 PI WPI; 1995-147431/19.
 DR
 XX
 XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 PS Claim 35; Page 75; 98pp; English.
 XX
 XX AAR73917 is the Rubella virus Thersien strain glycosylated membrane
 CC associated protein E2. It contains the meningitis related antigenic
 CC sequences (MRHAS) claimed in AAR73883-R73885 and AAR73897, which are
 CC recognised by a monoclonal antibody from the hybridoma Rubella
 CC virus (RV)-1. The claimed MRHAS peptides may be used in
 CC immunoassays to diagnose the presence of bacterial and/or viral
 CC meningitis agents in a sample, or in prophylactic and therapeutic
 CC against meningitis. The peptides may also be used as vaccines
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 7 AA;
 Query Match 42.9%; Score 3; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 Db ||| 3 QPP 5
 XX
 RESULT 66
 AAR73897
 ID AAR73897 standard; peptide; 7 AA.
 XX
 XX AAR73897;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-DEC-1995 (first entry)
 XX
 XX Rubella virus glycosylated membrane-associated protein E2 313-319.
 XX
 XX Rubella virus; glycosylated membrane associated protein E2; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS;
 KW RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial;
 XX viral; peptide 313-319; Thersien strain.
 XX
 OS Rubella virus.
 XX
 PN WO9509232-A2.
 XX
 PD 06-APR-1995.
 XX
 XX 28-SEP-1994; 94WO-CA00516.
 PF
 XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 XX Claim 35; Page 75; 98pp; English.
 PS
 XX AAR73916 is the Rubella virus strain M33 core structural polypeptide.
 CC It contains the meningitis related antigenic sequences (MRHAS)
 CC claimed in AAR73879-R73882, which are recognised by a monoclonal
 CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
 CC peptides may be used in immunoassays to diagnose the presence of
 CC bacterial and/or viral meningitis agents in a sample, or in
 PT meningitis - the peptide(s) corresp. to homologous antigenic

PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 PS Claim 35; Page 75; 98pp; English.
 XX
 XX AAR73915 is the Rubella virus Thersien strain glycosylated membrane
 CC associated protein E2. It contains the meningitis related antigenic
 CC sequences (MRHAS) claimed in AAR73883-R73885 and AAR73897, which are
 CC recognised by a monoclonal antibody from the hybridoma Rubella
 CC virus (RV)-1. The claimed MRHAS peptides may be used in
 CC immunoassays to diagnose the presence of bacterial and/or viral
 CC meningitis agents in a sample, or in prophylactic and therapeutic
 CC against meningitis. The peptides may also be used as vaccines
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 7 AA;
 Query Match 42.9%; Score 3; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 Db ||| 3 QPP 5
 XX
 RESULT 67
 AAR73879
 ID AAR73879 standard; peptide; 7 AA.
 XX
 XX AAR73879;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-DEC-1995 (first entry)
 XX
 XX Rubella virus strain M33 core structural peptide MRHAS 102-108.
 XX
 KW Rubella virus; strain M33; core structural polypeptide; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
 XX viral; peptide 102-108.
 XX
 OS Rubella virus.
 XX
 PN WO9509232-A2.
 XX
 PD 06-APR-1995.
 XX
 XX 28-SEP-1994; 94WO-CA00516.
 PF
 XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 XX Claim 35; Page 75; 98pp; English.
 PS
 XX AAR73916 is the Rubella virus strain M33 core structural polypeptide.
 CC It contains the meningitis related antigenic sequences (MRHAS)
 CC claimed in AAR73879-R73882, which are recognised by a monoclonal
 CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
 CC peptides may be used in immunoassays to diagnose the presence of
 CC bacterial and/or viral meningitis agents in a sample, or in

CC prophylactic and therapeutic meningitis treatments. The peptides
 CC may also be used as vaccines against meningitis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 7 AA;
 Query Match 42.9%; Score 3; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 ||||
 Db 3 QPP 5
 RESULT 68
 AAY20876
 ID AAY20876 standard; Protein; 7 AA.
 AC
 XX
 XX
 XX
 XX 22-JUL-1999 (first entry)
 DE Human presenilin 1 mutant protein fragment 22.
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9845322-A2.
 PN
 PD 15-OCT-1998.
 XX
 XX
 PF 02-APR-1998; 98WO-IB00705.
 XX
 XX
 PR 10-APR-1997; 97US-0043163.
 XX
 XX (UYUT-) RIJKSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 DR WPI; 1998-609901/51.
 DR N-PSDB; AAX75761.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA
 XX
 XX Disclosure; Figure 10; 258pp; English.
 PS
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be

CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 7 AA;
 Query Match 42.9%; Score 3; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPP 7
 ||||
 Db 2 QPP 4
 RESULT 69
 AAW61049
 ID AAW61049 standard; peptide; 7 AA.
 XX
 AC AAW61049;
 XX
 XX 25-SEP-1998 (first entry)
 DT Peptide from mouse IgG1 that is important for FcRn binding.
 DE
 DE Immunoglobulin G; IgG; FcRn binding; half-life; increase; decrease;
 KW treatment; idiopathic thrombocytopenic purpura; ITP;
 KW Kawasaki disease; AIDS; Guillain-Barre syndrome; dermatomyositis.
 XX
 XX Synthetic.
 OS
 OS Mus sp.
 XX
 XX WO9823289-A1.
 FN
 XX
 XX 04-JUN-1998.
 PD
 XX
 XX 26-NOV-1997; 97WO-US21437.
 PF
 XX
 XX 27-NOV-1996; 96US-0031607.
 PR
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 PA (UYBR-) UNIV BRANDEIS.
 XX
 XX Israel EJ, Simister NE;
 FI
 XX
 XX WPI; 1998-322461/28.
 DR
 XX
 XX New antibody having altered Fc receptor binding site - allows
 XX increased or decreased half-lives and clearance rates, useful for,
 PT e.g. tumour imaging or treatment of AIDS
 PT
 XX
 XX Example 2; Fig 2A; 32pp; English.
 PS
 CC AAW61048-57 represent partial amino acid sequence of different
 CC immunoglobulin G (IgG) molecules. These peptides have been identified
 CC as being important for FcRn binding. The specification describes a
 CC non-naturally occurring IgG having an altered amino acid sequence
 CC compared to native IgG, which binds to FcRn with increased or
 CC decreased affinity. FcRn is a receptor found on the intestinal surface
 CC of the neonate and is responsible passage of maternal milk IgG from the
 CC intestinal lumen to the systemic circulation via the intestinal
 CC epithelial cells. FcRn is also used to prevent clearance of circulating
 CC IgG from the circulation. Altering the binding site on an IgG for FcRn
 CC allows greater or lower affinity for the FcRn receptor, which
 CC subsequently increases or decreases the half-life of circulating IgG,
 CC respectively. IgG's with an increased half-life can be used to treat
 CC immune conditions or diseases such as idiopathic thrombocytopenic

CC purpura (ITP), Kawasaki disease, AIDS, Guillain-Barre syndrome and
 XX dermatomyositis.

SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
 DB 2 MHQ 4

RESULT 70

AA16906
 ID AAY16906 standard; peptide; 7 AA.

XX AC AAY16906;

XX DT 20-JUL-1999 (first entry)

XX DE Heat shock protein (hsp) binding peptide.

XX KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
 KW acquired immune deficiency; autoimmune disease.

XX OS Synthetic.

XX PN WO9922761-A1.

XX PD 14-MAY-1999.

XX PF 22-OCT-1998; 98WO-US22335.

XX PR 31-OCT-1997; 97US-0961707.

XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;
 PI Querfelli O, Rothman JE;

XX WPI; 1999-313177/26.

XX PT Identifying peptides which bind heat shock proteins

XX PS Examples; Page 20; 155pp; English.

CC The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target, and bound to a benzalkonium ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases.

XX SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6

DB 1 HQP 3

RESULT 71

AA16495

ID AAB16495 standard; Peptide; 7 AA.

XX AC AAB16495;

XX DT 27-OCT-2000 (first entry)

XX DE Linear peptide that binds to angiostatin SEQ ID # 86.

XX KW Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;
 KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
 KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;
 KW cerebral collateral; arteriovenous malformation; rubecosis; cancer;
 KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
 KW Helicobacter related disease; fracture; cat scratch fever.

XX OS Synthetic.

XX PN WO200032631-A2.

XX PD 08-JUN-2000.

XX PF 06-DEC-1999; 99WO-US28897.

XX PR 04-DEC-1998; 98US-0206059.

XX PA (ENTR-) ENTREMED INC.

XX PI MacDonald NJ, Sim KL;

XX WPI; 2000-412290/35.

XX PT New angiogenesis-inhibiting protein receptors, useful in methods for
 PT treating diseases and processes that are mediated by angiogenesis, such
 PT as solid tumours, psoriasis, scleroderma and myocardial angiogenesis -

XX PS Claim 1; Page 50; 100pp; English.

XX CC This invention relates to angiogenesis-inhibiting protein receptors, and
 CC the DNA sequences encoding them. Angiogenesis is the generation of new
 CC blood vessels into a tissue, and normally occurs in wound healing,
 CC foetal and embryonal development and the formation of the corpus luteum,
 CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and
 CC AAB16495) involved in angiogenesis, and has an amino acid sequence
 CC similar to that of a plasminogen fragment (see murine plasminogen
 CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.

CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
 CC AAB16495). Sequences AAB16451 and AAB16495 represent coding and protein
 CC sequences of human laminin. Laminin is an angiostatin binding protein,
 CC and some of the peptides of the invention share homology with regions of
 CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the
 CC angiogenesis-inhibiting protein receptor fragments of the invention. The
 CC peptides bind either angiostatin or endostatin and can be used in methods
 CC for treating diseases and processes that are mediated by angiogenesis,
 CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
 CC rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
 CC Helicobacter related diseases, fractures, placenta and cat scratch
 CC fever. They are useful for the detection and prognosis of cancer. DNA
 CC sequences A628204-A628241 encode the peptides of the invention.

XX SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

```

Db      |||
        2 QPP 4

RESULT 72
AAB17249
ID  AAB17249 standard; Peptide; 7 AA.
AC
XX
XX
DT  31-OCT-2000 (first entry)
XX
XX
DE  SH3 antagonist peptide sequence SEQ ID NO:305.
XX
XX
KW  Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW  immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW  MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW  cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW  vascular endothelial growth factor; matrix metalloproteinase;
KW  asthma; thrombosis; pharmaceutical.
XX
OS  Synthetic.
XX
XX
PN  WO200024782-A2.
XX
PD  04-MAY-2000.
XX
XX
PF  25-OCT-1999; 99WO-US25044.
XX
XX
PR  23-OCT-1998; 98US-0105371.
PR  22-OCT-1999; 99US-0428082.
XX
PA  (AMGE-) AMGEN INC.
XX
PI  Feige U, Liu C, Cheetham J, Boone TC;
XX
XX
DR  WPI; 2000-350702/30.
XX
XX
PT  Novel composition of matter comprising an Fc domain and
PT  pharmacologically active peptides, useful for treating cancer and
PT  autoimmune diseases -
XX
XX
PS  Claim 39; Page 302; 608pp; English.
XX
CC  The present invention describes composition of matter (I) comprising an
CC  Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC  (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
CC  independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC  -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC  where P1, P2, P3, and P4 = are each independently sequences of
CC  pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC  independently linkers; and a, b, c, d, e, and f = are each independently
CC  0 or 1, provided that at least 1 of a and b is 1. The composition can
CC  have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC  activities. DNAs, vectors and host cells from the present invention can
CC  be used for producing pharmaceutical compositions. The compositions are
CC  useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC  The use of an Fc domain (rather than a Fab domain) can provide a longer
CC  half-life or incorporate functions such as Fc receptor binding, protein
CC  A binding, complement fixation, and possibly placental transfer. AAB69443
CC  to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC  sequences used in the exemplification of the present invention.
XX
XX
Sequence 7 AA;

Query Match 42.9%; Score 3; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
    |||
Db  3 QPP 5

RESULT 73
AAY92768
ID  AAY92768 standard; peptide; 7 AA.
XX
XX
AC  AAY92768;
XX
XX
DT  29-AUG-2000 (first entry)
XX
XX
DE  Heptapeptide mimotope of surface LOS of serogroup B meningococcus.
XX
XX
KW  Heptapeptide; epitope; mimotope; surface lipo-oligosaccharide; LOS;
KW  meningitis; anti-bacterial; anti-inflammatory; vaccine.
XX
XX
OS  Neisseria meningitidis.
XX
XX
PN  WO200025814-A2.
XX
PD  11-MAY-2000.
XX
XX
PF  27-OCT-1999; 99WO-GB03559.
XX
XX
PR  30-OCT-1998; 98GB-0023835.
XX
XX
PA  (UNLO ) UNIV COLLEGE LONDON.
PA  (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX
XX
PI  Charalambous BM, Feavers IM;
XX
XX
DR  WPI; 2000-365403/31.
XX
XX
PT  Use of a mimotope of a surface lipooligosaccharide of a serogroup B
PT  meningococcus for a vaccine against serogroup B meningococci
XX
XX
PS  Claim 13; Page 26; 39pp; English.
XX
XX
CC  This is a preferred heptapeptide epitope mimotope of a surface
CC  lipooligosaccharide (LOS) of a serogroup B meningococcus. The mimotopes
CC  are useful in vaccines against serogroup B meningococci, especially
CC  Neisseria meningitidis, which causes meningitis. The LOS is a surface
CC  glycolipid that forms a major outer membrane component and possesses a
CC  terminal galactose acceptor sites for sialic acid. Sialylation of the LOS
CC  in immunotype B meningococci may enhance the ability of the organism to
CC  evade the human immune response. Therefore alternative target antigens on
CC  the surface of serogroup B meningococci are important.
XX
XX
Sequence 7 AA;

Query Match 42.9%; Score 3; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6
    |||
Db  4 QPP 6

RESULT 74
AAU72048
ID  AAU72048 standard; Peptide; 7 AA.
XX
XX
AC  AAU72048;
XX
XX
DT  26-FEB-2002 (first entry)
XX
XX
DE  Melanoma antigen, javelin peptide #34.
XX
XX
KW  Melanoma antigen; MART-1; MAGE-1; gpl00; cytostatic; immune response;
KW  immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYE501; GM2;
KW  tyrosinase related protein 1; tyrosinase related protein 2; vaccine;
KW  javelin molecule; melanoma antigen recognised by T cells-1; human.
XX
XX

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OS  Bacteriophage M13.
XX
PN  W0200178655-A2.
XX
PD  25-OCT-2001.
XX
PF  17-APR-2001; 2001WO-US12449.
XX
PR  17-APR-2000; 2000US-197462P.
XX
PA  (HOUG/) HOUGHTON A.
PA  (LIVI/) LIVINGSTON P.
PA  (ALAW/) AL-AWQATI Q.
PA  (MAYH/) MAYHEW M.
PA  (HOEM/) HOE M.
XX
PI  Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;
XX
DR  WPI; 2001-663092/76.
XX
XX  Anti cancer vaccine for the treatment of melanoma comprises a heat
PT  shock protein and a melanoma antigen i.e. tyrosinase -
XX
PS  Disclosure; Page 16; 150pp; English.
XX
CC  The invention relates to a method of induction of an immune response,
CC  comprising administration of an immunotherapeutic composition, comprising
CC  a heat shock protein, and a melanoma antigen, where the melanoma
CC  antigen is selected from tyrosinase, tyrosinase related protein 1,
CC  tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,
CC  NYESO1, MART antigens, GM2, antigenic portions and combinations of these.
CC  The melanoma antigen is covalently bound to a javelin molecule, where the
CC  melanoma antigen bound to the javelin molecule is non-covalently bound to
CC  the heat shock protein. The composition is useful for inducing an immune
CC  response for the treatment of melanoma. AAU71980-AAU72481 represent
CC  melanoma antigen peptides of the invention.
XX
SQ  Sequence 7 AA;

Query Match 42.9%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
Db 1 HQP 3

RESULT 75
AA43873
ID AA43873 standard; Peptide; 7 AA.
XX
AC AA43873;
XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #144.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytosatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX

```

```

PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
DR WPI; 2001-425937/46.
XX
XX  Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
PS Example 4; Page 101; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPFCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPFCs
CC or a population of different SPFCs consisting of immunogenic cancer cell
CC surface-associated SPFC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AA43707 to AA47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 5 QPP 7

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Search completed: November 25, 2003, 19:27:12
Job time : 19.8663 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 11.2326 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWNHQPP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

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17:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	15 US-10-281-652-24	Sequence 24, Appl
2	7	100.0	10	15 US-10-185-815-89	Sequence 89, Appl
3	6	85.7	19	12 US-10-372-736-3	Sequence 3, Appl
4	5	71.4	15	15 US-10-281-652-34	Sequence 34, Appl
5	4	57.1	10	9 US-09-794-346-1	Sequence 1, Appl
6	4	57.1	11	11 US-09-809-391-689	Sequence 689, Appl
7	4	57.1	11	12 US-09-882-171-689	Sequence 689, Appl
8	4	57.1	17	12 US-09-962-756-1752	Sequence 1752, Appl
9	4	57.1	20	12 US-10-195-730-261	Sequence 261, Appl
10	4	57.1	20	12 US-09-933-767-773	Sequence 773, Appl
11	4	57.1	20	15 US-10-023-282-773	Sequence 773, Appl
12	3	42.9	5	9 US-09-748-960-12	Sequence 12, Appl
13	3	42.9	5	9 US-09-765-086-223	Sequence 223, Appl
14	3	42.9	5	9 US-09-933-497B-26	Sequence 26, Appl
15	3	42.9	5	10 US-09-770-002-1	Sequence 1, Appl

16	3	42.9	5	11	US-09-940-727B-70	Sequence 70, Appl
17	3	42.9	6	15	US-10-097-065-334	Sequence 334, Appl
18	3	42.9	6	15	US-10-227-353-7	Sequence 7, Appl
19	3	42.9	6	15	US-10-281-652-13	Sequence 13, Appl
20	3	42.9	7	9	US-09-873-676-86	Sequence 86, Appl
21	3	42.9	7	10	US-09-821-687-7	Sequence 7, Appl
22	3	42.9	7	11	US-09-954-385-347	Sequence 347, Appl
23	3	42.9	7	12	US-10-052-578-176	Sequence 176, Appl
24	3	42.9	7	12	US-09-990-832C-10	Sequence 10, Appl
25	3	42.9	7	12	US-10-053-520-176	Sequence 176, Appl
26	3	42.9	7	12	US-10-286-457-92	Sequence 92, Appl
27	3	42.9	7	12	US-10-038-899-4	Sequence 4, Appl
28	3	42.9	7	12	US-10-220-033-21	Sequence 21, Appl
29	3	42.9	7	12	US-10-053-498B-176	Sequence 176, Appl
30	3	42.9	7	15	US-10-015-979-84	Sequence 84, Appl
31	3	42.9	7	15	US-10-281-652-1	Sequence 1, Appl
32	3	42.9	8	7	US-08-344-824-263	Sequence 263, Appl
33	3	42.9	8	10	US-09-765-614B-6	Sequence 6, Appl
34	3	42.9	8	10	US-09-925-715-2	Sequence 2, Appl
35	3	42.9	8	10	US-09-791-378-285	Sequence 285, Appl
36	3	42.9	8	10	US-09-883-825-35	Sequence 35, Appl
37	3	42.9	8	10	US-09-826-290-124	Sequence 124, Appl
38	3	42.9	8	11	US-09-999-724-58	Sequence 58, Appl
39	3	42.9	8	12	US-10-365-908-98	Sequence 98, Appl
40	3	42.9	8	12	US-09-823-382-11	Sequence 11, Appl
41	3	42.9	8	12	US-10-038-899-3	Sequence 3, Appl
42	3	42.9	8	12	US-10-357-929A-21	Sequence 21, Appl
43	3	42.9	8	15	US-10-158-596A-105	Sequence 105, Appl
44	3	42.9	8	15	US-10-017-193-4	Sequence 4, Appl
45	3	42.9	8	15	US-10-254-446A-232	Sequence 232, Appl
46	3	42.9	9	9	US-09-748-960-11	Sequence 11, Appl
47	3	42.9	9	10	US-09-780-053-165	Sequence 165, Appl
48	3	42.9	9	10	US-09-780-053-456	Sequence 456, Appl
49	3	42.9	9	10	US-09-780-053-517	Sequence 517, Appl
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51	3	42.9	9	10	US-09-862-179A-11	Sequence 11, Appl
52	3	42.9	9	10	US-09-862-179A-18	Sequence 18, Appl
53	3	42.9	9	10	US-09-017-743C-69	Sequence 69, Appl
54	3	42.9	9	11	US-09-938-864-108	Sequence 108, Appl
55	3	42.9	9	11	US-09-938-864-143	Sequence 143, Appl
56	3	42.9	9	11	US-09-938-864-148	Sequence 148, Appl
57	3	42.9	9	11	US-09-938-864-180	Sequence 180, Appl
58	3	42.9	9	11	US-09-938-864-243	Sequence 243, Appl
59	3	42.9	9	11	US-09-938-864-281	Sequence 281, Appl
60	3	42.9	9	11	US-09-791-477-108	Sequence 108, Appl
61	3	42.9	9	11	US-09-791-477-143	Sequence 143, Appl
62	3	42.9	9	11	US-09-791-477-148	Sequence 148, Appl
63	3	42.9	9	11	US-09-791-477-180	Sequence 180, Appl
64	3	42.9	9	11	US-09-791-477-283	Sequence 283, Appl
65	3	42.9	9	11	US-09-791-477-281	Sequence 281, Appl
66	3	42.9	9	11	US-09-785-019-108	Sequence 108, Appl
67	3	42.9	9	11	US-09-785-019-143	Sequence 143, Appl
68	3	42.9	9	11	US-09-785-019-148	Sequence 148, Appl
69	3	42.9	9	11	US-09-785-019-180	Sequence 180, Appl
70	3	42.9	9	11	US-09-785-019-243	Sequence 243, Appl
71	3	42.9	9	11	US-09-785-019-281	Sequence 281, Appl
72	3	42.9	9	12	US-09-932-165-66	Sequence 66, Appl
73	3	42.9	9	12	US-09-932-165-669	Sequence 669, Appl
74	3	42.9	9	12	US-09-932-165-1013	Sequence 1013, Appl
75	3	42.9	9	12	US-09-932-165-1212	Sequence 1212, Appl
76	3	42.9	9	12	US-09-932-165-1222	Sequence 1222, Appl
77	3	42.9	9	12	US-10-155-883B-47	Sequence 47, Appl
78	3	42.9	9	12	US-10-155-883B-50	Sequence 50, Appl
79	3	42.9	9	12	US-10-271-617-11	Sequence 11, Appl
80	3	42.9	9	12	US-10-022-066-34	Sequence 34, Appl
81	3	42.9	9	12	US-10-022-066-488	Sequence 488, Appl
82	3	42.9	9	12	US-10-365-908-80	Sequence 80, Appl
83	3	42.9	9	12	US-10-038-899-2	Sequence 2, Appl
84	3	42.9	9	12	US-10-119-536A-11	Sequence 11, Appl
85	3	42.9	9	12	US-10-195-835-108	Sequence 108, Appl
86	3	42.9	9	12	US-10-195-835-143	Sequence 143, Appl
87	3	42.9	9	12	US-10-195-835-148	Sequence 148, Appl
88	3	42.9	9	12	US-10-195-835-180	Sequence 180, Appl

89 3 42.9 9 12 US-10-195-835-243 Sequence 243, App
90 3 42.9 9 12 US-10-195-835-281 Sequence 281, App
91 3 42.9 9 12 US-10-286-333-108 Sequence 108, App
92 3 42.9 9 12 US-10-286-333-143 Sequence 143, App
93 3 42.9 9 12 US-10-286-333-148 Sequence 148, App
94 3 42.9 9 12 US-10-286-333-180 Sequence 180, App
95 3 42.9 9 12 US-10-286-333-243 Sequence 243, App
96 3 42.9 9 12 US-10-286-333-281 Sequence 281, App
97 3 42.9 9 15 US-10-125-635A-108 Sequence 108, App
98 3 42.9 9 15 US-10-125-635A-143 Sequence 143, App
99 3 42.9 9 15 US-10-125-635A-148 Sequence 148, App
100 3 42.9 9 15 US-10-125-635A-180 Sequence 180, App

ALIGNMENTS

RESULT 1
US-10-281-652-24
; Sequence 24, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-24

Query Match 100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQP 7
Db 1 SWMHQP 7

RESULT 2
US-10-185-815-89
; Sequence 89, Application US/10185815
; Publication No. US20030096354A1
; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Segment of CAPHI beta casein precursor
US-10-185-815-89

Query Match 100.0%; Score 7; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQP 7
Db 1 SWMHQP 7

RESULT 3
US-10-372-736-3
; Sequence 3, Application US/10372736
; Publication No. US20030166223A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE REFERENCE: 2005-B
; CURRENT APPLICATION NUMBER: US/10/372,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide substrate
US-10-372-736-3

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Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQP 6
Db 12 SWMHQP 17

RESULT 4
US-10-281-652-34
; Sequence 34, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-34

Query Match          71.4%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHOPP 7
Db 1 MHOPP 5

RESULT 5
US-09-794-346-1
; Sequence 1, Application US/09794346
; Patent No. US20010031857A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Memo Peptides, Process for Their Preparation and Use Thereof
; FILE REFERENCE: 02481.1728
; CURRENT APPLICATION NUMBER: US/09/794,346
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: EP 00104114.4
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: PCT/EP 01/01661
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: Memmonielia echinata, FH 227
; OTHER INFORMATION: 1, DSM 1319
US-09-794-346-1

Query Match          57.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHOP 6
Db 1 MHOP 4

RESULT 6
US-09-809-391-689
; Sequence 689, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 689
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-689

Query Match          57.1%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOPP 7
Db 1 HOPP 4

RESULT 7
US-09-882-171-689
; Sequence 689, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
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; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,596

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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
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; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 57.1%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOPP 7

DB 1 HOPP 4

RESULT 8

US-09-962-756-1752
; Sequence 1752, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTIA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAPFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051USI
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1752
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1752

Query Match 57.1%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6
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Db 12 MHQP 15

RESULT 9
US-10-195-730-261
; Sequence 261, Application US/10195730
; Publication No. US2003014492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 261
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-730-261

Query Match 57.1%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQPP 7
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Db 11 HQPP 14

RESULT 10
US-09-933-767-773
; Sequence 773, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
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; PRIOR APPLICATION NUMBER: 60/085,925
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; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-773

Query Match      57.1%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 HOPP 7
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Db      1 HOPP 4

RESULT 11
US-10-023-282-773
; Sequence 773, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
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; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-773

Query Match          57.1%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HOPP 7
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Db      1 HOPP 4

RESULT 12
US-09-748-960-12
; Sequence 12, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855-2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: CDRL1 of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-12

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 WMH 4
      ||||
Db      3 WMH 5

RESULT 13
US-09-765-086-223
; Sequence 23, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredeesen, Dale E.

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; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-223

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HOP 6
      ||||
Db      2 HOP 4

RESULT 14
US-09-933-497B-26
; Sequence 26, Application US/09933497B
; Patent No. US20020098193A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Elizabeth S.
; TITLE OF INVENTION: IMMUNOGLOBULIN-LIKE DOMAINS WITH INCREASED HALF LIVES
; FILE REFERENCE: UTSD:483
; CURRENT APPLICATION NUMBER: US/09/933,497B
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/013,563
; PRIOR FILING DATE: 1996-03-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-09-933-497B-26

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
      ||||
Db      2 MHQ 4

RESULT 15
US-09-770-002-1
; Sequence 1, Application US/09770002
; Patent No. US20020110558A1
; GENERAL INFORMATION:
; APPLICANT: Peter Lloyd Amlot
; APPLICANT: Max H. Schreier
; APPLICANT: Karin Schreier
; TITLE OF INVENTION: Use of CD25 binding molecules in the
; FILE REFERENCE: 4-30583A/30967C1
; CURRENT APPLICATION NUMBER: US/09/770,002
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/EP99/05316

```

;; PRIOR FILING DATE: 1999-07-26
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: mus musculus
;; FEATURE:
US-09-770-002-1

Query Match 42.9%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WNH 4
|||
DB 3 WNH 5

RESULT 16
US-09-940-727B-70
;; Sequence 70, Application US/09940727B
;; Publication No. US2003007793A1
;; GENERAL INFORMATION:
;; APPLICANT: Landry, Donald W
;; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
;; FILE REFERENCE: 0575/51400-B
;; CURRENT APPLICATION NUMBER: US/09/940,727B
;; CURRENT FILING DATE: 2002-09-04
;; PRIOR APPLICATION NUMBER: 09/214,095
;; PRIOR FILING DATE: 1998-12-28
;; PRIOR APPLICATION NUMBER: PCT/US97/10965
;; PRIOR FILING DATE: 1997-06-25
;; PRIOR APPLICATION NUMBER: 08/672,345
;; PRIOR FILING DATE: 1996-06-25
;; NUMBER OF SEQ ID NOS: 121
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 70
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: mouse
US-09-940-727B-70

Query Match 42.9%; Score 3; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WNH 4
|||
DB 3 WNH 5

RESULT 17
US-10-097-065-334
;; Sequence 334, Application US/10097065
;; Publication No. US20030055236A1
;; GENERAL INFORMATION:
;; APPLICANT: Moore, Paul A. et al.
;; TITLE OF INVENTION: 110 Human Secreted Proteins
;; FILE REFERENCE: PZ021PI
;; CURRENT APPLICATION NUMBER: US/10/097,065
;; CURRENT FILING DATE: 2002-03-14
;; PRIOR APPLICATION NUMBER: PCT/US98/27059
;; PRIOR FILING DATE: 1998-12-17
;; PRIOR APPLICATION NUMBER: 60/070,923
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,007
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,057
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,006
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,369

;; PRIOR FILING DATE: 1997-12-19
;; PRIOR APPLICATION NUMBER: 60/068,367
;; PRIOR FILING DATE: 1997-12-19
;; PRIOR APPLICATION NUMBER: 60/068,368
;; PRIOR FILING DATE: 1997-12-19
;; PRIOR APPLICATION NUMBER: 60/068,169
;; PRIOR FILING DATE: 1997-12-19
;; PRIOR APPLICATION NUMBER: 60/068,053
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,064
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,054
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,008
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,365
;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 672
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 334
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-097-065-334

Query Match 42.9%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6
|||
DB 4 HQP 6

RESULT 18
US-10-227-353-7
;; Sequence 7, Application US/10227353
;; Publication No. US20030087383A1
;; GENERAL INFORMATION:
;; APPLICANT: CLARE, JEFFREY J.
;; ROMANOS, MICHAEL A.
;; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
;; STREET: 2200 Clarendon Blvd., Suite 1400
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22201
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/227,353
;; FILING DATE: 26-Aug-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/460,269C
;; FILING DATE: 02-Jun-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lebovitz, Richard M.
;; REGISTRATION NUMBER: 37,067
;; REFERENCE/DOCKET NUMBER: Popov-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 243-6333
;; TELEFAX: (703) 243-6410
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid


```

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-227-353-7

Query Match          42.9%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
   |||
Db 4 QPP 6

RESULT 19
US-10-281-652-13
; Sequence 13, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265,00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-13

Query Match          42.9%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
   |||
Db 3 QPP 5

RESULT 20
US-09-873-676-86
; Sequence 86, Application US/09873676
; Patent No. US2002007289A1
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-347
```

```

; OTHER INFORMATION: Synthetic Peptide
US-09-873-676-86

Query Match          42.9%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
   |||
Db 2 QPP 4

RESULT 21
US-09-821-687-7
; Sequence 7, Application US/09821687
; Patent No. US20020106724A1
; GENERAL INFORMATION:
; APPLICANT: MIKOSHIBA, KATSUHIKO
; APPLICANT: MIZUTANI, AKIHIRO
; TITLE OF INVENTION: RNA-BINDING PROTEIN
; FILE REFERENCE: 081356/0162
; CURRENT APPLICATION NUMBER: US/09/821,687
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP 2000-299812
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-821-687-7

Query Match          42.9%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6
   |||
Db 2 QPP 4

RESULT 22
US-09-954-385-347
; Sequence 347, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gestel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-347

Query Match          42.9%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 23

US-10-052-578-176
; Sequence 176, Application US/10052578
; Publication No. US2003013478A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 176
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-052-578-176

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
|||
Db 1 HQP 3

RESULT 24

US-09-990-832C-10
; Sequence 10, Application US/09990832C
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/P11910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-10

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 4 QPP 6

RESULT 25

US-10-038-899-4

; Sequence 4, Application US/10038899

; Publication No. US20030186406A1

US-10-053-520-176
; Sequence 176, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 176
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-520-176

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
|||
Db 1 HQP 3

RESULT 26

US-10-286-457-92
; Sequence 92, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPC1-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 92
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, be
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-92

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 1 QPP 3

RESULT 27

US-10-038-899-4

; Sequence 4, Application US/10038899

; Publication No. US20030186406A1

GENERAL INFORMATION:
APPLICANT: KIKUCHI, KOKICHI
SATO, NORIYUKI
SAHARA, HIROMITSU
YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
SUZUKI, MANABU
HAMURO, JUNJI
TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCQUELLEND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/038,899
FILING DATE: 08-Jan-2002
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/723,116
FILING DATE: 30-SEP-1996
APPLICATION NUMBER: JP 253491/1995
FILING DATE: 29-SEP-1995
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 2 SWM 4

RESULT 28
US-10-220-033-21
Sequence 21, Application US/10220033
Publication No. US20030186906A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
and a molecule binding to an expression product of that

TITLE OF INVENTION: Gene
FILE REFERENCE: P68119050
CURRENT APPLICATION NUMBER: US/10/220,033
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: PCT/EP01/02694
PRIOR FILING DATE: 2001-03-10
PRIOR APPLICATION NUMBER: EP00105190.3
PRIOR FILING DATE: 2000-03-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
OTHER INFORMATION: obtained by screening randomly synthesized
peptides
OTHER INFORMATION: peptides
US-10-220-033-21

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 1 QPP 3

RESULT 29
US-10-053-498B-176
Sequence 176, Application US/10053498B
Publication No. US2003019409A1
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
APPLICANT: Rothman, James E.
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
APPLICANT: Hartl, Ulrich
APPLICANT: Querfelli, Ouathek
APPLICANT: Moroi, Yoichi
TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
FILE REFERENCE: 11746/46002
CURRENT APPLICATION NUMBER: US/10/053,498B
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 08/961,707
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 321
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 176
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-176

Query Match 42.9%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
Db 1 HQP 3

RESULT 30
US-10-015-979-84
Sequence 84, Application US/10015979
Publication No. US20030036050A1
GENERAL INFORMATION:
APPLICANT: Quax, Wilhelmus J.

APPLICANT: Verhaert, Raymond M.D.
APPLICANT: Beekwilder, Martinus J.
APPLICANT: Aehle, Wolfgang
TITLE OF INVENTION: Enzyme Selection
FILE REFERENCE: 2183-5207US
CURRENT APPLICATION NUMBER: US/10/015,979
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: PCT/NL00/00399
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/138,443
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 84
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CB4 mutant isolated by selection
OTHER INFORMATION: tion
NAME/KEY: SITE
LOCATION: (1)..(7)
OTHER INFORMATION:
US-10-015-979-84
Query Match 42.9%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 WNH 4
Db 5 WNH 7
RESULT 31
US-10-281-652-1
Sequence 1, Application US/10281652
Publication No. US20030091606A1
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: HUGHES, Thomas K.
TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/10/281,652
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/09/641,803
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-281-652-1
Query Match 42.9%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QPP 7
Db 2 QPP 4
RESULT 32

US-08-344-824-263
Sequence 263, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-263
Query Match 42.9%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QPP 7
Db 4 QPP 6
RESULT 33
US-09-765-614B-6
Sequence 6, Application US/09765614B
Patent No. US20020102215A1
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial

```
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-09-765-614B-6

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 34
US-09-925-715-2
; Sequence 2, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCES: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
US-09-925-715-2

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 35
US-09-791-378-285
; Sequence 285, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCES: SCHIZOPHRENIA
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 285
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-285

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 1 QPP 3
```

```
RESULT 36
US-09-883-825-35
; Sequence 35, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20020151024Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; INFO: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-883-825-35

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 4 WMH 6

RESULT 37
US-09-826-290-124
; Sequence 124, Application US/09826290
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
```

```

; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-124

Query Match      42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 38
US-09-999-724-58
; Sequence 58, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, INRE
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-999-724-58

Query Match      42.9%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

```

```

Db 2 QPP 4

RESULT 39
US-10-365-908-98
; Sequence 98, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-98

Query Match      42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 40
US-09-829-382-11
; Sequence 11, Application US/09829382
; Publication No. US20030175293A1
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Wizemann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,382
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,065
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

```

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-158
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-829-382-11

Query Match 42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 41
US-10-038-899-3
Sequence 3, Application US/10038899
Publication No. US20030186406A1
GENERAL INFORMATION:
APPLICANT: KIKUCHI, KOKICHI
SAHARA, HIROMITSU
YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
SUZUKI, MANABU
HAMURO, JUNJI
TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/038,899
FILING DATE: 08-Jan-2002
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/723,116
FILING DATE: 30-SEP-1996
APPLICATION NUMBER: JP 253491/1995
FILING DATE: 29-SEP-1995
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-038-899-3

Query Match 42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3
Db 2 SWM 4

RESULT 42
US-10-357-929A-21
Sequence 21, Application US/10357929A
Publication No. US20030216322A1
GENERAL INFORMATION:
APPLICANT: Tatiana I. Samoylova
APPLICANT: Valery A. Petrenko
APPLICANT: Nancy R. Cox
APPLICANT: Nancy E. Morrison
APPLICANT: Henry J. Baker
APPLICANT: Ludmila P. Globa
TITLE OF INVENTION: Peptides for Recognition and Targeting
TITLE OF INVENTION: of Glial Cell Tumors
FILE REFERENCE: 35721/259047
CURRENT APPLICATION NUMBER: US/10/357,929A
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 10/357,929
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 60/354,188
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 8
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-357-929A-21

Query Match 42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6
Db 6 HQP 8

RESULT 43
US-10-158-596A-105
Sequence 105, Application US/10158596A
Publication No. US20030068900A1
GENERAL INFORMATION:
APPLICANT: Belcher, Angela
APPLICANT: Flynn, Christine
TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYST.
FILE REFERENCE: 119927-1052
CURRENT APPLICATION NUMBER: US/10/158,596A
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/296,013
PRIOR FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide retrieved from phage biopanning
US-10-158-596A-105

Query Match 42.9%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 4 MHQ 6

RESULT 44
US-10-017-193-4
; Sequence 4, Application US/10017193
; Publication No. US20030113478A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Mai Huong
; APPLICANT: Chiu, Phillip
; TITLE OF INVENTION: Surface Coating Method and Coated Device
; FILE REFERENCE: 52200-8010
; CURRENT APPLICATION NUMBER: US/10/017,193
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attachment peptide from fibronectin
US-10-017-193-4

Query Match 42.9%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 45
US-10-254-446A-232
; Sequence 232, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopant
US-10-254-446A-232

Query Match 42.9%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 4 MHQ 6

RESULT 46
US-09-748-960-11
; Sequence 11, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; APPLICANT: Allison, David Edward
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855.2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(9)
; OTHER INFORMATION: CDR3 of the light chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-11

Query Match 42.9%; Score 3; DB 9; Length 9;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
Db 5 HQP 7

RESULT 47
US-09-780-053-165
; Sequence 165, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Rid
; APPLICANT: Mary Faris
; APPLICANT: Elana Ievin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.SUSUI
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-165

Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 5 QPP 7

RESULT 48
US-09-780-053-456
; Sequence 456, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-456

Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 4 QPP 6

RESULT 49
US-09-780-053-517
; Sequence 517, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-517

Query Match 42.9%; Score 3; DB 10; Length 9;

QY 5 QPP 7

Db 4 QPP 6

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

US-09-780-053-517

```

; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-017-743C-69

Query Match          42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 54
US-09-938-864-108
; Sequence 108, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-108

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 4 MHQ 6

RESULT 55
US-09-938-864-143
; Sequence 143, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864

```

```

; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-143

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
      |||
Db      1 MHQ 3

```

RESULT 56

```

US-09-938-864-148
; Sequence 148, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-148

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
      |||
Db      2 MHQ 4

```

RESULT 57

```

US-09-938-864-180
; Sequence 180, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5

```

```

; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-180

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
      |||
Db      5 MHQ 7

```

RESULT 58

```

US-09-938-864-243
; Sequence 243, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-243

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
      |||
Db      6 MHQ 8

```

RESULT 59

```

US-09-938-864-281
; Sequence 281, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

```

; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-281

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 1 MHQ 3

RESULT 60

US-09-791-477-108
; Sequence 108, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-108

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 4 MHQ 6

RESULT 61

US-09-791-477-143
; Sequence 143, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-143

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 1 MHQ 3

RESULT 62

US-09-791-477-148
; Sequence 148, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-148

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 2 MHQ 4

RESULT 63

US-09-791-477-180
; Sequence 180, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-180

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
|||
Db 5 MHQ 7

RESULT 64

US-09-791-477-243

```

; Sequence 243, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791.477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-243

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
        |||
Db      6 MHQ 8

```

RESULT 65

```

US-09-791-477-281
; Sequence 281, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791.477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-281

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
        |||
Db      1 MHQ 3

```

RESULT 66

```

US-09-785-019-108
; Sequence 108, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

```

```

; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-108

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
        |||
Db      4 MHQ 6

```

RESULT 67

```

US-09-785-019-143
; Sequence 143, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-143

```

```

Query Match      42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 MHQ 5
        |||
Db      1 MHQ 3

```

RESULT 68

```

US-09-785-019-148
; Sequence 148, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-148

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
Db 2 MHQ 4

RESULT 69
US-09-785-019-180
; Sequence 180, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-180

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
Db 5 MHQ 7

RESULT 70
US-09-785-019-243
; Sequence 243, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-785-019-243

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
Db 6 MHQ 8

RESULT 71
US-09-785-019-281
; Sequence 281, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-281

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
Db 1 MHQ 3

RESULT 72
US-09-932-165-66
; Sequence 66, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAPPAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-66

Query Match 42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 73

US-09-932-165-669
; Sequence 669, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Catf2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-669

Query Match 42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 74

US-09-932-165-1013
; Sequence 1013, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Catf2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1013
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1013

Query Match 42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 5 QPP 7

RESULT 75

US-09-932-165-1212
; Sequence 1212, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Catf2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1212
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1212

Query Match 42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 1 QPP 3

Search completed: November 25, 2003, 20:37:01
Job time : 12.2326 secs

ALIGNMENTS

```
RESULT 1
US-09-641-803-24
; Sequence 24, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR FILING DATE: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-24

Query Match      100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SWMHQPP 7
Db      1 SWMHQPP 7

RESULT 2
US-08-870-529-3
; Sequence 3, Application US/08870529
; Patent No. 6080557
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: IL-1/TNF-(-ACTIVATED KINASE (ITAK),
; TITLE OF INVENTION: AND METHODS OF MAKING AND USING THE SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,529
; FILING DATE: 06-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.418
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-870-529-3

Query Match      85.7%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SWMHQP 6
Db      12 SWMHQP 17

RESULT 3
US-09-544-794-3
; Sequence 3, Application US/09544794
; Patent No. 6541232
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE REFERENCE: 2005-B
; CURRENT APPLICATION NUMBER: US/09/544,794
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide substrate
US-09-544-794-3

Query Match      85.7%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SWMHQP 6
Db      12 SWMHQP 17

RESULT 4
US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match          71.4%   Score 5;   DB 4;   Length 15;
Best Local Similarity 100.0%;   Pred. No. 0.81;
Matches 5;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      3 MHQPP 7
Db       1 MHQPP 5

RESULT 5
US-09-149-476-689
; Sequence 689, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
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; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/056,637
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,636
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,831
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
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; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
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; EARLIER APPLICATION NUMBER: 60/047,590
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; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER APPLICATION NUMBER: 60/056,909
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; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060

; EARLIER FILING DATE: 1997-10-02
Query Match 57.1%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred.No.14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HOPP 7
DB 1 HOPP 4
RESULT 6
US-09-205-258-773
; Sequence 773, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
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; EARLIER APPLICATION NUMBER: 60/049,020
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; EARLIER APPLICATION NUMBER: 60/048,876
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; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
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; EARLIER APPLICATION NUMBER: 60/048,971
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; EARLIER APPLICATION NUMBER: 60/048,964
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; EARLIER APPLICATION NUMBER: 60/048,899
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; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
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; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-773

Query Match 57.1%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQPP 7
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Db 1 HQPP 4

RESULT 7
US-08-810-720-12
; Sequence 12, Application US/08810720
; Patent No. 6037527
; GENERAL INFORMATION:
; APPLICANT: Barton, Kenneth A.
; APPLICANT: Umbeck, Paul F.
; TITLE OF INVENTION: INSECTICIDAL COTTON PLANTS (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,720
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386

; REFERENCE/DOCKET NUMBER: 670513.90163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608/251-5000
; TELEFAX: 608/251-9166
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-810-720-12

Query Match 42.9%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
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Db 2 QPP 4

RESULT 8
US-08-014-979-52
; Sequence 52, Application US/08014979
; Patent No. 5510240
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,979
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,972
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-014-979-52

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
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Db 1 WMH 3

RESULT 9
 US-07-946-421-4
 ; Sequence 4, Application US/07946421
 ; Patent No. 5558864
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Kettleborough, Catherine A.
 ; APPLICANT: Saldanha, Jose
 ; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
 ; TITLE OF INVENTION: Antibodies
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
 ; STREET: 2200 Clarendon Boulevard, Suite 1400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/946,421
 ; FILING DATE: 06-NOV-1992
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/EP92/00480
 ; FILING DATE: 04-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 911933892
 ; FILING DATE: 06-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hamlet-King, Diana
 ; REGISTRATION NUMBER: 33,302
 ; REFERENCE/DOCKET NUMBER: Merck 1430
 ; TELEPHONE: 703-243-6333
 ; TELEFAX: 703-243-6410
 ; TELEX: 64191
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-07-946-421-4

Query Match 42.9%; Score 3; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
 Db 3 WMH 5

RESULT 10
 US-08-318-970B-1
 ; Sequence 1, Application US/08318970B
 ; Patent No. 5589573
 ; GENERAL INFORMATION:
 ; APPLICANT: Hideaki HAGIWARA, et al.
 ; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
 ; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
 ; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Office of Sherman and Shalloway
 ; STREET: 413 N. Washington Street
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA

ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
 ; OPERATING SYSTEM: MS DOS 3.3
 ; SOFTWARE: Word Perfect, Version 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/318,970B
 ; FILING DATE: October 6, 1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Richard A. Steinberg
 ; REGISTRATION NUMBER: 26,588
 ; REFERENCE/DOCKET NUMBER: S-2371
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 549-2282
 ; TELEFAX: (703) 836-0106
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: H-CDRI-1
 ; OTHER INFORMATION: hypervariable region
 ; US-08-318-970B-1

Query Match 42.9%; Score 3; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
 Db 3 WMH 5

RESULT 11
 US-08-672-345C-70
 ; Sequence 70, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 70:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-70

Query Match 42.9%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 WMH 4
|||
Db 3 WMH 5

RESULT 12
US-08-774-354B-2
; Sequence 2, Application US/08774354B
; Patent No. 6063427
; GENERAL INFORMATION:
; APPLICANT: Michiko WATANABE
; TITLE OF INVENTION: METHOD FOR PRODUCING A
; TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington, D.C.
; STATE:
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,354B
; FILING DATE: December 27, 1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER: 653-96F029US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
US-08-774-354B-2

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 13
US-09-258-754-278
; Sequence 278, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 278
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-278

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6
|||
Db 2 HQP 4

RESULT 14
US-09-042-107-278
; Sequence 278, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 278
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-278

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6
|||
Db 2 HQP 4

RESULT 15
US-08-811-463-26
; Sequence 26, Application US/08811463C
; Patent No. 6277375
; GENERAL INFORMATION:
; APPLICANT: Ward, Elizabeth S.

; TITLE OF INVENTION: IMMUNOGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
; FILE REFERENCE: UTSD:483
; CURRENT APPLICATION NUMBER: US/08/811,463C
; CURRENT FILING DATE: 1997-03-03
; EARLIER APPLICATION NUMBER: 50/013,563
; EARLIER FILING DATE: 1996-03-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-08-811-463-26

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
|||
Db 2 MHQ 4

RESULT 16
US-09-214-095D-70
; Sequence 70, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-70

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|||
Db 3 WMH 5

RESULT 17
US-09-406-532-5
; Sequence 5, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: 15B8 heavy chain CDR 1
US-09-406-532-5

Query Match 42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|||
Db 3 WMH 5

RESULT 18
US-08-479-089A-7
; Sequence 7, Application US/08479089A
; Patent No. 6383487
; GENERAL INFORMATION:
; APPLICANT: Amlot, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammisuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6383487artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,089A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/669,545
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019323
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Diane E.
; REGISTRATION NUMBER: 31,104
; REFERENCE/DOCKET NUMBER: 100-7617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6924
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-479-089A-7

Query Match 42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|||
Db 3 WMH 5

RESULT 19
US-09-082-358B-31
; Sequence 31, Application US/09082358B
; Patent No. 6469153
; GENERAL INFORMATION:
; APPLICANT: Goff, Stephen P.
; APPLICANT: Li, Xingqiang
; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
; TITLE OF INVENTION: EIP-1, and EIP-3
; FILE REFERENCE: 0575/54804
; CURRENT APPLICATION NUMBER: US/09/082,358B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 5
; TYPE: PRT
; ORGANISM: murine
US-09-082-358B-31

Query Match 42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 20
US-07-669-545B-7
; Sequence 7, Application US/07669545B
; Patent No. 6521230
; GENERAL INFORMATION:
; APPLICANT: Amlot, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammisuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6521230artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,545B
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9005962
; FILING DATE: 16-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019323
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Diane E.
; REGISTRATION NUMBER: 31,104
; REFERENCE/DOCKET NUMBER: 100-7617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6924
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-07-669-545B-7

Query Match 42.9%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 21
5217869-43
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:43
; LENGTH: 5
5217869-43

Query Match 42.9%; Score 3; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 WMH 4
Db 1 WMH 3

RESULT 22
5464756-28
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:28
; LENGTH: 5
5464756-28

Query Match 42.9%; Score 3; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 SWM 3
Db 2 SWM 4

RESULT 23
US-08-253-854-40
; Sequence 40, Application US/08253854
; Patent No. 5504190
; GENERAL INFORMATION:

APPLICANT: Houghten, Richard A.
APPLICANT: Cuervo, Julio H.
APPLICANT: Pinilla, Clemencia
APPLICANT: Appel Jr., Jon R.
APPLICANT: Blondelle, Silvie
TITLE OF INVENTION: Synthesis Of Equimolar Multiple
TITLE OF INVENTION: Oligomer Mixtures, Especially Of Oligopeptide Mixtures
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler,
ADDRESS: Milinacow, Ltd.
STREET: 180 No. 5504190th Stetson Avenue, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: PRL-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-253-854-40

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 4 WMH 6

RESULT 24
US-08-127-499A-22
Sequence 22, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A

FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-22

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 25
US-08-482-847-22
Sequence 22, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-22

Query Match

42.9%; Score 3; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.5e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 26

US-08-237-716-7
; Sequence 7, Application US/08237716
; Patent No. 5589384
; GENERAL INFORMATION:
; APPLICANT: LIPSCOMBE, Martin J
; APPLICANT: CHARLES, Ian G
; APPLICANT: FAIRWEATHER, Neil F
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vandethye, P.C.
; STREET: 1100 No. 5589384th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,716
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,003
; FILING DATE: 11-JUN-1992
; APPLICATION NUMBER: GB 9112553.4
; FILING DATE: 11-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-237-716-7

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 4 QPP 6

RESULT 27

US-08-704-170-89
; Sequence 89, Application US/08704170
; Patent No. 5707626
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR

; TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 No. 5707626th Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,850
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-704-170-89

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 28

US-08-460-269C-7
; Sequence 7, Application US/08460269C
; Patent No. 6197548
; GENERAL INFORMATION:
; APPLICANT: CLARE, JEFFREY J.
; ROMANOS, MICHAEL A.
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd., Suite 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,269C
; FILING DATE: 02-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067

```
;
; REFERENCE/DOCKET NUMBER: Popov-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 243-6333
; TELEFAX: (703) 243-6410
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-460-269C-7

Query Match          42.9%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 4 QPP 6

RESULT 29
US-09-641-803-13
; Sequence 13, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641-803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-13

Query Match          42.9%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 30
PCT-US94-02631-89
; Sequence 89, Application PC/TUS9402631
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
```

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;
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02631
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,850
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US94-02631-89

Query Match          42.9%; Score 3; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 31
US-08-169-524-3
; Sequence 3, Application US/08169524
; Patent No. 5496706
; GENERAL INFORMATION:
; APPLICANT: Kuusela, Pentti
; APPLICANT: Hilden, Pekka
; TITLE OF INVENTION: Methods and Materials for the
; TITLE OF INVENTION: Detection of
; TITLE OF INVENTION: Staphylococcus Aureus
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-8402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 28113/31832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-169-524-3

```

```

Query Match          42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 5 QPP 7
Db 1 QPP 3

```

```

RESULT 32
US-08-081-539-113
; Sequence 113, Application US/08081539
; Patent No. 5501962
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKeary, John P.
; APPLICANT: Olin, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; TITLE OF INVENTION: Chimeric Hybrid Polypeptides
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,539
; FILING DATE: 19930621
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-081-539-113

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```

Query Match          42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 5 QPP 7
Db 1 QPP 3

```

```

RESULT 33
US-08-127-499A-3

```

```

; Sequence 3, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INB1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-3

```

```

Query Match          42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 QPP 7
Db 3 QPP 5

```

```

RESULT 34
US-08-127-499A-7
; Sequence 7, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993

```

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-7

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 35
US-08-127-499A-10
Sequence 10, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-10

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 36
US-08-127-499A-25
Sequence 25, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-10

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 36
US-08-127-499A-25
Sequence 25, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-25

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 3 QPP 5

RESULT 37
US-08-466-647-113
Sequence 113, Application US/08466647
Patent No. 5543141
GENERAL INFORMATION:
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olins, Peter O.
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
TITLE OF INVENTION: Chimeric Hybrid Polypeptides
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
ADDRESSEE: Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,647
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,539
FILING DATE: 21-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-466-647-113

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 1 QPP 3

RESULT 38
US-08-482-847-3
Sequence 7, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-3

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 3 QPP 5

RESULT 39
US-08-482-847-7
Sequence 7, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-7

Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 3 QPP 5

Wed Nov 26 09:07:13 2003

RESULT 40
US-08-482-847-10
; Sequence 10, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-482-847-10
Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 Qpp 7
Db 3 Qpp 5
RESULT 41
US-08-482-847-25
; Sequence 25, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-482-847-25
Query Match 42.9%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 Qpp 7
Db 3 Qpp 5
RESULT 42
US-08-723-116-4
; Sequence 4, Application US/08723116
; Patent No. 5837248
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KIKICHI
; APPLICANT: SATO, NORIYUKI
; APPLICANT: SAHARA, HIROMITSU
; APPLICANT: YASOJIMA, TAKAHIRO
; APPLICANT: WADA, YOSHIMASA
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,116
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 253491/1995
; FILING DATE: 29-SEP-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; US-08-723-116-4

Query Match 42.9%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3
|||
Db 2 SWM 4

RESULT 43
US-08-774-354B-4
; Sequence 4, Application US/08774354B
; Patent No. 6063427
; GENERAL INFORMATION:
; APPLICANT: Michiko WATANABE
; TITLE OF INVENTION: METHOD FOR PRODUCING A
; TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington, D.C.
; STATE:
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,354B
; FILING DATE: December 27, 1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER: 653-96F029US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; US-08-774-354B-4

Query Match 42.9%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 4 QPP 6

RESULT 44
US-09-103-808-4
; Sequence 4, Application US/09103808
; Patent No. 6368852
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; SAITO, NORIYUKI
; SAHARA, HIROMITSU
; YASOJIMA, TAKAHIRO
; WADA, YOSHIMASA
; SUZUKI, MANABU
; HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,808
; FILING DATE: 24-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/723,116
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN

; SEQUENCE DESCRIPTION: SEQ ID NO: 4;
US-09-103-808-4

Query Match 42.9%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3
|||
Db 2 SWM 4

RESULT 45
US-09-641-803-1
; Sequence 1, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOSH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641.803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-1

Query Match 42.9%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 46
US-07-872-644-35
; Sequence 35, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; PHOSPHODIESTERASES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; BICKNELL, STREET
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-872-644-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|||
Db 4 WMH 6

RESULT 47
US-08-291-349A-5
; Sequence 5, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; INHIBITORS OF RETROVIRAL INFECTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1234
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1,8
OTHER INFORMATION: /note= "FMS (1892-1899)"
OTHER INFORMATION: fibronectin fragment : FN-C/H-V"
US-08-291-349A-5

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 48
US-08-297-494-35
; Sequence 35, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,494
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 558077land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-297-494-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
|||
Db 4 WMH 6

RESULT 49
US-07-990-296-3
; Sequence 3, Application US/07990296
; Patent No. 5591719
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: Allen, Janice B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; TITLE OF INVENTION: Method for Treating Acute and
; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/990,296
; FILING DATE: 19921210
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600.252-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Fragment of the 33 kD carboxy
; NAME/KEY: terminal heparin-binding fragment of the A
; NAME/KEY: chain of fibronectin
; LOCATION: Represents isolated fibronectin
; LOCATION: Residues 1892-1899 from all plasma isoforms
; LOCATION: of fibronectin
US-07-990-296-3

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db 2 QPP 4

RESULT 50
US-08-297-510-35
; Sequence 35, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: Allen, Janice B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; TITLE OF INVENTION: Method for Treating Acute and
; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/990,296
; FILING DATE: 19921210
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600.252-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Fragment of the 33 kD carboxy
; NAME/KEY: terminal heparin-binding fragment of the A
; NAME/KEY: chain of fibronectin
; LOCATION: Represents isolated fibronectin
; LOCATION: Residues 1892-1899 from all plasma isoforms
; LOCATION: of fibronectin
US-08-297-510-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Charbonneau, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,510
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5602019and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-297-510-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 4 WMH 6

RESULT 51
US-08-479-532-35
; Sequence 35, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Charbonneau, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
```

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; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-479-532-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 4 WMH 6

RESULT 52
US-08-455-526-35
; Sequence 35, Application US/08455526
; Patent No. 5783553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,526
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/297,494
; FILING DATE: 29-AUG-1994
```

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
|||
Db 2 SWM 4

RESULT 55
US-08-480-133A-3
; Sequence 3, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; APPLICANT: Billups, Kevin L.
; APPLICANT: Everett, Jeffrey E.
; TITLE OF INVENTION: Method for Treating Inflammatory
; DISEASES Using Polypeptides with Fibronectin Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5840691west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,133A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600-308US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-133A-3

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 56
US-08-699-965-2
; Sequence 2, Application US/08699965
; Patent No. 5853744
; GENERAL INFORMATION:
; APPLICANT: MOORADIAN, DANIEL L.
; APPLICANT: FIELDS, GREGG B.
; TITLE OF INVENTION: METHOD FOR MODIFYING A SUBSTRATE SURFACE
; TO INCLUDE A BIOMOLECULE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH, GERHARDT & SCHWAPPACH, P.A.
; STREET: 119 No. 5853744th Fourth Street, Suite 203
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/699,965
; FILING DATE: 20-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00300101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-699-965-2

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 57
US-08-435-149-6
; Sequence 6, Application US/08435149
; Patent No. 5866402
; GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; APPLICANT: CREASEY, ABLA A.
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0989.001
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-149-6

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 58
US-09-025-706-10
Sequence 10, Application US/09025706
Patent No. 5958874
GENERAL INFORMATION:
APPLICANT: Clark, Richard A
APPLICANT: Greiling, Doris
APPLICANT: Gallit, James
TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
EXTRACELLULAR MATRIX FOR WOUND HEALING
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaecle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bramer, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87653.97R263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 59
US-08-394-748A-13
Sequence 13, Application US/08394748A
Patent No. 6013628
GENERAL INFORMATION:
APPLICANT: Skubitz, Amy P.N.
APPLICANT: Furcht Leo T.
APPLICANT: Balles, Mark
APPLICANT: Gregerson, Dale S.
APPLICANT: Agarwal, Anita
APPLICANT: Wright, Martha M.
APPLICANT: Murali, Shobana
TITLE OF INVENTION: Method for Treating Conditions of the Eye
USING POLYPEPTIDES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6013628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,748A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600.307US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: FN-C/H-V

US-08-394-748A-13
Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 60
US-09-139-491-35
Sequence 35, Application US/09139491
Patent No. 6015677
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry

APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/139,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/297,494
FILING DATE:
FILING DATE:
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6015677and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-139-491-35

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
|||
Db 4 WMH 6

RESULT 61
US-08-774-354B-5
Sequence 5, Application US/08/74354B
Patent No. 6063427
GENERAL INFORMATION:
APPLICANT: Michiko WATANABE
TITLE OF INVENTION: METHOD FOR PRODUCING A
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington, D.C.
STATE:
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,354B
FILING DATE: December 27, 1996
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER: 653-96F029US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-08-774-354B-5

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 5 QPP 7

RESULT 62
US-08-916-913A-3
Sequence 3, Application US/08916913A
Patent No. 6121027
GENERAL INFORMATION:
APPLICANT: Clapper, David L.
APPLICANT: Swanson, Melvin J.
APPLICANT: Hu, Sheau-ping
APPLICANT: Amos, Richard A.
APPLICANT: Everson, Terrence P.
TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH
TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOIETIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fredrikson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-97
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,913A
FILING DATE: 15 August 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: No. 6121027e
; FILING DATE: No. 6121027e
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-916-913A-3

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db |||
2 QPP 4

RESULT 63
US-09-025-622-10
; Sequence 10, Application US/09025622
; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Grilling, Doris
; TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bramer, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-025-622-10

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db |||
2 QPP 4

us-09-641-801-24.oligo.ra1

; APPLICATION NUMBER: No. 6121027e
; FILING DATE: No. 6121027e
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-916-913A-3

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db |||
2 QPP 4

RESULT 64
US-08-847-065-11
; Sequence 11, Application US/08847065
; Patent No. 6245335
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Wizemann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,065
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-847-065-11

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db |||
2 QPP 4

RESULT 65
US-08-960-054A-6
; Sequence 6, Application US/08960054A
; Patent No. 6261537
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/klaiveness/054
; CURRENT APPLICATION NUMBER: US/08/960,054A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
```


; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-960-054A-6

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 66
US-08-958-993A-6
; Sequence 6, Application US/08958993A
; Patent No. 6264917
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/993
; CURRENT APPLICATION NUMBER: US/08/958,993A
; CURRENT FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-958-993A-6

Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 67
US-08-959-206A-2
; Sequence 2, Application US/08959206A
; Patent No. 6331289
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/08/959,206A
; CURRENT FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-959-206A-2

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
|||
Db 2 QPP 4

RESULT 68
US-09-103-808-3
; Sequence 3, Application US/09103808
; Patent No. 6368852
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; SATO, NORIYUKI
; SAHARA, HIROMITSU
; YASOJIMA, TAKAHIRO
; WADA, YOSHIMASA
; SUZUKI, MANABU
; HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTIN
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,808
; FILING DATE: 24-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/723,116
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-103-808-3

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
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Db 2 SWM 4

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RESULT 69
US-09-101-751A-58
; Sequence 58, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, INRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: US/09/101,751A
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (..)
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence
US-09-101-751A-58

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 70
US-09-591-564-3
; Sequence 3, Application US/09591564
; Patent No. 6514734
; GENERAL INFORMATION:
; APPLICANT: Clapper, David L.
; APPLICANT: Swanson, Melvin J.
; APPLICANT: Hu, Sheau-Ping
; APPLICANT: Amos, Richard A.
; APPLICANT: Everson, Terrence P.
; TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY
; ACTIVE MOISTIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fredrikson & Byron, P.A.
; STREET: 900 Second Avenue South
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-3397
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows-97
; SOFTWARE: ASCII files
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/591,564
; FILING DATE: 09-Jun-2000
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/916,913
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7077
; TELEFAX: (612) 347-7088
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-591-564-3

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 71
PCT-US92-03222-35
; Sequence 35, Application PC/TUS9203222
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03222
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
PCT-US92-03222-35

Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 4 WMH 6

RESULT 72

PCT-US93-11781-3
; Sequence 3, Application PC/TUS9311781
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; APPLICANT: Morrill Hall
; APPLICANT: 100 Church Street, S.E.
; APPLICANT: Minneapolis, Minnesota 55455
; APPLICANT: U.S.A.
; APPLICANT: Represented By The Secretary of Health
; APPLICANT: and Human Services
; APPLICANT: 200 Independence Avenue S.W.
; APPLICANT: Washington, D.C. 20201
; APPLICANT: United States of America
; TITLE OF INVENTION: Polypeptides Useful for Treating
; TITLE OF INVENTION: Inflammatory Disorders
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 Northwest Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11781
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600.283-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-11781-3

Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 73

PCT-US95-02478-13
; Sequence 13, Application PC/TUS9502478
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for Treating Conditions
; TITLE OF INVENTION: Of the Eye Using Polypeptides
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/203,458
; APPLICATION NUMBER: 28-FEB-1994
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; STRAIN: FN-C/H-V
PCT-US95-02478-13

Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 74

US-08-139-054-7
; Sequence 7, Application US/08139054
; Patent No. 5578710
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothea
; APPLICANT: Dony, Carola
; APPLICANT: Rudolph, Rainer
; TITLE OF INVENTION: IMPROVED ACTIVATION OF RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 1725 K. St. N.W. Suite 1000
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/139,054
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/837,779
; FILING DATE:
; APPLICATION NUMBER: DE P 41 05 480.6
; FILING DATE: 21-FEB-1991
; ATTORNEY/AGENT INFORMATION:

NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: 920053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)659-2930
TELEFAX: (202)887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-139-054-7

Query Match 42.9%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
Db 7 Qpp 9

RESULT 75
US-08-723-116-2
Sequence 2, Application US/08723116
Patent No. 5837248
GENERAL INFORMATION:
APPLICANT: KIKUCHI, KOKICHI
APPLICANT: SATO, NORIYUKI
APPLICANT: SAHARA, HIROMITSU
APPLICANT: YASOJIMA, TAKAHIRO
APPLICANT: WADA, YOSHINASA
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723.116
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 253491/1995
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN
US-08-723-116-2

Query Match 42.9%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 2 SWM 4

Search completed: November 25, 2003, 20:30:00
Job time : 5.65698 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 6.86047 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPLPPTVMFP 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4	40.0	8	2	SI0783
2	4	40.0	12	2	PN0663
3	4	40.0	13	2	I84603
4	4	40.0	19	2	PH1352
5	4	40.0	20	2	PC2030
6	3	30.0	8	2	SI6324
7	3	30.0	9	2	B38740
8	3	30.0	10	2	PC2171
9	3	30.0	10	2	SI8396
10	3	30.0	10	2	C39745
11	3	30.0	11	1	XASNBA
12	3	30.0	11	2	C61497
13	3	30.0	11	2	I33098
14	3	30.0	13	2	A60856
15	3	30.0	13	2	SI5755
16	3	30.0	13	2	A40207
17	3	30.0	14	2	PQ0152
18	3	30.0	14	2	C33098
19	3	30.0	14	2	PH1566
20	3	30.0	14	2	PH1348
21	3	30.0	14	2	H83778
22	3	30.0	15	2	PQ0545
23	3	30.0	15	2	B39109
24	3	30.0	15	2	S29386
25	3	30.0	15	2	PA0060
26	3	30.0	15	2	B61457
27	3	30.0	16	2	F44908
28	3	30.0	16	2	A54877
29	3	30.0	16	2	B54877

30	3	30.0	16	2	E58503
31	3	30.0	16	2	S01104
32	3	30.0	17	2	SI5754
33	3	30.0	17	2	S32587
34	3	30.0	17	2	S59481
35	3	30.0	17	2	I55612
36	3	30.0	18	2	S04229
37	3	30.0	18	2	PC2280
38	3	30.0	18	2	S39845
39	3	30.0	18	2	B45138
40	3	30.0	18	2	SI0452
41	3	30.0	18	2	A54195
42	3	30.0	19	2	S60633
43	3	30.0	19	2	C32735
44	3	30.0	19	2	B32735
45	3	30.0	19	2	B61409
46	3	30.0	19	2	A34467
47	3	30.0	20	2	S21737
48	3	30.0	20	2	S29817
49	3	30.0	20	2	A39328
50	3	30.0	20	2	A37111
51	3	30.0	20	2	A54519
52	3	30.0	20	2	T44453
53	3	30.0	20	2	PH1380
54	3	30.0	20	2	S65605
55	3	30.0	20	2	A61093
56	3	30.0	20	2	F24417
57	3	30.0	20	2	S03954
58	3	30.0	20	4	I53672
59	2	20.0	3	3	I78890
60	2	20.0	4	2	A32039
61	2	20.0	4	2	S33508
62	2	20.0	5	1	H08084
63	2	20.0	5	2	JN0860
64	2	20.0	5	2	E42364
65	2	20.0	5	2	P50324
66	2	20.0	5	2	B37988
67	2	20.0	5	2	A60411
68	2	20.0	5	2	G44817
69	2	20.0	5	2	I44817
70	2	20.0	5	2	E44817
71	2	20.0	5	2	C44817
72	2	20.0	5	2	A44817
73	2	20.0	6	2	A61049
74	2	20.0	6	2	A27696
75	2	20.0	6	2	B27696
76	2	20.0	6	2	A19780
77	2	20.0	6	2	I67345
78	2	20.0	6	4	A35039
79	2	20.0	7	2	PH1408
80	2	20.0	7	2	S08606
81	2	20.0	7	2	A61081
82	2	20.0	7	2	E61491
83	2	20.0	7	2	S71299
84	2	20.0	7	2	PC1316
85	2	20.0	7	2	P02883
86	2	20.0	7	2	B39040
87	2	20.0	7	2	I48105
88	2	20.0	7	2	I48086
89	2	20.0	7	2	S66442
90	2	20.0	7	2	A39690
91	2	20.0	7	2	A56718
92	2	20.0	7	2	A56648
93	2	20.0	8	2	PH1407
94	2	20.0	8	2	A31570
95	2	20.0	8	2	B24749
96	2	20.0	8	2	S43971
97	2	20.0	8	2	PL0184
98	2	20.0	8	2	S21273
99	2	20.0	8	2	B39745
100	2	20.0	8	2	S21288

superoxide dismuta
hypothetical prote
actin 6 - soybean
L-ascorbate peroxi
hydroxyproline-ric
thyroid hormone re
N4-(beta-N-acetylgl
prolylendopeptidas
2-aminobenzoate-Co
arsenite oxidase I
hypothetical prote
Na+/K+-exchanging
H+-transporting tw
thyroglobulin - sh
genome polyprotein
36K microfibril-as
coulmarin 7-monooxy
cytochrome P450 2C
noechis II-5b non
ribulose-bisphosph
tubulin alpha chai
acetyl-CoA synthet
alpha-amylase (EC
dimeric protein (B
glue protein - Cal
interphotoreceptor
acidic fibroblast
somatotropin - syn
tyrosine-melanocyt
starvation-induced
proctolin - Americ
peptidyl-dipeptida
flagellar protein
ribulose-bisphosph
acid proteinase li
proctolin - Atlant
27.5 kda structura
27.5K structural p
28.5K structural p
28K structural pro
halo-toxin - Pseud
contraction-inhibi
transferrin - bovi
MHC H2-K-k cell su
hypothetical colla
Ig heavy chain V r
hypothetical prote
tryptophyllin, bas
seed protein ws-5
ICL2 protein - Par
large granule L3 C
Ig heavy chain CRD
calsequestrin, fas
dihydrofolate redu
DNA topoisomerase
glutathione S-tran
neural cell adhesi
carnocin UI49 - Ca
Na+-transporting A
Ig heavy chain V r
angiotensin-conver
neuropeptide B - b
tumor-associated a
capsid protein VP-
cellulase (EC 3.2.
endoglycosylcerami
lectin - potato (f

ALIGNMENTS

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RESULT 1
SI0783
enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: SI0783
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins', identified mainly as serum proteins. Major 'enamelin' is albu
A;Reference number: SI0780; MUID:90336641; PMID:2379503
A;Accession: SI0783
A;Molecule type: protein
A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein

Query Match          40.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
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Db 2 PLPP 5

RESULT 2
PN0663
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: PN0663
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A;Reference number: PN0662; MUID:94156881; PMID:8113213
A;Accession: PN0663
A;Molecule type: protein
A;Residues: 1-12 <YOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: glycoprotein; skeletal muscle

Query Match          40.0%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
   ||||
Db 3 PLPP 6

RESULT 3
I84603
deoxynucleotidyltransferase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I84603
R;Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A;Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A;Reference number: 145884; MUID:87213162; PMID:3579900
A;Accession: I84603
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-13 <RES>
A;Cross-references: GB:M26144; NID:g951194; PIDN:AAA74588.1; PID:g951195
C;Genetics:
A;Gene: GDB:DNNT
A;Cross-references: GDB:119100; OMIM:187410
A;Map position: 10q23-10q24

Query Match          40.0%; Score 4; DB 2; Length 13;
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
   ||||
Db 8 QPLP 11

RESULT 4
PHI352
IG heavy chain DJ region (clone C100-115) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PHI352
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor ly
A;Reference number: PHI302; MUID:93094761; PMID:1460419
A;Accession: PHI352
A;Molecule type: DNA
A;Residues: 1-19 <WAS>
A;Note: the authors translated the stop codon for residue 2 as X
C;Keywords: heterotrimer; immunoglobulin

Query Match          40.0%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
   ||||
Db 8 PPTV 11

RESULT 5
PC2030
tumor-derived adhesion factor - human (fragment)
N;Alternate names: 30K protein
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jan-2000
R;Akaogi, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.;
Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994
A;Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder
A;Reference number: PC2030; MUID:94161713; PMID:8117260
A;Accession: PC2030
A;Molecule type: protein
A;Residues: 1-20 <AKA>
A;Experimental source: cell line EJ-1
C;Comment: This protein relates with the aberrant cell adhesion of cancer cells.

Query Match          40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
   ||||
Db 16 PLPP 19

RESULT 6
SI6324
hypothetical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: SI6324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely link
A;Reference number: SI6323; MUID:91266907; PMID:1675603
A;Accession: SI6324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <RUB>
```

A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 30.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
|||
Db 6 LPP 8

RESULT 7

B38740
I9 kappa chain C region (PY20) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: B38740

R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991

A;Title: Heavy and light chain variable region sequences and antibody properties of anti-
A;Reference number: A38740; MUID:91177923; PMID:1706720

A;Accession: B38740

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-9 <RUF>

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
|||
Db 5 PTV 7

RESULT 8

PC2171
triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fragm

C;Species: Rhizopus niveus

C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: PC2171

R;Kobno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994

A;Title: Purification, characterization, and crystallization of two types of lipase from
A;Reference number: PC2171; MUID:94319059; PMID:7765029

A;Accession: PC2171

A;Molecule type: protein

A;Residues: 1-10 <KOH>

C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.

C;Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
|||
Db 5 LPP 7

RESULT 9

S18396
probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter Hansenii (fragm

C;Species: Acetobacter Hansenii

C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C;Accession: S18396

R;Levy, H.R.; Cook, C.

Arch. Biochem. Biophys. 291, 161-167, 1991

A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase fr
A;Reference number: S18396; MUID:92027789; PMID:1929428

A;Accession: S18396

A;Molecule type: protein

A;Residues: 1-10 <LEV>

A;Experimental source: ATCC 23769

C;Function:

A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phosphat

A;Pathway: pentose phosphate pathway

C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
|||
Db 3 LPP 5

RESULT 10

C39745

sphingomyelinase - Rhodococcus sp. (fragment)

C;Species: Rhodococcus sp.

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993

C;Accession: C39745

R;Ito, M.; Ikegami, Y.; Yamagata, T.

J. Biol. Chem. 266, 7919-7926, 1991

A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidases.
ble using these activator proteins.

A;Reference number: A39745; MUID:91210321; PMID:1850427

A;Accession: C39745

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ITO>

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
|||
Db 3 PLP 5

RESULT 11

XASNB4

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysi

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; ve

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
|||
Db 3 LPP 5

RESULT 12

C61497

seed protein ws-18 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: C61497

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis

A:Reference number: A61491; MUID:89351606; PMID:2765119

A:Accession: C61497

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <HR>

C:Keywords: glycoprotein; seed

Query Match 30.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7

Db 3 PTV 5

RESULT 13

I33098

173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C:Accession: I33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: I33098

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <NC>

Query Match 30.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5

Db 2 LPP 4

RESULT 14

A60856

inhibin alpha chain - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: A60856

R:Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wetterhall

J. Endocrinol. 113, 213-221, 1987

A:Title: Isolation of inhibin from ovine follicular fluid.

A:Reference number: A60856; MUID:87224684; PMID:3585232

A:Accession: A60856

A:Molecule type: protein

A:Residues: 1-13 <LEV>

C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.

C:Superfamily: inhibin

C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PTP 4

Db 4 PTP 6

RESULT 15

S15755

actin 7 - soybean (fragment)

C:Species: Glycine max (soybean)

C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999

C:Accession: S15755

A:Reference number: S15755; MUID:89351606; PMID:2765119

A:Accession: C61497

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <HR>

C:Keywords: glycoprotein; seed

R:Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated region

A:Reference number: S15754; MUID:91346640; PMID:2102831

A:Accession: S15755

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <PEA>

A:Cross-references: EMBL:X17120; NID:gl8527; PIDN:CAA34980.1; PID:gl8528

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3

Db 8 QPL 10

RESULT 16

A40207

cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)

C:Species: Dictyostelium discoideum

C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 31-Dec-1993

C:Accession: A40207

R:Gao, E.N.; Shier, P.; Siu, C.H.

J. Biol. Chem. 267, 9409-9415, 1992

A:Title: Purification and partial characterization of a cell adhesion molecule (gp150)

A:Reference number: A40207; MUID:92250549; PMID:1577768

A:Accession: A40207

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <GAO>

C:Keywords: glycoprotein

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6

Db 3 PPT 5

RESULT 17

PQ0152

18K iron-sulfur protein - Chlamydomonas reinhardtii chloroplast (fragment)

N:Alternate names: frxB homolog

C:Species: chloroplast Chlamydomonas reinhardtii

C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-Sep-1993

C:Accession: PQ0152

R:Wu, M.; Nie, Z.Q.; Yang, J.

Plant Cell 1, 551-557, 1989

A:Title: The 18-KD protein that binds to the chloroplast DNA replicative origin is an

A:Reference number: PQ0152; MUID:92404720; PMID:2562513

A:Accession: PQ0152

A:Molecule type: protein

A:Residues: 1-14 <WUM>

C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10

Db 1 MFP 3

RESULT 18.

C33098 223K exantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C:Accession: C33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: C33098

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <NIC>

Query Match 30.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5

Db 2 LPP 4

RESULT 19

PH1566

Cerebrin 30 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C:Accession: PH1566

R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.

J. Neurochem. 61, 533-540, 1993

A:Title: Micropurification of two human cerebrospinal fluid proteins by high performance

A:Reference number: PH1566; MUID:93329419; PMID:8336140

A:Accession: PH1566

A:Molecule type: protein

A:Residues: 1-14 <LEO>

Query Match 30.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3

Db 9 QPL 11

RESULT 20

PH1348

Ig heavy chain DJ region (clone C100-106) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1348

R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1348

A:Molecule type: DNA

A:Residues: 1-14 <WAS>

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6

Db 4 PPT 6

RESULT 21

H83778

hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: H83778

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans ar

submitted to the Protein Sequence Database, May 1990

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H83778

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-14 <STO>

A:Cross-references: GB:AP001510; GB:BA000004; NID:gl0173440; PIDN:BA804751.1; GSPDB:CB

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH1032

Query Match 30.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8

Db 8 TVM 10

RESULT 22

PQ0545

capsid protein VP19C - human herpesvirus 1 (fragment)

C:Species: human herpesvirus 1

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: PQ0545

R:Davidson, M.D.; Rixon, F.J.; Davidson, A.J.

J. Gen. Virol. 73, 2709-2713, 1992

A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpe

A:Reference number: PQ0544; MUID:93019027; PMID:1328483

A:Accession: PQ0545

A:Molecule type: protein

A:Residues: 1-15 <DAV>

A:Experimental source: strain 17

C:Genetics:

A:Gene: UL38

C:Keywords: capsid protein

Query Match 30.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4

Db 5 PLP 7

RESULT 23

B39109

hypothetical 1.5K protein - hepatitis C virus

N:Alternate names: hypothetical protein 2

C:Species: hepatitis C virus

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999

C:Accession: B39109; JQ1585

R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekan

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identific

A:Reference number: A39109; MUID:91156678; PMID:1705704

A:Accession: B39109

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-15 <HAN>

A:Cross-references: GB:M58406

R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A:Title: Cloning and sequencing of the structural region and expression of putative c

A:Reference number: JQ1584; MUID:92300349; PMID:1318944

A:Accession: JQ1585

A:Molecule type: genomic RNA

A:Residues: 1-15 <KUM>

A:Experimental source: strain U.K.

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
|||
Db 10 PLP 12

RESULT 24

S29386

C:Species: Desulfovibrio vulgaris

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999

C:Accession: S29386

R:Pierik, A.J.; Wolbert, R.B.G.; Portier, G.L.; Verhagen, M.F.J.M.; Hagen, W.R.

Eur. J. Biochem. 212, 237-245, 1993

A:Title: Nigerythrin and rubrerythrin from Desulfovibrio vulgaris each contain two monon

A:Reference number: S29385; MUID:93185629; PMID:8383040

A:Accession: S29386

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <PIE>

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
|||
Db 8 PTV 10

RESULT 25

PA0060

C:Species: Fusarium sporotrichioides (fragment)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C:Accession: PA0060

R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A:Reference number: PA0051

A:Accession: PA0060

A:Molecule type: protein

A:Residues: 1-15 <CHO>

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
|||
Db 4 PLP 6

RESULT 26

B61457

C:Species: Tetrahymena pyriformis (strain W) (fragment)

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999

C:Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification

A:Reference number: A61457; MUID:90095988; PMID:2689637

A:Accession: B61457

A:Molecule type: protein

A:Residues: 1-15 <BAN>

C:Genetics:

A:Genetic code: SGC5

A:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; mo

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
|||
Db 2 LPP 4

RESULT 27

F44908

C:Species: Streptomyces olivaceoviridis (fragment)

C:Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000

C:Accession: F44908

R;Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.

J. Bacteriol. 174, 3450-3454, 1992

A:Title: Chitinases of Streptomyces olivaceoviridis and significance of processing fo

A:Reference number: A44908; MUID:92276319; PMID:1592803

A:Accession: F44908

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <ROM>

A:Experimental source: ATCC 11238

A:Note: sequence extracted from NCBI backbone (NCBIP:104594)

C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
|||
Db 6 MFP 8

RESULT 28

AS4877

C:Species: alpha-conotoxin Pn1A [validated] - cone shell (Conus pennaceus)

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000

C:Accession: AS4877

R;Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zl

Biochemistry 33, 9523-9529, 1994

A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r

A:Reference number: AS4877; MUID:94347719; PMID:8068627

A:Accession: AS4877

A:Molecule type: protein

A:Residues: 1-16 <PAI>

R;Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A:Reference number: A66355; PDB:1PEN

A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
|||
Db 5 LPP 7

```

RESULT 29
B54877
A:Gene: conotoxin PnIB - cone shell (Conus pennaceus)
A:Cross-references: FlyBase:FBgn0002036
Query Match      30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LPP 5
      |||
Db      5 LPP 7

RESULT 30
E58503
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)
N:Alternate names: 21.3K bladder and kidney stone protein
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 05-Mar-1999
C:Accession: E58503
R:Binette, J. P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: E58503
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <Bin>
A:Experimental source: human bladder and kidney stones
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Keywords: metalloprotein; oxidoreductase

Query Match      30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LPP 5
      |||
Db      5 LPP 7

RESULT 31
S01104
hypothetical protein 3 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jul-2000
C:Accession: S01104
R:Eveleth, D.D.; Marsh, J.L.
Mol. Gen. Genet. 209, 290-298, 1987
A:Title: Overlapping transcription units in Drosophila: sequence and structure of the C
A:Reference number: S01102; MUID:88038375; PMID:3478553
A:Accession: S01104
A:Molecule type: DNA
A:Residues: 1-16 <EVE>
A:Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29407.1; PID:g7762
C:Genetics:

```

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A:Gene: Cs
A:Cross-references: FlyBase:FBgn0002036
Query Match      30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PTV 7
      |||
Db      13 PTV 15

RESULT 32
S15754
actin 6 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
C:Accession: S15754; S08049
R:Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A:Reference number: S15754; MUID:91346640; PMID:2102831
A:Accession: S15754
A:Molecule type: DNA
A:Residues: 1-17 <PEA>
A:Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526
C:Superfamily: actin
C:Keywords: cytoskeleton

Query Match      30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPL 3
      |||
Db      8 QPL 10

RESULT 33
S32587
L-ascorbate peroxidase (EC 1.11.1.11) isozyme II - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C:Accession: S32587; S15878
R:Kubo, A.; Saji, H.; Tanaka, K.; Tanaka, K.; Kondo, N.
Plant Mol. Biol. 18, 691-701, 1992
A:Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidops
A:Reference number: S20866; MUID:92216045; PMID:1558944
A:Accession: S32587
A:Molecule type: protein
A:Residues: 1-17 <KUB>
A>Note: this is a revision to the sequence from reference S15878
R:Tanaka, K.; Takeuchi, E.; Kubo, A.; Sakaki, T.; Haraguchi, K.; Kawamura, Y.
Arch. Biochem. Biophys. 286, 371-375, 1991
A:Title: Two immunologically different isozymes of ascorbate peroxidase from spinach
A:Reference number: S15878; MUID:91378325; PMID:1897962
A:Accession: S15878
A:Molecule type: protein
A:Residues: 1,3-17 <TAN>
A>Note: this sequence has been revised in reference S20866
C:Keywords: chloroplast; oxidoreductase

Query Match      30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PTV 7
      |||
Db      5 PTV 7

RESULT 34
S59481

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hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C>Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C:Accession: S59481
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A:Title: Specificity in the immobilisation of cell wall proteins in response to different
A:Reference number: S59481; MUID:96011753; PMID:7548825
A:Accession: S59481
A:Molecule type: protein
A:Residues: 1-17 <WOJ>
C:Keywords: glycoprotein; hydroxyproline
F:6,8,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
   |||
Db 4 LPP 6

RESULT 35
I55612
thyroid hormone receptor beta - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I55612
R:Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.
J. Clin. Invest. 94, 506-515, 1994
A:Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th
A:Reference number: I55612; MUID:94314950; PMID:8040303
A:Accession: I55612
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-17 <RSS>
A:Cross-references: GB:S72623; NID:G633779; PIDN:AAB31420.1; PID:G633780
C:Genetics:
A:Gene: TRbeta

Query Match 30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
   |||
Db 5 LPP 7

RESULT 36
S04229
N4-(beta-N-acetylglucosaminyl)-L-asparaginase (BC 3.5.1.26) 24K chain - rat (fragment)
N:Alternate names: glycosylasparaginase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C:Accession: S04229
R:Tollersrud, O.K.; Aronson Jr., N.N.
Biochem. J. 260, 101-108, 1989
A:Title: Purification and characterization of rat liver glycosylasparaginase.
A:Reference number: S04228; MUID:89374025; PMID:2775174
A:Accession: S04229
A:Molecule type: protein
A:Residues: 1-18 <TOL>
C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
C:Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
   |||

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Db 3 PLP 5

RESULT 37
PC2280
prolylendopeptidase-inhibiting peptide - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-May-1997
C:Accession: PC2280
R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.
Biochem. Biophys. Res. Commun. 202, 809-815, 1994
A:Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.
A:Reference number: PC2280; MUID:94324571; PMID:8048952
A:Accession: PC2280
A:Molecule type: protein
A:Residues: 1-18 <OHM>
A:Experimental source: brain
C:Superfamily: cytoskeletal keratin

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
   |||
Db 4 PLP 6

RESULT 38
S39845
2-aminobenzoate-CoA ligase, anaerobic - Pseudomonas sp. (strain KB740) (fragment)
C:Species: Pseudomonas sp.
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S39845
R:Altenschmidt, U.; Fuchs, G.
Eur. J. Biochem. 205, 721-727, 1992
A:Title: Novel aerobic 2-aminobenzoate metabolism. Purification and characterization
from a denitrifying Pseudomonas sp.
A:Reference number: S22402; MUID:92241310; PMID:1315272
A:Accession: S39845
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10, 'X', 12-14, 'X', 16-18 <ALT>

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
   |||
Db 12 LPP 14

RESULT 39
B45138
arsenite oxidase I - Alcaligenes faecalis (fragment)
C:Species: Alcaligenes faecalis
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C:Accession: B45138
R:Anderson, G.L.; Williams, J.; Hille, R.
J. Biol. Chem. 267, 23674-23682, 1992
A:Title: The purification and characterization of arsenite oxidase from Alcaligenes f
A:Reference number: A45138; MUID:93054722; PMID:1331097
A:Accession: B45138
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <AND>
A>Note: sequence extracted from NCBI backbone (NCBIP:118543)

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3 LPP 5
|||
Db 9 LPP 11

RESULT 40

S10452
hypothetical protein (bpha 5' region) - *Aspergillus niger*
C;Species: *Aspergillus niger*
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C;Accession: S10452
R;van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A;Reference number: S10452
A;Accession: S10452
A;Molecule type: DNA
A;Residues: 1-18 <VAN>
A;Cross-references: EMBL:X52521; NID:g2336; PID:g2337

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
|||
Db 4 QPL 6

RESULT 41

A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)
C;Species: *Squalus acanthias* (spiny dogfish)
C;Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002
C;Accession: A54195
R;Bermann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase
A;Reference number: A54195; MUID:94297020; PMID:8025109
A;Accession: A54195

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <ESM>
A;Experimental source: rectal gland
A;Note: sequence extracted from NCBI backbone (NCBIP:149363)
C;Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
|||
Db 9 PPT 11

RESULT 42

S60633
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion
C;Species: mitochondrion *Artemia* sp. (brine shrimp)
A;Variety: strain La Mata
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
C;Accession: S60633
R;Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
J. Mol. Evol. 38, 156-168, 1994
A;Title: Speciation in the *Artemia* genus: mitochondrial DNA analysis of bisexual and parthenogenetic strains
A;Reference number: S60624; MUID:94223692; PMID:8169960
A;Accession: S60633

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-19 <PER>
A;Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
A;Experimental source: strain La Mata
A;Note: the source is designated as *Artemia parthenogenetica*

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Genetics:
A;Gene: ATP8
A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; c

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
|||
Db 6 PLP 8

RESULT 43

C32735
thyroglobulin - pig (fragment)
C;Species: *Sus scrofa domestica* (domestic pig)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
C;Accession: C32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: C32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
|||
Db 10 QPL 12

RESULT 44

B32735
thyroglobulin - sheep (fragment)
C;Species: *Ovis orientalis aries*, Ovis ammon aries (domestic sheep)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
C;Accession: B32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: B32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
|||
Db 10 QPL 12

RESULT 45

B61409

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genome polyprotein (clone L3/S2) - Skalica virus (fragment)
C:Species: Skalica virus
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Nov-2000
C:Accession: B61409
R:Guirakho, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M.
J. Gen. Virol. 72, 333-338, 1991
A:Title: The relationship between the flaviviruses Skalica and Langat as revealed by mon
A:Reference number: A61409; MUID:91132129; PMID:1847173
A:Accession: B61409
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: genomic RNA
A:Residues: 1-19 <GUI>
C:Superfamily: yellow fever virus genome polyprotein

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
   |||
Db 1 LPP 3

RESULT 46
A34467
36K microfibril-associated protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Jun-1993
C:Accession: A34467
R:Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Hayakawa
J. Biol. Chem. 264, 17437-17444, 1989
A:Title: Isolation and characterization of a new 36-kDa microfibril-associated glycoprotein
A:Reference number: A34467; MUID:90008913; PMID:2793866
A:Accession: A34467
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <KOB>

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
   |||
Db 16 QPL 18

RESULT 47
S21737
coumarin 7-monooxygenase (EC 1.14.14.-) cytochrome P450 2A7 - western baboon (fragment)
N:Alternate names: coumarin 7-hydroxylase
C:Species: Papio papio (western baboon)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Mar-1999
C:Accession: S21737
R:Dalet-Beluche, I.; Boulenc, X.; Fabre, G.; Maurel, P.; Bonfils, C.
Eur. J. Biochem. 204, 641-648, 1992
A:Title: Purification of two cytochrome P450 isozymes related to CYP2A and CYP3A gene fa
A:Reference number: S21176; MUID:92174920; PMID:1541278
A:Accession: S21737
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <DAL>
C:Genetics:
A:Gene: CYP2A7
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
   |||

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Db 16 TVM 18

RESULT 48
S29817
cytochrome P450 2C23 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
C:Accession: S29817
R:Marie, S.; Roussel, F.; Cresteil, T.
Biochim. Biophys. Acta 1172, 124-130, 1993
A:Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
A:Reference number: S29817; MUID:93176794; PMID:7679925
A:Accession: S29817
A:Molecule type: mRNA
A:Residues: 1-20 <MAR>
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; transmembrane protein

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
   |||
Db 4 PLP 6

RESULT 49
A39328
notechis II-5b nontoxic venom protein - common tiger snake (fragment)
C:Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
C:Accession: A39328
R:Yang, C.C.; Chang, L.S.; Wu, F.S.
Toxicol. 29, 1337-1344, 1991
A:Title: Venom constituents of Notechis scutatus scutatus (Australian tiger snake) fr
A:Reference number: A39328; MUID:92263371; PMID:1814009
A:Accession: A39328
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <YAN>
C:Superfamily: phospholipase A2

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
   |||
Db 17 QPL 19

RESULT 50
A37111
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C>Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 12-Apr-1995
C:Accession: A37111
R:Sato, M.H.; Hisabori, T.; Yoshida, M.
J. Biol. Chem. 265, 13419-13422, 1990
A:Title: The 55-kDa polypeptide released from spinach thylakoid membranes with 1 M Li
A:Reference number: A37111; MUID:90337936; PMID:2143183
A:Accession: A37111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <SAT>
C:Superfamily: ribulose-bisphosphate carboxylase small chain
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 LPP 5
      |||
Db      18 LPP 20

RESULT 51
A54519
tubulin alpha chain - Leishmania enriettii (fragment)
C:Species: Leishmania enriettii
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 13-Aug-1999
C:Accession: A54519
R:Wirth, D.F.; Slater, C.
Mol. Biochem. Parasitol. 9, 83-92, 1983
A:Title: Isolation and characterization of an alpha-tubulin gene from Leishmania enriettii
A:Reference number: A54519; MUID:84142075; PMID:6321982
A:Accession: A54519
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <WIR>
A:Cross-references: GB:M28001; NID:gi159409; PIDN:AAA29273.1; PID:gi159410
C:Superfamily: tubulin

Query Match      30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PTV 7
      |||
Db      2 PTV 4

RESULT 52
T44453
acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44453
R:Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.
J. Bacteriol. 180, 5559-5566, 1998
A:Title: Molecular characterization and regulation of an operon encoding a system for
A:Reference number: 222777; MUID:99008987; PMID:9791103
A:Accession: T44453
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-20 <NTS>
A:Cross-references: EMBL:AF012537; NID:G26668593; PIDN:AAC71069.1; PID:G2668594
A:Experimental source: strain PAOI

Query Match      30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLP 4
      |||
Db      11 PLP 13

RESULT 53
PH1380
alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)
C:Species: Bacillus sp.
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 07-May-1999
C:Accession: PH1380
R:Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992
A:Title: Purification and some properties of a Haim-sensitive alpha-amylase from newly
A:Reference number: PH1380; MUID:93113087; PMID:1369074
A:Accession: PH1380
A:Molecule type: protein
A:Residues: 1-20 <KAW>
A:Experimental source: strain N0.195
C:Comment: This enzyme has an optimum pH of 7.0.

```

interphotoreceptor retinoid-binding protein - bush baby (fragment)
 N:Alternate names: interstitial retinol-binding protein
 C:Species: Galago sp. (bush baby)
 C>Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 18-Jun-1993
 C:Accession: F24417
 R:Pong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
 A:Reference number: A91365; MUID:86301171; PMID:3743780
 A:Accession: F24417
 A:Molecule type: protein
 A:Residues: 1-20 <PON>

Query Match 30.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
 |||
 Db 5 QPL 7

RESULT 57
 S03954
 acidic fibroblast growth factor - pig (fragment)
 N:Alternate names: alpha-endothelial cell growth factor
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
 C:Accession: S03954
 R:Quinkler, W.; Maasberg, M.; Bernotat-Dantelowski, S.; Luethe, N.; Sharma, H.S.; Schape
 Eur. J. Biochem. 181, 67-73, 1989
 A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
 A:Reference number: S03953; MUID:89231704; PMID:2714282
 A:Accession: S03954

A:Molecule type: protein
 A:Residues: 1-20 <QUI>
 C:Keywords: growth factor

Query Match 30.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 |||
 Db 3 LPP 5

RESULT 58
 I53672
 somatotropin - synthetic
 C:Species: synthetic
 C>Date: 07-Jun-1996 #sequence_revision 31-Jul-1997 #text_change 19-May-2000
 C:Accession: I53672
 R:Bogosian, G.; Bilyeu, K.; O'Neil, J.P.
 Gene 133, 17-22, 1993

A:Title: Genome rearrangements by residual IS10 elements in strains of Escherichia coli
 A:Reference number: I53672; MUID:94040791; PMID:8224890
 A:Accession: I53672
 A:Molecule type: DNA
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-20 <BOG>
 A:Cross-references: GB:S67119; NID:g455674; PIDN:AB28847.1; PID:g455675
 A>Note: partial sequence of bovine somatotropin synthesized and expressed in Escherichia

Query Match 30.0%; Score 3; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
 |||
 Db 1 MFP 3

RESULT 59

I78890
 tyrosine protein kinase - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: I78890
 R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak,
 Oncogene 9, 3437-3448, 1994
 A:Title: Two distinct protein isoforms are encoded by ntck, a csk-related tyrosine pro
 A:Reference number: I58407; MUID:95060800; PMID:7970703
 A:Accession: I78890
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3 <RES>
 A:Cross-references: GB:IJ33339; NID:g609536; PIDN:AAA64432.1; PID:g609538
 C:Genetics:
 A:Gene: p52ntk

Query Match 20.0%; Score 2; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 |||
 Db 2 PT 3

RESULT 60
 A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
 C:Accession: A32039
 R:Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989
 A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact
 A:Reference number: A32039; MUID:89123285; PMID:2563371
 A:Accession: A32039

A:Molecule type: protein
 A:Residues: 1-4 <HOR>
 A:Experimental source: brain
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
 |||
 Db 2 PL 3

RESULT 61
 S53508
 starvation-induced ribonuclease - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 C:Accession: S53508
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995
 A:Title: cDNA structure and regulatory properties of a family of starvation-induced r
 A:Reference number: S53506; MUID:95201242; PMID:7894013
 A:Accession: S53508
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <KOE>

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
||
Db 2 PT 3

RESULT 62

HOROKA

proctolin - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
C:Accession: A01644
R:Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A:Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects
A:Reference number: A93048; PMID:76074708; PMID:576
A:Accession: A01644
A:Molecule type: protein
A:Residues: 1-5 <STA>
A>Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmacological properties as the natural peptide.
R:O'Shea, M.; Adams, M.E.
Science 213, 567-569, 1981
A:Title: Pentapeptide (proctolin) associated with an identified neuron.
A:Reference number: A94260; PMID:81225865; PMID:6113690
A:Contents: annotation; biological source
C:Comment: This peptide is found in the lateral white neurons, which occur (in the cockroach) innervate the striated hindgut muscles in insects and stimulate contraction of these muscles.
C:Superfamily: proctolin
C:Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
||
Db 3 LP 4

RESULT 63

JN0860
peptidyl-diesterase A inhibitory peptide C107 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0860
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide from the lateral white neurons of angiotensin I-converting enzyme inhibitory peptide.
A:Reference number: JN0859; PMID:94080036; PMID:7764272
A:Accession: JN0860
A:Molecule type: protein
A:Residues: 1-5 <MAT>
A:Experimental source: intestine
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory peptide.
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
||
Db 2 LP 3

RESULT 64

B42364
flagellar protein flir - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C:Accession: B42364
R:Voogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991

A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and flagellar assembly.
A:Reference number: A42364; PMID:91258342; PMID:1646201
A:Accession: B42364
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <VOG>
A:Cross-references: GB:M62408

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
||
Db 4 LP 5

RESULT 65

PS0324
ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C:Accession: PS0324
R:Tsuigita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0324
A:Molecule type: protein
A:Residues: 1-5 <TSU>
A:Experimental source: leaf, chlorophyll

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
||
Db 4 PT 5

RESULT 66

B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C:Species: Physarum polycephalum
C>Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C:Accession: B37988
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J.
J. Biol. Chem. 265, 19898-19903, 1990
A:Title: Purification and characterization of a novel intracellular acid proteinase from Physarum polycephalum.
A:Reference number: A37988; PMID:91060608; PMID:2246266
A:Accession: B37988
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <MUR>

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
||
Db 3 PP 4

RESULT 67

A60411
proctolin - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
C:Accession: A60411
R:Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, R.; Peptides 11, 205-211, 1990
A:Title: Identification of proctolin in the central nervous system of the horseshoe crab.

A;Reference number: A60411; MUID:90287800; PMID:2356151
A;Accession: A60411
A;Molecule type: protein
A;Residues: 1-5 <GRO>
C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse
C;Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
||
Db 3 LP 4

RESULT 68

G44817
27.5 kDa structural protein - Leuconostoc oenos phase P32 (fragment)

C;Species: Leuconostoc oenos phase P32
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: G44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: G44817

A;Molecule type: protein
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 69

I44817

27.5K structural protein - Leuconostoc oenos phase P37 (fragment)

C;Species: Leuconostoc oenos phase P37
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: I44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: I44817

A;Molecule type: protein
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 70

E44817

27.5K structural protein - Leuconostoc oenos phase P54 (fragment)

C;Species: Leuconostoc oenos phase P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: E44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.

A;Note: sequence extracted from NCBI backbone (NCBIP:70330)

A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: E44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 71

C44817

28.5K structural protein - Leuconostoc oenos phase PAt5-12 (fragment)

C;Species: Leuconostoc oenos phase PAt5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: C44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: C44817

A;Molecule type: protein
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 72

A44817

28K structural protein - Leuconostoc oenos phase PZt11-15 (fragment)

C;Species: Leuconostoc oenos phase PZt11-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: A44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: A44817

A;Molecule type: protein
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 2 TV 3

RESULT 73

A61049

halo-toxin - Pseudomonas syringae pv. mori

C;Species: Pseudomonas syringae pv. mori

A;Note: host mulberry tree

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C;Accession: A61049
R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, Chem. Lett. 00, 679-680, 1989

A;Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas

A:Reference number: A61049
A:Accession: A61049
A:Molecule type: protein
A:Residues: 1-6 <KAJ>
A>Note: sequence confirmed by synthesis
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C:Keywords: toxin

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FP 10
||
Db 2 FP 3

RESULT 74

A27696
contraction-inhibiting peptide I - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995
C:Accession: A27696
R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
A:Title: Structures and actions of Mytilus inhibitory peptides.
A:Reference number: A90142; PMID:88240357; PMID:3377776
A:Accession: A27696
A:Molecule type: protein
A:Residues: 1-6 <HIR>
C:Keywords: amidated carboxyl end
F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MF 9
||
Db 4 MF 5

RESULT 75

B27696
contraction-inhibiting peptide II - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995
C:Accession: B27696
R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
A:Title: Structures and actions of Mytilus inhibitory peptides.
A:Reference number: A90142; PMID:88240357; PMID:3377776
A:Accession: B27696
A:Molecule type: protein
A:Residues: 1-6 <HIR>
C:Keywords: amidated carboxyl end
F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MF 9
||
Db 4 MF 5

Search completed: November 25, 2003, 19:36:10
Job time : 7.86047 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 3.54651 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QLPPTVMFP 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	30.0	8	1 CPD1_ENTFA	P13269 enterococcu
2	3	30.0	9	1 RT33_BOVIN	P82926 bos taurus
3	3	30.0	11	1 BPPH_AGRHA	P01021 agkistrodon
4	3	30.0	11	1 TIN4_HOFTI	P82654 holoibatr
5	3	30.0	12	1 TIN2_HOFTI	P82652 holoibatr
6	3	30.0	12	1 TIN3_HOFTI	P82653 holoibatr
7	3	30.0	13	1 ACT7_SOYBN	P15987 glycine max
8	3	30.0	14	1 ECDC_LYMDI	P80940 lymantria d
9	3	30.0	16	1 CXAA_CONPE	P50984 conus penna
10	3	30.0	16	1 CXAB_CONPE	P50985 conus penna
11	3	30.0	17	1 ACT6_SOYBN	P15986 glycine max
12	3	30.0	18	1 UC21_MAIZE	P80627 zea mays (m
13	3	30.0	20	1 BULB_NARPS	P80554 narcissus p
14	3	30.0	20	1 CPB7_PAPSP	P80055 papio sp. (
15	2	20.0	5	1 EI04_LITRU	P82100 litoria rub
16	2	20.0	5	1 PAP2_PARMA	P81864 pardachirus
17	2	20.0	5	1 PRCT_PERAM	P01373 periplaneta
18	2	20.0	6	1 CIP1_MYTED	P13736 mytilus edu
19	2	20.0	6	1 CIP2_MYTED	P13737 mytilus edu
20	2	20.0	6	1 TMOF_SARBU	P41495 sarcophaga
21	2	20.0	6	1 TRPI_PSEPU	P36414 pseudomonas
22	2	20.0	6	1 VP19_HSV1K	P23210 herpes slimp
23	2	20.0	7	1 LANC_CARUI	P36960 carnobacter
24	2	20.0	7	1 MNPI_LEPDE	P42984 leptinotars
25	2	20.0	7	1 TPFV_PACDA	P83455 pachymedusa
26	2	20.0	7	1 UF04_MOUSE	P38642 mus musculu
27	2	20.0	7	1 UN06_PINPS	P81675 pinus pinas
28	2	20.0	8	1 ACI_THUAL	P18691 thunnus alb
29	2	20.0	8	1 ALL5_CALVO	P41841 calliphora
30	2	20.0	8	1 ALL6_CVDPO	P82157 cydia pomon
31	2	20.0	8	1 COM2_CONPU	P58785 conus purpu
32	2	20.0	8	1 NPB_BOVIN	P15507 bos taurus
33	2	20.0	8	1 PPK2_PERAM	P82692 periplaneta

RESULT 1

ALIGNMENTS

34	2	20.0	9	1	AL10_CARMA	P81813 carcinus ma
35	2	20.0	9	1	COXB_THUOB	P80975 thunnus obe
36	2	20.0	9	1	FAR3_PENMO	P8318 penaeus mon
37	2	20.0	9	1	FAR4_PENMO	P8319 penaeus mon
38	2	20.0	9	1	FAR5_ASCSU	P43170 ascaris suu
39	2	20.0	9	1	FAR9_ASCSU	P43172 ascaris suu
40	2	20.0	9	1	FLA2_TREHY	P80159 treponema h
41	2	20.0	9	1	FRF1_SARBU	P83350 sarcophaga
42	2	20.0	9	1	KNL3_BOMVA	P83058 bomina var
43	2	20.0	9	1	LMT3_LOCMI	P41489 locusta mig
44	2	20.0	9	1	OXYA_SQUAC	P42999 squalus aca
45	2	20.0	9	1	OXYT_EISFO	P42998 eisenia foe
46	2	20.0	9	1	OXYT_RABIT	P32878 oryctolagus
47	2	20.0	9	1	SAMP_MUSCA	P13095 mustelus ca
48	2	20.0	9	1	TKC1_CALVO	P41517 calliphora
49	2	20.0	9	1	UPA3_HUMAN	P30089 homo sapien
50	2	20.0	9	1	YBFR_AZOVI	P25825 azotobacter
51	2	20.0	10	1	AH3_PRUSE	P29261 prunus sero
52	2	20.0	10	1	AL15_CARMA	P81822 carcinus ma
53	2	20.0	10	1	BPP2_BOTIN	P30422 bothrops in
54	2	20.0	10	1	BPP2_BOTJA	P30422 bothrops ja
55	2	20.0	10	1	BPP8_BOTIN	P30426 bothrops in
56	2	20.0	10	1	BPP_VIPAS	P31351 vipera aspi
57	2	20.0	10	1	BRK_ONCMY	O9prz1 oncorhynch
58	2	20.0	10	1	CAT8_SHEEP	P83205 ovis aries
59	2	20.0	10	1	COXM_RAT	P80431 rattus norv
60	2	20.0	10	1	COXQ_RABIT	P80336 oryctolagus
61	2	20.0	10	1	COXQ_SHEEP	P80337 ovis aries
62	2	20.0	10	1	FAR6_PANRE	P82660 panagrellus
63	2	20.0	10	1	GON1_ALLMI	P37041 alligator m
64	2	20.0	10	1	GON3_ONCKE	P20367 oncorhynch
65	2	20.0	10	1	GONL_SQUAC	P27429 squalus aca
66	2	20.0	10	1	LABA_JATMU	P13270 jatrophu mu
67	2	20.0	10	1	LPK2_LOCMI	P41488 locusta mig
68	2	20.0	10	1	NS1_MYCTU	P81135 mycobacteri
69	2	20.0	10	1	ODP2_BOVIN	P11180 bos taurus
70	2	20.0	10	1	PVK_LOCMI	P83382 locusta mig
71	2	20.0	10	1	Q205_COMTE	P80465 comamonas t
72	2	20.0	10	1	SLAP_BACTG	P43325 bacillus th
73	2	20.0	10	1	TEMK_RANTE	P56923 rana tempor
74	2	20.0	10	1	TKL2_LOCMI	P16224 locusta mig
75	2	20.0	10	1	TMOF_AEDAE	P19425 aedes aegyp
76	2	20.0	10	1	UHA3_HUMAN	P40930 homo sapien
77	2	20.0	10	1	UPA2_HUMAN	P30088 homo sapien
78	2	20.0	10	1	UPA5_HUMAN	P30091 homo sapien
79	2	20.0	10	1	UPA9_HUMAN	P30095 homo sapien
80	2	20.0	10	1	URE3_MORMO	P17339 morganelle
81	2	20.0	11	1	BPP3_BOTIN	P30423 bothrops in
82	2	20.0	11	1	BPP4_BOTIN	P30424 bothrops in
83	2	20.0	11	1	BPP_AGRHP	P04562 agkistrodon
84	2	20.0	11	1	BRK_MEGFL	P12797 megascollia
85	2	20.0	11	1	BFG_CLOPA	P81350 clostridium
86	2	20.0	11	1	LADD_ONCMY	P81018 oncorhynch
87	2	20.0	11	1	LPW_THETH	P05624 thermus the
88	2	20.0	11	1	MLG_THETS	P41989 theromyzon
89	2	20.0	11	1	MORN_HUMAN	P01163 homo sapien
90	2	20.0	11	1	NXSN_PSETE	P59072 pseudonaja
91	2	20.0	11	1	POQC_PSEFL	P55173 pseudomonas
92	2	20.0	11	1	PVK1_PERAM	P41837 periplaneta
93	2	20.0	11	1	TKN1_PSEGU	P42986 pseudophryn
94	2	20.0	11	1	TKN1_UPEHU	P08612 uperoleia r
95	2	20.0	11	1	TKN2_PSEGU	P42987 pseudophryn
96	2	20.0	11	1	TKN3_PSEGU	P42988 pseudophryn
97	2	20.0	11	1	TKN4_PSEGU	P42989 pseudophryn
98	2	20.0	11	1	TKN5_PSEGU	P42990 pseudophryn
99	2	20.0	11	1	TKN_ELEMO	P01293 eleodone mos
100	2	20.0	12	1	FAR7_PENMO	P83322 penaeus mon

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CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -1- FUNCTION: cPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOGIN PLASMID PF1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VMP 9
DB 3 VMP 5

RESULT 2
RT33 BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT Identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
DB 5 QPL 7

RESULT 3
BPPB_AKHA STANDARD; PRT; 11 AA.
ID BPPB_AKHA

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AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydus blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad. B, Phys. Biol. Sci. 46:176-181(1970).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 3 LPP 5

RESULT 4
TIM4_HOPTI STANDARD; PRT; 11 AA.
ID TIM4_HOPTI
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
FT SEQUENCE 11 AA; 1248 MW; 117D88FD37605DCB CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 3 LPP 5

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Db          7 PLP 9

RESULT 5
TIN2 HOPTI          STANDARD;          PRT;          12 AA.
AC P82652.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE-Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD_RES 12 12 AMIDATION.
FT SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match          30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 PLP 4
Db          7 PLP 9

RESULT 6
TIN3 HOPTI          STANDARD;          PRT;          12 AA.
AC P82653.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE-Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD_RES 12 12 AMIDATION.
FT SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match          30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 PLP 4
Db          7 PLP 9

RESULT 7
ACT7 SOYBN          STANDARD;          PRT;          13 AA.
ID ACT7_SOYBN
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SACT7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne.
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X17120; CAA34980.1; -.
CC PIR; S15755; S15755.
CC InterPro; IPR004001; Actin.
CC InterPro; IPR004000; Actin_like.
CC PROSITE; PS00406; ACTINS 1; PARTIAL.
CC PROSITE; PS00432; ACTINS 2; PARTIAL.
CC PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match          30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 QPL 3
Db          8 QPL 10

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RESULT 8
ECDC LYMDI      STANDARD;      PRT;      14 AA.
AC P80940;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide C (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
[1]
RN SEQUENCE.
RP MEDLINE=97387807; PubMed=9243792;
RX Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -1- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match      30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
   |||
Db 9 PLP 11

RESULT 9
CXAB_CONPE      STANDARD;      PRT;      16 AA.
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1B.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
[1]
RN SEQUENCE.
RP TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
[2]
RN SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
[3]
RN X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrman J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;

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RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
antagonist, alpha-conotoxin Pn1A from Conus pennaceus.";
RL Structure 4:417-423(1996).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A54877; A54877.
DR FDB; 1PEN; 21-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match      30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
   |||
Db 5 LPP 7

RESULT 10
CXAB_CONPE      STANDARD;      PRT;      16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1B.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
[1]
RN SEQUENCE.
RP TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
[2]
RN SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
[3]
RN X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.-H., Gehrman J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin Pn1B:
RT comparison with alpha-conotoxins Pn1A and GI.";

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OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
RA Partis M.D., Barker P., Thomas B.;
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
FT UNSURE 2 2 OR N.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 13 LPP 15

RESULT 14
CPA7_PAPSP
ID CPA7_PAPSP STANDARD; PRT; 20 AA.
AC P80055;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 2A7 (EC 1.14.14.1) (CYP1A7) (P450 FI) (Coumarin 7-
hydroxylase) (Fragment).
GN CYP2A7.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=52174920; PubMed=1541278;
RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
RT "Purification of two cytochrome P450 isozymes related to CYP2A and
RT CYP3A gene families from monkey (baboon, Papio papio) liver
RT microsomes. Cross reactivity with human forms."
RL Eur. J. Biochem. 204:641-648 (1992).
CC -!- FUNCTION: EXHIBITS A HIGH COUMARIN 7-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- INDUCTION: By phenobarbital.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro; IPR001128; Cytochrome P450.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
FT UNSURE 14 14
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2045 MW; 693102A1F0B50C96 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8
Db 16 TVM 18

RESULT 15
E104_LITRU
ID E104_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RC Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RA "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TV 7
Db 3 TV 4

RESULT 16
PAP2_PAPMA
ID PAP2_PAPMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardaxinus marmoratus (Red sea moles sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleoidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moles sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 FP 10
Db 4 FP 5

RESULT 17
PRCT_PERAM

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ID PRCT_PIRAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]_SEQUENCE.
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]_SEQUENCE.
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]_SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]_SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HORORA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B4600000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
DB 3 LP 4

RESULT 18
CIP1 MYTED STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]_SEQUENCE.
RP SEQUENCE.
RX TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
MUSCLES.
CC -!- SIMILARITY: TO MIP I.
DR PIR; B27696; B27696.
KW Hormone; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MF 9
DB 4 MF 5

RESULT 20
TMOF SARBU STANDARD; PRT; 6 AA.
AC P41495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcoptera; Insecta; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]_SEQUENCE.
RP SEQUENCE.
RX TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
MUSCLES.
CC -!- SIMILARITY: TO MIP II.
DR PIR; A27696; A27696.
KW Hormone; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MF 9
DB 4 MF 5

RESULT 19
CIP2 MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]_SEQUENCE.
RP SEQUENCE.
RX TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
MUSCLES.
CC -!- SIMILARITY: TO MIP I.
DR PIR; B27696; B27696.
KW Hormone; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MF 9
DB 4 MF 5

RESULT 20
TMOF SARBU STANDARD; PRT; 6 AA.
AC P41495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcoptera; Insecta; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OX Sarcophagidae; Sarcophaga.
 RN NCBI_TaxID=7385;
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Byllemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 de Loof A.;
 RT "Sequencing and characterization of trypsin modulating oostatic
 factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
 (Sarcophaga) bullata";
 RL Regul. Pept. 50:61-72(1994).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 DEVELOPMENT.
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 EPITHELIUM AFTER A BLOOD MEAL.
 KW Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PT 6
 DB 2 PT 3
 RESULT 21
 TRPI_PSEPU
 ID -TRPI_PSEPU STANDARD; PRT; 6 AA.
 AC P38414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TrpBA operon transcriptional activator (Fragment).
 GN TRPI.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=3303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPG1 C1S;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
 putida";
 RL Biochimie 71:521-531(1989).
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYXR FAMILY OF TRANSCRIPTIONAL
 REGULATORS.
 CC
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 CC
 CC EMBL; X13299; CAA31660.1; -;
 DR InterPro: IPR000847; HTH_Lyxr.
 DR PROSITE: PS00044; HTH_LYXR_FAMILY; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON_TER 6

SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LP 4
 DB 5 LP 6
 RESULT 22
 VP19_HSVIK
 ID -VP19_HSVIK STANDARD; PRT; 6 AA.
 AC P23210;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)
 DE (Capsid protein VP19C) (Fragment).
 GN UL38.
 OS Herpes simplex virus (type 1 / strain KOS).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
 Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 expression of UL38, a true late gene involved in capsid assembly";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 EMBEDDED. BINDS DNA.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M57646; AAA45830.1; -;
 DR Capsid assembly; Coat protein; DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PL 3
 DB 5 PL 6
 RESULT 23
 LANC_CARUI
 ID -LANC_CARUI STANDARD; PRT; 7 AA.
 AC P36960;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lantibiotic carmocin U149 (Fragment).
 OS Carnobacterium sp. (strain U149).
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 OC Carnobacterium.
 OX NCBI_TaxID=35782;
 RN [1]
 RP SEQUENCE.

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RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON_TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
   ||
Db 5 QP 6

RESULT 24
MNPL LEPDE
ID MNPL LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropeptide 1 (Led-MNP-I).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelini;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RT Peptides 16:365-374(1995).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
   ||
Db 5 PL 6

RESULT 25
TPFY_PACDA
ID TPHY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-1 (Pdt-1).
OS Pachymedusa dactyloides (Giant Mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;

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[1]
RN SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactyloides tryptophyllin-1 (pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; Cerebral; NAS.
DR GO; GO:0045986; P: negative regulation of smooth muscle contractility; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3
   7
FT MOD_RES 7
   7
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
   ||
Db 2 PP 3

RESULT 26
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC NON_TER 7
   7
FT NON_TER 7
   7
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
   ||
Db 3 PP 4

RESULT 27
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
[1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=92274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 KDa.
FT NON TER 1 1
FT NON TER 7 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
Db 5 LP 6

RESULT 28
ACI_THUAL
ID ACI_THUAL STANDARD; PRT; 8 AA.
AC P1691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neochannus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PT 6
Db 1 PT 2

RESULT 29
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.

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OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
[2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -|- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -|- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; B47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION (20%).
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 2 PP 3

RESULT 30
ALL6_CVDPO
ID ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
Db 1 LP 2

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RESULT 31
COW2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD_RES 4 4 D-LEUCINE
FT SEQUENCE 8 AA; 890 MW; 75A36767232CEB8 CRC64;
SQ SEQUENCE 8 AA; 890 MW; 75A36767232CEB8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
DB 5 LP 6

RESULT 32
NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Pratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 OP 2
DB 4 OP 5

RESULT 33
PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRK-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
FT SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 34
AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98321193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the

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RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
Db 3 QP 4

RESULT 35
COXE_THUOB
ID FAR3_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
CC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR, S77984; S77984.
DR PROSITE, PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
Db 3 QP 4

RESULT 36
FAR3_PENMO
ID FAR3_PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
DE of the giant tiger prawn Penaeus monodon."
DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk; PubMed=11959015;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
Db 2 QP 3

RESULT 37
FAR4_PENMO
ID FAR4_PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
CC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk; PubMed=11959015;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
Db 2 QP 3

RESULT 38
FAR5_ASCSU
ID FAR5_ASCSU STANDARD; PRT; 9 AA.
AC P43170;

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DT	01-NOV-1995 (Rel. 32, Created)	
DT	01-NOV-1995 (Rel. 32, Last sequence update)	
DT	01-FEB-1996 (Rel. 33, Last annotation update)	
DE	FMRFamide-like neuropeptide AF5.	
OC	Ascaris suum (Pig roundworm) (Ascaris lumbricoides).	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;	
OC	Ascarididae; Ascaris.	
OC	NCBI_TaxID=6253;	
RN	[1]	
RP	SEQUENCE.	
RX	MEDLINE=95380362; PubMed=7651904;	
RA	Cowden C., Stretton A.O.W.;	
RT	"Eight novel FMRFamide-like neuropeptides isolated from the nematode	
RT	RT Ascaris suum.";	
RL	Peptides 16:491-500(1995).	
CC	- - SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)	
CC	FAMILY.	
KW	Neuropeptide; Amidation.	
FT	MOD_RES 9 9	AMIDATION.
SQ	SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 CRC64;	
	Query Match 20.0%; Score 2; DB 1; Length 9;	
	Best Local Similarity 100.0%; Pred.No. 1.3e+05;	
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	5 PT 6	
DB	4 PT 5	
RESULT 39		
FAR9 ASCSU		
ID FAR9 ASCSU STANDARD; PRT; 9 AA.		
AC P43172;		
DT 01-NOV-1995 (Rel. 32, Created)		
DT 01-NOV-1995 (Rel. 32, Last sequence update)		
DT 01-FEB-1996 (Rel. 33, Last annotation update)		
DE FMRFamide-like neuropeptide AF9.		
OC Ascaris suum (Pig roundworm) (Ascaris lumbricoides).		
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;		
OC Ascarididae; Ascaris.		
OC NCBI_TaxID=6253;		
RN [1]		
RP SEQUENCE.		
RX MEDLINE=95380362; PubMed=7651904;		
RA Cowden C., Stretton A.O.W.;		
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode		
RT RT Ascaris suum.";		
RL Peptides 16:491-500(1995).		
CC - - SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)		
CC FAMILY.		
KW Neuropeptide; Amidation.		
FT MOD_RES 9 9	AMIDATION.	
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;		
	Query Match 20.0%; Score 2; DB 1; Length 9;	
	Best Local Similarity 100.0%; Pred.No. 1.3e+05;	
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2 PL 3	
DB	6 PL 7	
RESULT 40		
FLA2 TREHY		
ID FLA2 TREHY STANDARD; PRT; 9 AA.		
AC P80159;		
DT 01-FEB-1995 (Rel. 31, Created)		
DT 01-FEB-1995 (Rel. 31, Last sequence update)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)		
DE (Fragment).		

RESULT 42
KML3_BOMVA
ID KML3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RN SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP TISSUE=Skin secretion;
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens."
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -|- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;
Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 PP 5
Db 2 PP 3
RESULT 43
LMT3_LOCFI
ID LMT3_LOCFI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RP TISSUE=Brain;
RA Schoofa L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family."
PL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -|- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;
Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
Db 3 QP 4
RESULT 44
OXYA_SQUAC
ID OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RN SEQUENCE.
RP MEDLINE=73031727; PubMed=5083097;
RX Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RN SEQUENCE.
RP MEDLINE=72128038; PubMed=4622083;
RX Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376BB444404B CRC64;
Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PL 3
Db 7 PL 8
RESULT 45
OXYT_EISFO
ID OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RN SEQUENCE.
RP TISSUE=Pituitary;
RC MEDLINE=94121660; PubMed=8292046;
RX Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -|- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO

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CC *PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; PC2021; PC2021.
DR InterPro; IPR000981; Neutryp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
DB 7 PT 8

RESULT 46
OXYT RABIT
ID -OXYT RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus),
OS Balanoptera physalus (Finback whale),
OS Tachyglossus aculeatus aculeatus (Australian echidna), and
OS Hydrolagus colliei (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104 (1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H.amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429 (1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B.physalus;
RX Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192 (1964).
RN [4]
RP SEQUENCE.
RC SPECIES=A.aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophysial hormones and evolution of tetrapods.";
RN [5]
RP SEQUENCE.
RC SPECIES=H.colliei;
RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophysial hormone in the holocephalian
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RT elasmobranch fish, Hydrolagus collei.";
RL J. Endocrinol. 45:597-606 (1969).
CC -1- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro; IPR000981; Neutryp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1 6
FT MOD RES 9 9
FT SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
DB 7 PL 8

RESULT 47
SAMP MUSCA
ID -SAMP MUSCA STANDARD; PRT; 9 AA.
AC P19035;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
OC NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894 (1983).
CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1 >9
FT NON TER 9
FT SEQUENCE 9 AA; 965 MW; D05B5735B386769 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FP 10
DB 2 FP 3
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RESULT 48

TKC1 CALVO STANDARD; PRT; 9 AA.
 ID TKC1 CALVO
 AC P41517;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin I.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clotens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, Calliphora vomitoria, that have resemblances to
 RT tachykinins.";
 RL Peptides 15:761-768 (1994).
 CC -|- FUNCTION: MYOACTIVE PEPTIDE.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 9
 FT AMIDATION.
 SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 PT 6
 DB 2 PT 3

RESULT 49

UPA3 HUMAN STANDARD; PRT; 9 AA.
 ID UPA3 HUMAN
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714 (1992).
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON-TER 1
 FT NON-TER 9
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PL 3
 DB 2 PL 3

RESULT 50

YBFR AZOVI STANDARD; PRT; 9 AA.
 ID YBFR AZOVI
 AC P25825;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in bfr 3'region (Fragment).
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196129; PubMed=1549605;
 RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
 RA Stiefel E.I.;
 RT "Unification of the ferritin family of proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423 (1992).
 CC -----
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 CC -----

EMBL; M83692; AAA22122.1; -.
 DR PIR; B41983; B41983.
 KW Hypothetical protein.
 FT NON-TER 9

SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PP 5
 DB 3 PP 4

RESULT 51

AH3 PRUSE STANDARD; PRT; 10 AA.
 ID AH3 PRUSE
 AC P29261;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
 DE isozyme II) (AH II) (Fragment).
 OS Prunus serotina (Black cherry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=23207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Li C.P., Swain E., Poulton J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
 RL Plant Physiol. 100:282-290 (1992).
 CC -|- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
 CC glucose.
 CC -|- SUBUNIT: Monomer.
 CC -|- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
 CC EMBRYONAL TISSUES.
 CC -|- PTM: GLYCOSYLATED.

KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 Db 3 PP 4

RESULT 52

AL19_CARMA STANDARD; PRT; 10 AA.
 AC P81822;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Carcinustatin 19.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTROSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1101 MW; 96687CDSAB569AB1 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 Db 2 PT 3

RESULT 53

BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.

DR PIR; B37196; B37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C741773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 Db 9 PP 10

RESULT 54

BPP2_BOTJA STANDARD; PRT; 10 AA.
 AC P01022;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
 DE inhibitor V-6-II).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=72118526; PubMed=4334402;
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
 RA Kocy O.;

RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
 RT jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.

DR PIR; A01255; XAVI6B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 Db 9 PP 10

RESULT 55

BPP8_BOTIN STANDARD; PRT; 10 AA.
 AC P30426;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8723;
 RN [1]

```

RP SEQUENCE.
RX TISSUE=Venom;
RA MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: H37196; H37196
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 9 PP 10

RESULT 56
BPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RA MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 9 PP 10

RESULT 57
BRK ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.

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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma.";
RL FEBS Lett. 334:75-78 (1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR: S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PL 3
Db 8 PL 9

RESULT 58
CATB SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
GN CTSSB.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta; PubMed=12506352;
RX MEDLINE=22394055; PubMed=12506352;
RA El Amiri B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Moko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (by similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro: IPR000169; SHPtot acite
DR PROSITE; PS00640; THIOI_PROTEASE_ASN; PARTIAL.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

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Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
 ||
 1 LP 2

Db

RESULT 59
 COXM RAT
 ID COXM RAT STANDARD; PRT; 10 AA.
 AC P80431;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
 DE (Fragment).
 DE COX7B.
 GN Rattus norvegicus (Rat).
 OS
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome c oxidase in developing rat heart. Enzymic properties and
 RT amino-terminal sequences suggest identity of the fetal heart and the
 RT adult liver isoform.";
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC PIR; S65387; S65387.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1210 MW; CFC70BB771A33326 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 ||
 7 PT 8

Db

RESULT 60
 COXQ RABIT
 ID COXQ RABIT STANDARD; PRT; 10 AA.
 AC P80336;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
 DE (Fragment).
 DE COX8H.
 GN Oryctolagus cuniculus (Rabbit).
 OS
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart, and Liver;
 RA Freund R., Kadenbach B.;
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.

CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 ||
 9 PT 10

Db

RESULT 61
 COXQ SHEEP
 ID COXQ SHEEP STANDARD; PRT; 10 AA.
 AC P80337;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
 DE (Fragment).
 DE Ovis aries (Sheep).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart, and Liver;
 RA Freund R., Kadenbach B.;
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
 ||
 9 PT 10

Db

RESULT 62
 FAR6 PANRE
 ID FAR6 PANRE STANDARD; PRT; 10 AA.
 AC P82660;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRFamide-related
 RT peptides (FarPs) from free-living nematode, Panagrellus redivivus.";
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.

CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1132 MW; CB13P4C9D776C76D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
 ||
 Db 5 QP 6

RESULT 63

CON1_ALLMI
 ID GON1_ALLMI STANDARD; PRT; 10 AA.
 AC P37041; P20407;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)
 DE (Luliberin I).
 OS Alligator mississippiensis (American alligator).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=91352338; PubMed=1882082;
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
 RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure of two forms of gonadotropin-releasing hormone
 RT from brains of the American alligator (Alligator mississippiensis).";
 RL Regul. Pept. 33:105-116(1991).

CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GNRH family.

DR PIR; A60066; RHA01.
 DR InterPro; IPR002012; GNRH.
 DR Pfam; PF00446; GNRH; 1.
 DR PROSITE; PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QP 2
 ||
 Db 8 QP 9

RESULT 64

GON3_ONCKE
 ID GON3_ONCKE STANDARD; PRT; 10 AA.
 AC P20367; P81751;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-RH III)
 DE (Luliberin III).
 GN GNRH3.
 OS Oncorhynchus keta (Chum salmon), and
 OS Clupea pallasii (Pacific herring).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8018, 30724;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=O. keta;
 RX MEDLINE=83195140; PubMed=6341999;
 RA Sherwood N., Eiden U., Brownstein M., Spiess J., Rivier J., Vale W.;
 RT "Characterization of a teleost gonadotropin-releasing hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
 RN [2]

RP SEQUENCE, AND FUNCTION

RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
 RX MEDLINE=20114351; PubMed=10650929;
 RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing
 RT hormones, including a novel form, from an ancient teleost, herring.";
 RL Endocrinology 141:505-512(2000).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GNRH family.

DR PIR; A21114; A21114.

DR InterPro; IPR002012; GNRH.

DR Pfam; PF00446; GNRH; 1.

DR PROSITE; PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 10 10 AMIDATION

SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
 ||
 Db 8 LP 9

RESULT 65

GONL_SQUAC
 ID GONL_SQUAC STANDARD; PRT; 10 AA.
 AC P27429;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH)
 DE (Luliberin).
 OS Squalus acanthias (Spiny dogfish).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 CC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 OX NCBI_TaxID=7797;
 RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=92335300; PubMed=1631133;

RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,

RA Naborniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;

RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in

RT dogfish brain provides insight into GNRH evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).

CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GNRH family.

DR PIR; A46030; A46030.

DR InterPro; IPR002012; GNRH.

DR Pfam; PF00446; GNRH; 1.

DR PROSITE; PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 10 10 AMIDATION

SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
||
Db 8 LP 9

RESULT 66

LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Jatropha.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
multifida L. (Euphorbiaceae). Isolation and sequence determination
by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE
CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY
SEEMS TO BE BASED ON AN INTERACTION WITH C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR
TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1E362 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
||
Db 5 TV 6

RESULT 67

LPK2_LOCMI STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOW-PK-2) (FXPL-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=94094539; PubMed=7903606;
RX Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
de Loof A.;
RT "Isolation, identification and synthesis of locustapyrokinin II from
Locusta migratoria, another member of the FXPL-amide peptide
family."
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC

CC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
||
Db 4 PT 5

RESULT 68

NS1_MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37Rv;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
the genome of strain H37Rv.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
||
Db 4 PL 5

RESULT 69

ODP2_BOVIN STANDARD; PRT; 10 AA.
AC P11180;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipamide acetyltransferase component of pyruvate dehydrogenase
complex (EC 2.3.1.12) (E2) (Fragment).
GN DIAT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
RT "Primary structure around the lipase-attachment site on the E2
component of bovine heart pyruvate dehydrogenase complex."
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall


```

CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyl-dihydrolipoamide
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
CC COFACTOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro: IPR003016; Lipoyl.
KW Lipoyl.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
KW Lipoyl.
FT NON TER 1 1 LIPOYL.
FT BINDING 5 5
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1066 MW; 889BECDAADD33AB1 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
Db |||
7 TV 8

RESULT 70
PVK_LOCMI ID PVK LOCMI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (Lom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.
RT "Identification of the abundant neuropeptide from abdominal
RT perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
CC contraction of the heart and stimulates amplitude and tonus of the
CC foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MCD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FP 10
Db |||
7 FP 8

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RESULT 71
Q2OB_COMTE ID Q2OB COMTE STANDARD; PRT; 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinolone 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RX Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
CC 1,2-DIHYDROQUINOLINE.
CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first
CC step.
CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON TER 10
SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FP 10
Db |||
3 FP 4

RESULT 72
SLAP_BACTG ID SLAP BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RX Luckevich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 9 FP 10
Db 5 FP 6

RESULT 73
TEMK_RANTE
ID TEMK_RANTE STANDARD; PRT; 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
Db 2 LP 3

RESULT 74
TKL2_LOCMI
ID TKL2_LOCMI STANDARD; PRT; 10 AA.
AC P16224;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
Db 2 PL 3

RESULT 75
TMOF_AEDAE
ID TMOF_AEDAE STANDARD; PRT; 10 AA.
AC F19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=835326;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
Db 5 PP 6

Search completed: November 25, 2003, 19:28:23
Job time : 3.61794 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 18.7791 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPLPPTVMEP 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: SPREMBL 23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_nhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvirus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	40.0	12	Q8KZ86	Q8KZ86 acinetobact
2	4	40.0	12	Q9BZ49	Q9BZ49 homo sapien
3	4	40.0	13	Q9L8K1	Q9L8K1 enterococcu
4	4	40.0	13	Q14182	Q14182 homo sapien
5	4	40.0	15	Q40562	Q40562 nicotiana t
6	4	40.0	15	Q40563	Q40563 nicotiana t
7	4	40.0	18	Q84129	Q84129 influenzavi
8	4	40.0	19	Q9RBV1	Q9RBV1 pseudomonas
9	4	40.0	20	Q9UCA8	Q9UCA8 homo sapien
10	4	40.0	20	Q9S8A8	Q9S8A8 secale cere
11	4	40.0	20	Q9PRN3	Q9PRN3 petromyzon
12	3	30.0	9	P83157	P83157 anabaena sp
13	3	30.0	9	Q9TWV0	Q9TWV0 anthopleura
14	3	30.0	9	Q9S8J8	Q9S8J8 cryza sativ
15	3	30.0	9	Q935G1	Q935G1 salmonella
16	3	30.0	10	Q9R5T2	Q9R5T2 acetobacter

17	3	30.0	10	4	Q14096	Q14096 homo sapien
18	3	30.0	10	11	Q9QVF7	Q9QVF7 rattus sp.
19	3	30.0	10	11	Q8VHM9	Q8VHM9 mus musculus
20	3	30.0	10	12	Q8JV78	Q8JV78 polyomaviru
21	3	30.0	10	13	Q90ZV8	Q90ZV8 psittacus e
22	3	30.0	11	4	O60761	O60761 homo sapien
23	3	30.0	11	4	Q9UCR1	Q9UCR1 homo sapien
24	3	30.0	11	6	Q9GL48	Q9GL48 sus scrofa
25	3	30.0	11	10	Q9S8Z9	Q9S8Z9 psophocarpu
26	3	30.0	12	4	Q9P116	Q9P116 homo sapien
27	3	30.0	12	4	Q9NTQ2	Q9NTQ2 homo sapien
28	3	30.0	12	6	Q9TRU1	Q9TRU1 bos taurus
29	3	30.0	12	10	P82329	P82329 pisum sativ
30	3	30.0	13	4	Q14890	Q14890 homo sapien
31	3	30.0	13	4	Q9UNV6	Q9UNV6 homo sapien
32	3	30.0	13	6	Q9TRW6	Q9TRW6 bos taurus
33	3	30.0	13	10	Q42373	Q42373 solanum tub
34	3	30.0	13	11	O88176	O88176 mus musculu
35	3	30.0	14	8	Q9TK7	Q9TK7 chlamydomon
36	3	30.0	14	10	P82326	P82326 pisum sativ
37	3	30.0	14	11	O70599	O70599 rattus norv
38	3	30.0	14	16	Q9KE26	Q9KE26 bacillus ha
39	3	30.0	15	2	Q9R5D5	Q9R5D5 chromatium
40	3	30.0	15	6	Q9TR62	Q9TR62 cryotolagus
41	3	30.0	15	11	Q9QV25	Q9QV25 rattus sp.
42	3	30.0	15	12	Q63353	Q63353 herpes simp
43	3	30.0	16	2	Q9RSK7	Q9RSK7 streptomyce
44	3	30.0	16	4	Q9NNZ2	Q9NNZ2 homo sapien
45	3	30.0	16	5	O18378	O18378 drosophila
46	3	30.0	16	8	P92732	P92732 fejeervarya
47	3	30.0	17	2	O8VME2	O8VME2 pseudomonas
48	3	30.0	17	2	P97135	P97135 mycobacteri
49	3	30.0	17	4	O15276	O15276 homo sapien
50	3	30.0	17	4	Q96P96	Q96P96 homo sapien
51	3	30.0	17	6	Q9TRU8	Q9TRU8 bos taurus
52	3	30.0	17	10	P83061	P83061 spinacia ol
53	3	30.0	17	12	O8B4C4	O8B4C4 hepatitis b
54	3	30.0	18	2	Q9RSU2	Q9RSU2 pseudomonas
55	3	30.0	18	2	Q9RSF9	Q9RSF9 alcaligenes
56	3	30.0	18	2	Q9RAV9	Q9RAV9 campylobact
57	3	30.0	18	2	Q9EYW5	Q9EYW5 erwinia ste
58	3	30.0	18	2	Q9R4C6	Q9R4C6 agrobacteri
59	3	30.0	18	4	Q96F98	Q96F98 homo sapien
60	3	30.0	18	4	Q16244	Q16244 homo sapien
61	3	30.0	18	4	O8NFB4	O8NFB4 homo sapien
62	3	30.0	18	10	Q9S915	Q9S915 triticum tu
63	3	30.0	19	2	Q9K4X0	Q9K4X0 planktothri
64	3	30.0	19	4	Q9UC80	Q9UC80 homo sapien
65	3	30.0	19	4	O8NFL2	O8NFL2 homo sapien
66	3	30.0	19	4	Q9UCK6	Q9UCK6 homo sapien
67	3	30.0	19	8	Q31887	Q31887 artemia par
68	3	30.0	19	8	Q9GI97	Q9GI97 sargassum p
69	3	30.0	19	10	Q9S8F5	Q9S8F5 beta vulgar
70	3	30.0	19	12	Q69099	Q69099 herpes simp
71	3	30.0	19	13	Q9PRT0	Q9PRT0 gallus gall
72	3	30.0	19	13	Q9PRN4	Q9PRN4 petromyzon
73	3	30.0	19	15	Q9ORF8	Q9ORF8 human immun
74	3	30.0	19	15	Q905E8	Q905E8 human immun
75	3	30.0	20	2	Q9R4M9	Q9R4M9 pseudomonas
76	3	30.0	20	2	Q931L1	Q931L1 vibrio harv
77	3	30.0	20	2	O53370	O53370 escherichia
78	3	30.0	20	2	O50180	O50180 pseudomonas
79	3	30.0	20	2	Q46499	Q46499 desulfovibr
80	3	30.0	20	2	Q9R5E8	Q9R5E8 bacillus sp
81	3	30.0	20	4	Q9ET45	Q9ET45 homo sapien
82	3	30.0	20	4	Q9UCB7	Q9UCB7 homo sapien
83	3	30.0	20	4	Q9URC8	Q9URC8 homo sapien
84	3	30.0	20	5	Q25281	Q25281 leishmania
85	3	30.0	20	7	Q8WLP7	Q8WLP7 macaca mula
86	3	30.0	20	10	Q9S8H1	Q9S8H1 hordeum vul
87	3	30.0	20	11	Q9QW31	Q9QW31 rattus sp.
88	3	30.0	20	11	Q9QVG0	Q9QVG0 rattus sp.
89	2	20.0	5	13	P83308	P83308 gallus gall

90 P70804 azotobacter
 91 O50556 actinobacil
 92 Q54248 streptomyc
 93 O34028 sphingomona
 94 P92214 amblyopyrum
 95 P92393 hordeum vul
 96 P92403 lophopyrum
 97 P92427 peridictyon
 98 P92430 aegilops ta
 99 P92221 bromus iner
 100 P92425 pseudoroegn

ALIGNMENTS

RESULT 1
 Q8KZ86 PRELIMINARY; PRT; 12 AA.
 ID Q8KZ86
 AC Q8KZ86;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Class I integron DNA integrase (Fragment).
 GN INT11.
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]_TaxID=470;
 RP SEQUENCE FROM N.A.
 RC STRAIN=204A;
 RA Dolzani L., Gombac F., Lagatolla C., Riccio M.L., Rossolini G.M.,
 RA Tonin E., Monti-Bragadin C.;
 RT "Carriage of class I and II integrons in Italian clinical isolates of
 RT Acinetobacter baumannii.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ313334; CAC85941.1; -.
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1296 MW; 904268B8F5E376DC1 CRC64;

Query Match 40.0%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db 7 PLPP 10
 RESULT 2
 Q9BZ49 PRELIMINARY; PRT; 12 AA.
 ID Q9BZ49
 AC Q9BZ49;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Glycophorin C (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
 RA Zimmerman P.A.;
 RT "The association of the glycophorin C exon 3 deletion with
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
 RT Guinea.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF342984; AAK01459.1; -.
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1296 MW; 904268B8F5E376DC1 CRC64;

SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;
 Query Match 40.0%; Score 4; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 Db 7 PLPP 10
 RESULT 3
 Q9L8K1 PRELIMINARY; PRT; 13 AA.
 ID Q9L8K1
 AC Q9L8K1;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE Vans (Fragment).
 GN VANSB.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BM4281;
 RX MEDLINE=20307504; PubMed=10846225;
 RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
 RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin
 RT resistant enterococci and characterization of two novel insertion
 RT sequences.";
 RL Microbiology 146:1469-1479(2000).
 DR EMBL; AF201896; AAF73374.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1502 MW; 8D0E282189F9672A CRC64;

Query Match 40.0%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6
 Db 7 LPPT 10
 RESULT 4
 Q14182 PRELIMINARY; PRT; 13 AA.
 ID Q14182
 AC Q14182;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE Deoxynucleotidyltransferase (Fragment).
 GN DNTT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87213162; PubMed=3579900;
 RA Koizumi O., Kaneda T., Morishita R.;
 RT "Analysis of human terminal deoxynucleotidyl transferase cDNA
 RT expressible in mammalian cells.";
 RL Biochem. Biophys. Res. Commun. 144:185-190(1987).
 DR EMBL; M26144; AAA74588.1; -.
 KW Transferase.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 40.0%; Score 4; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 QPLP 4
Db      8 QPLP 11

RESULT 5
Q40562 PRELIMINARY; PRT; 15 AA.
ID Q40562;
AC Q40562;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-A2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565(1994).
DR EMBL; L16786; AAA73564.1; -.
KW GTP-binding.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1707 MW; 8AB89F924EA30CAF CRC64;

Query Match 40.0%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLP 4
Db      3 QPLP 6

RESULT 6
Q40563 PRELIMINARY; PRT; 15 AA.
ID Q40563;
AC Q40563;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-B2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565(1994).
DR EMBL; L16788; AAA73565.1; -.
KW GTP-binding.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFAF CRC64;

Query Match 40.0%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLP 4
Db      8 QPLP 11

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLP 4
Db      4 QPLP 7

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
Q84129 PRELIMINARY; PRT; 18 AA.
ID Q84129;
AC Q84129;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg
DE 8), COOH terminus of NS1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates."
RL Virology 128:512-517(1983).
DR EMBL; K00959; AAA43541.1; -.
DR InterPro; IPR000256; Flu_Ns1.
DR Pfam; PF00600; Flu_Ns1; I.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FFEBEF CRC64;

Query Match 40.0%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      12 PLPP 15

RESULT 8
Q9RBV1 PRELIMINARY; PRT; 19 AA.
ID Q9RBV1;
AC Q9RBV1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Integrase (Fragment).
OS Pseudomonas sp. R9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=101164;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R9; TRANSPOSON=Tn1404;
RX MEDLINE=20011227; PubMed=10543801;
RA Schnabel E.L., Jones A.L.;
RT "Distribution of tetracycline resistance genes and transposons among
RT phylloplane bacteria in Michigan apple orchards."
RL Appl. Environ. Microbiol. 65:4898-4907(1999).
DR EMBL; AF157798; RAD47998.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2065 MW; 19EF26DDCA6290F0 CRC64;

Query Match 40.0%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      7 PLPP 10

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RESULT 9
Q9UCAB PRELIMINARY; PRT; 20 AA.
ID Q9UCAB
AC Q9UCAB;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Tumor-derived adhesion factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94161713; PubMed=8117260;
RA Akaogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
RA Yasumitsu H., Umeda M., Miyazaki K.;
RT "Cell adhesion activity of a 30-KDa major secreted protein from human
RT bladder carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 198;1046-1053(1994).
SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0A8BD CRC64;

Query Match 40.0%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 16 PLPP 19

RESULT 10
Q9S8A8 PRELIMINARY; PRT; 20 AA.
ID Q9S8A8
AC Q9S8A8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Gamma-35 SECALIN isoform P9-12 (COELIAC immunoreactive protein)
DE (Fragment).
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE.
RX MEDLINE=96283789; PubMed=8679669;
RA Rocher A., Calero M., Soriano F., Mendez E.;
RT "Identification of major rye secalins as coeliac immunoreactive
RT proteins.";
RL Biochim. Biophys. Acta 1295:13-22(1996).
SQ SEQUENCE 20 AA; 2249 MW; 96D3DA4098BB5C80 CRC64;

Query Match 40.0%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
Db 16 QPLP 19

RESULT 11
Q9PRN3 PRELIMINARY; PRT; 20 AA.
ID Q9PRN3
AC Q9PRN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Melanotropin MSH-B.

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OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 20 AA; 2403 MW; AC4DAD67C69AB0D CRC64;

Query Match 40.0%; Score 4; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
Db 17 QPLP 20

RESULT 12
P83157 PRELIMINARY; PRT; 9 AA.
ID P83157
AC P83157;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlenmann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR PROSITE; PS00088; SOD MN; PARTIAL.
KW Oxidoreductase; Iron; Metal-binding.
FT NON TER 9
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 6 PLP 8

RESULT 13
Q9TWV0 PRELIMINARY; PRT; 9 AA.
ID Q9TWV0
AC Q9TWV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Antho-RPAMIDE-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]

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RP SEQUENCE.
RX MEDLINE=93126143; PubMed=1480510;
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Arg-Pro-NH2 (Antho-Ramide),
RT an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db |||
1 LPP 3

RESULT 14
Q9S8J8 PRELIMINARY; PRT; 9 AA.
AC Q9S8J8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE OryzATENSIN=BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and Characterization of Oryzatenin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.";
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Gramene; Q9S8J8; -.
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 30.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db |||
6 PLP 8

RESULT 15
Q9J35G1 PRELIMINARY; PRT; 9 AA.
ID Q9J35G1;
AC Q9J35G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1.01C.
OS Salmonella typhi.
OG Plasmid pHCM1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

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RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Iarsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AJ513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FDC77776D86767 CRC64;

Query Match 30.0%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db |||
1 PLP 3

RESULT 16
Q9R5T2 PRELIMINARY; PRT; 10 AA.
ID Q9R5T2;
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]
RP SEQUENCE
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D7767 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db |||
3 LPP 5

RESULT 17
Q14096 PRELIMINARY; PRT; 10 AA.
ID Q14096;
AC Q14096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYP2B6 gene cryptic exon 3A of cytochrome P45011B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174922; PubMed=2308828;
RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT "Alternative splicing in the human cytochrome P45011B6 gene: use of a
RT cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL Nucleic Acids Res. 18:189-189(1990).
DR EMBL; X16864; CAA34754.1; -.

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SQ SEQUENCE 10 AA; 885 MW; 4181B9D87DC77767 CRC64;
Query Match 30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 3 LPP 5

RESULT 18
Q9QVF7 PRELIMINARY; PRT; 10 AA.
AC Q9QVF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92135065; PubMed=1777418;
RA Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA Yasuda T., Koike T.;
RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT cDNA cloning and inter-species differences of beta 2-GPI in
RT alternation of anticardiolipin binding.";
RL Int. Immunol. 3:1217-1221(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1100 MW; 94E681B767376EA1 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 5 PLP 7

RESULT 19
Q8VHM9 PRELIMINARY; PRT; 10 AA.
AC Q8VHM9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interferon receptor 2a, (Fragment).
GN IFNAR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The organization, transcriptional regulation and chromosomal
RT localization of the locus encoding the gene for the murine type I
RT interferon receptor, Ifnar2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF440786; AAL40944.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 1 LPP 3

RESULT 20
Q8JV78 PRELIMINARY; PRT; 10 AA.
AC Q8JV78;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303946; AAM97796.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 7 LPP 9

RESULT 21
Q90ZV8 PRELIMINARY; PRT; 10 AA.
AC Q90ZV8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Adenylate kinase (Fragment).
OS Psittacus erithacus (grey parrot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.
OX NCBI_TaxID=57247;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapiro L.H., Dumbacher J.P.;
RT "Adenylate kinase intron 5: a new nuclear locus for avian
RT systematics.";
RL Auk 118:248-255(2001).
DR EMBL; AF307895; AAK43534.1; -.
KW Kinase.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;

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Matches. 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6
Db |||
3 PPT 5

RESULT 22

O60761 PRELIMINARY; PRT; 11 AA.
ID O60761
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NPT-1 protein (Fragment).
GN NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207718; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
RA Tatsumi S., Moxita K., Takeda E.;
RT "Characterization of the 5' flanking region of the human NPT-1
RT Na+/phosphate cotransporter gene.";
RL Biochim. Biophys. Acta 1396:267-272 (1998).
DR EMBL; D83236; BAA25645.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db |||
7 LPP 9

RESULT 23

Q9UCR1 PRELIMINARY; PRT; 11 AA.
ID Q9UCR1
AC Q9UCR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Kruszsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffrman E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529 (1992).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db |||
3 QPL 5

RESULT 24

Q9GL48 PRELIMINARY; PRT; 11 AA.
ID Q9GL48
AC Q9GL48;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE G protein-coupled receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagasaka T., Bouliday G., Couplon S., Coulon F., Tesson L.,
RA Heslan J.-M., Soullou J.-P., Charreau B.;
RT "Alternative double screening for differentially expressed genes by
RT modified RNA differential display and semi-quantitative Reverse
RT Northern blot.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319662; AAG33870.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6
Db |||
2 PPT 4

RESULT 25

Q9S8Z9 PRELIMINARY; PRT; 11 AA.
ID Q9S8Z9
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W1 peptide (Fragment).
OS Paophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Paophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735 (1992).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BACBD77772D1 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
Db |||
3 PTV 5

RESULT 26

Q9P116 PRELIMINARY; PRT; 12 AA.
ID Q9P116
AC Q9P116;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Apolipoprotein E receptor 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Korschneck I., Gharehbaghi-Schnell E., Lang I., Binder R.B.;
RL "Expression of Apolipoprotein E Receptor 2 in atherosclerosis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF129170; AAF66440.1; -.
KW Lipoprotein; Receptor.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1467 MW; 4E89354104044877 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 1 PPT 3

RESULT 27
Q9NTQ2 PRELIMINARY; PRT; 12 AA.
ID Q9NTQ2
AC Q9NTQ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE DJ402L9.1 (Mu opiate receptor (MOR1)) (Fragment).
GN DJ402L9.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillimore B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132774; CAB76846.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1296 MW; 68479422BDAB1DDB CRC64;

Query Match 30.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 10 PLP 12

RESULT 28
Q9TRU1 PRELIMINARY; PRT; 12 AA.
ID Q9TRU1
AC Q9TRU1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 43 kDa CYANOGEN bromide fragment PEAK 7 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA MEDLINE=92132498; PubMed=1734497;

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RA Velby O.P., Sletten K., Husby G., Nordatoga K.;
RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
of bovine kidney.";
RL Scand. J. Immunol. 35:63-69(1992).
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1257 MW; 0D5C94FDE9B76AA4 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
Db 7 PTV 9

RESULT 29
P82329 PRELIMINARY; PRT; 12 AA.
ID P82329
AC P82329;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT111) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1244 MW; CBE0AD74B3D5B862 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 9 LPP 11

RESULT 30
Q14890 PRELIMINARY; PRT; 13 AA.
ID Q14890
AC Q14890;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mucin (Fragment).
GN MUC5AC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tracheobronchial mucosa;
RA Guyonnet-Duperrat V., Audie J., Debailleul V., Laine A., Buisine M.,

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RA Zouitina-Gallieue S., Pigmy P., Degand P., Aubert J., Porchet N.;
RT "Characterization of the human mucin gene MUC5AC: a consensus
RT cysteine-rich domain for lip15 mucin genes.";
RL Biochem. J. 0:0-0(1994).
DR EMBL; Z34280; CAA84034.1; -.
FT NON_TER 1 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;

Query Match
Best Local Similarity 30.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 6 LPP 8

RESULT 31
Q9UNV6 PRELIMINARY; PRT; 13 AA.
AC Q9UNV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN IMPA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Detera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
SQ SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF085628; AAD22141.1; -.
DR EMBL; AF085627; AAD22141.1; JOINED.
FT NON_TER 1 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match
Best Local Similarity 30.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
DB 9 PTV 11

RESULT 32
Q9TRW6 PRELIMINARY; PRT; 13 AA.
AC Q9TRW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein p25, peptide F3 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
RL FEBS Lett. 289:37-43(1991).
FT NON_TER 1 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1375 MW; 2C2822494805D1B7 CRC64;

Query Match
Best Local Similarity 30.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
DB 6 PTV 8

RESULT 33
Q42373 PRELIMINARY; PRT; 13 AA.
AC Q42373;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Patatin class 1 (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamids; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4113;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=88226014; PubMed=3371664;
RA Mignery G.A., Pikaard C.S., Park W.D.;
RT "Molecular characterization of the patatin multigene family of
RT potato.";
RL Gene 62:27-44(1988).
DR EMBL; M18882; AAA33830.1; -.
DR EMBL; M18881; AAA33829.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1456 MW; 916595F37A6E29D5 CRC64;

Query Match
Best Local Similarity 30.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
DB 11 TVM 13

RESULT 34
O88176 PRELIMINARY; PRT; 13 AA.
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
RX STRAIN=Balb-c; TISSUE=Liver;

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RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RL of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db |||
3 PLP 5

RESULT 35
Q9T2K7 PRELIMINARY; PRT; 14 AA.
AC Q9T2K7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 18-Kda chloroplast DNA-binding iron-sulfur protein (Fragment).
OS Chlamydomonas reinhardtii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RX MEDLINE=92404720; PubMed=2562513;
RA Wu M., Nie Z.Q., Yang J.;
RT "The 18-kD protein that binds to the chloroplast DNA replicative
RT origin is an iron-sulfur protein related to a subunit of NADH
RT dehydrogenase.";
RL Plant Cell 1:551-557(1989).
SQ SEQUENCE 14 AA; 1698 MW; 7799E02B12C200CB CRC64;

Query Match 30.0%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
Db |||
1 MFP 3

RESULT 36
P82326 PRELIMINARY; PRT; 14 AA.
AC P82326;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS Pisum sativum (Garden pea)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";

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RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0. ITS MW IS: 18.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON TER 14
FT NON TER 14
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db |||
5 LPP 7

RESULT 37
O70599 PRELIMINARY; PRT; 14 AA.
AC O70599;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sauer M.;
RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.
DR EMBL; AJ006455; CAA07030.1; -.
KW Kinase; Transferase.
FT NON TER 14
FT NON TER 14
SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
Db |||
7 PTV 9

RESULT 38
Q9KE26 PRELIMINARY; PRT; 14 AA.
AC Q9KE26;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein BH1032.
GN BH1032.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001510; BAB04751.1; -.
KW Hypothetical protein; Complete proteome.

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SQ SEQUENCE 14 AA; 1697 MW; A9A302145A7AE8A6 CRC64;

Query Match 30.0%; Score 3; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
|||
DB 8 TVM 10

RESULT 39

Q9R5D5 PRELIMINARY; PRT; 15 AA.

ID Q9R5D5; AC Q9R5D5; DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 40 kDa protein (Fragment).
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochrochromatium.
OX NCBI_TaxID=1049;
RN [1]
RP SEQUENCE
RX MEDLINE=93146381; PubMed=1490603;
RA Liebergessel M., Schmidt B., Steinbuechel A.;
RT "Isolation and identification of granule-associated proteins relevant for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum D.";
RT FEMS Microbiol. Lett. 78:227-232(1992).
RL
SQ SEQUENCE 15 AA; 1834 MW; 215B7FCFCF65BB8E CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10
|||
DB 1 MFP 3

RESULT 40

Q9TR62 PRELIMINARY; PRT; 15 AA.

ID Q9TR62; AC Q9TR62; DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Apolipoprotein A-IV (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE
RX MEDLINE=95329112; PubMed=7605356;
RA Mezdour H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low apolipoprotein A-IV level in rabbit sera.";
RL Atherosclerosis 113:171-178(1995).
SQ SEQUENCE 15 AA; 1761 MW; DE115BB7351F0ABC CRC64;

Query Match 30.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
|||
DB 9 TVM 11

RESULT 41

Q9QV25 PRELIMINARY; PRT; 15 AA.

ID Q9QV25; AC Q9QV25; DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE sigma receptor cyclophilin-like component (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=94322640; PubMed=8046989;
RA Schuster D.I., Ehrlich G.K., Murphy R.B.;
RT "Purification and partial amino acid sequence of a 28 kDa cyclophilin-like component of the rat liver sigma receptor.";
RL Life Sci. 55:151-151(1994).
SQ SEQUENCE 15 AA; 1622 MW; 95E384B4EC8D14D4 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
|||
DB 3 PTV 5

RESULT 42

Q69353 PRELIMINARY; PRT; 15 AA.

ID Q69353; AC Q69353; DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HSV-2 (333) N terminus of 17.8 kDa protein gene (0.642 mu) (Fragment).
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85033906; PubMed=6092683;
RA Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,
RA Wagner B.K.;
RT "Herpes simplex virus types 1 and 2 homology in the region between 0.58 and 0.68 map units.";
RL J. Virol. 52:615-623(1984).
DR EMBL; K03360; AAA45840.1; -.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1603 MW; 20B04D60BA4507FE CRC64;

Query Match 30.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
|||
DB 11 QPL 13

RESULT 43

Q9RSK7 PRELIMINARY; PRT; 16 AA.

ID Q9RSK7; AC Q9RSK7; DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 23.4-kDa chitinase (Fragment).
OS Streptomyces olivaceoviridis (Streptomyces corchorusii).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92276319; PubMed=1592803;
 RA Ronaguera A., Menge U., Breves R., Diekmann H.;
 RT "Chitinases of Streptomycetes olivaceoviridis and significance of
 processing for multiplicity";
 RL J. Bacteriol. 174:3450-3454(1992).
 FT NON TER 1
 FT NON TER 16
 SQ SEQUENCE 16 AA; 2014 MW; 0F732A24DC14CE01 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MFP 10
 Db 6 MFP 8

RESULT 44

Q9NNZ2 PRELIMINARY; PRT; 16 AA.
 ID Q9NNZ2
 AC Q9NNZ2
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
 DE Integrin alpha-2 subunit (Fragment).
 GN ITGA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98421383; PubMed=9746778;
 RA Krizik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
 RA Kunicki T.J.;
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
 that are associated with differences in platelet alpha2 beta1
 density";
 RL Blood 92:2382-2388(1998).
 DR EMBL; AF062039; AAF77577.1; -.
 FT NON TER 16
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
 Db 10 PLP 12

RESULT 45

O18378 PRELIMINARY; PRT; 16 AA.
 ID O18378
 AC O18378
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Hypothetical 1.5 kDa protein in ANON-37CS 5'REGION (ORF3).
 GN ANON-37CC.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88038375; PubMed=3478553;
 RA Eveleth D.D., Marsh J.L.;
 RT "Overlapping transcription units in Drosophila: sequence and structure
 of the Cs gene";
 RL Mol. Genet. 209:290-298(1987).
 DR EMBL; X05991; CAA29407.1; -.
 DR Flybase; FBgn026744; anon-37cc.
 KW Hypothetical protein.
 SQ SEQUENCE 16 AA; 1543 MW; F6F881ED5A799277 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
 Db 13 PTV 15

RESULT 46

P92732 PRELIMINARY; PRT; 16 AA.
 ID P92732
 AC P92732
 DT 01-MAY-1997 (TRENBLrel. 03, Created)
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE NADH dehydrogenase subunit II (Fragment).
 GN ND2.
 OS Fejervarya limnocharis (Boie's wart frog).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Fejervarya.
 OX NCBI_TaxID=1110108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 rearrangement of the vertebrate mitochondrial genome";
 RL Mol. Biol. Evol. 14:91-104(1997).
 DR EMBL; U71324; AAB48287.1; -.
 KW Mitochondrion.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1860 MW; DD1C1017F8B19DEE CRC64;

Query Match 30.0%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MFP 10
 Db 5 MFP 7

RESULT 47

Q8VME2 PRELIMINARY; PRT; 17 AA.
 ID Q8VME2
 AC Q8VME2
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE PARC protein (Fragment).
 GN PARC.
 OS Pseudomonas putida.
 OG Plasmid pW0.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Greated A., Lamberton L., Williams P.A., Thomas C.M.;

RT "Complete nucleotide sequence of IncP-9 plasmid pMW0.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ344068; CAC68875.1; -.
 KW Plasmid.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1903 MW; A58E0B85C365A399 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
 Db 14 QPL 16

RESULT 48

P97135 ID P97135 PRELIMINARY; PRT; 17 AA.
 AC P97135;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GyA protein (Fragment).
 GN GyA.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Ra;
 RX MEDLINE=95072534; PubMed=7981652;
 RA Madhusudan K., Ramesh V., Nagaraja V.;
 RT "Molecular cloning of gyra and gyrB genes of Mycobacterium
 tuberculosis: analysis of nucleotide sequence."
 RL Biochem. Mol. Biol. Int. 33:651-660(1994).
 DR EMBL; X78888; CAA55487.1; -.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1916 MW; EF0E750A3E365AE CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 Db 6 LPP 8

RESULT 49

O15276 ID O15276 PRELIMINARY; PRT; 17 AA.
 AC O15276;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mitochondrial translation elongation factor EF-1u (Fragment).
 GN TUFM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jacobs H.T., Smurthwaite L., Koshy R.;
 RT "Human genomic sequences encoding mitochondrial elongation factor EF-
 Tu: Evidence for post-endosymbiotic intron insertion."
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y11797; CAA72493.1; -.
 KW Elongation factor.
 FT NON TER 1 1
 SQ SEQUENCE 17 17

Query Match 30.0%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
 Db 17

SQ SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0A7E CRC64;
 Query Match 30.0%; Score 3; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
 Db 13 LPP 15

RESULT 50

Q96P96 ID Q96P96 PRELIMINARY; PRT; 17 AA.
 AC Q96P96;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NHP2-like protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
 RT "Characterization of TPA-responsive genes in U937 cells using ordered
 RT differential display PCR."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401217; AAL02173.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEFC CRC64;

Query Match 30.0%; Score 3; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
 Db 14 PLP 16

RESULT 51

Q9TRU8 ID Q9TRU8 PRELIMINARY; PRT; 17 AA.
 AC Q9TRU8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Leukemia inhibitory factor, LIF-INHIBITOR of aortic endothelial cell
 DE growth (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92115728; PubMed=1370585;
 RA Ferrara N., Winer J., Henzel W.J.;
 RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial
 RT cell growth: identification as leukemia inhibitory factor."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).
 FT NON TER 1 1
 SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
 Db 17

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Db          2 PLP 4

RESULT 52
P83061
ID P83061 PRELIMINARY; PRT; 17 AA.
AC P83061
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RA Kieselbach T.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR InterPro: IPR001179; FKBP_PPIase.
KW Isomerase; Rotamase; Chlotoplast.
FT NON TER 17
FT SEQUENCE 17 AA; 1771 MW; E2013F998EFBF908 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 3 LPP 5

RESULT 53
Q8B4C4
ID Q8B4C4 PRELIMINARY; PRT; 17 AA.
AC Q8B4C4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Precore.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Vatsali C., Acharya S.K., Panda S.K.;
RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic
RT sequence of HBV from nine patients with seronegative viral
RT hepatitis."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161158; AAO12630.1; -
FT SEQUENCE 17 AA; 1908 MW; 0B63A9BF82802568 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7
Db 15 PTV 17

RESULT 54

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Q9R5U2
ID Q9R5U2 PRELIMINARY; PRT; 18 AA.
AC Q9R5U2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 2-amino-benzoate-CoA LIGASE=E3 (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RA MEDLINE=91358327; PubMed=1885526;
RA Alteschmidt U., Oswald B., Fuchs G.;
RT "Purification and characterization of benzoate-coenzyme A ligase and
RT 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
RT sp."
RL J. Bacteriol. 173:5494-5501(1991).
FT NON TER 1
FT NON TER 18
FT SEQUENCE 18 AA; 2061 MW; C43F8799692771EF CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 12 LPP 14

RESULT 55
Q9R5F9
ID Q9R5F9 PRELIMINARY; PRT; 18 AA.
AC Q9R5F9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Arsenite oxidase, AOI (Fragment).
OS Alcaligenes faecalis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=511;
RN [1]
RP SEQUENCE.
RA MEDLINE=93054722; PubMed=1331097;
RA Anderson G.L., Williams J., Hille R.;
RT "The purification and characterization of arsenite oxidase from
RT Alcaligenes faecalis, a molybdenum-containing hydroxylase."
RL J. Biol. Chem. 267:23674-23682(1992).
FT NON TER 1
FT NON TER 18
FT SEQUENCE 18 AA; 1938 MW; 4EDDC418B71A4574 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 9 LPP 11

RESULT 56
Q9R4V9
ID Q9R4V9 PRELIMINARY; PRT; 18 AA.
AC Q9R4V9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 10 kDa heat shock- and alkaline PH-induced protein (Fragment).
OS Campylobacter jejuni.

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OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 RN NCBI_TaxID=197;
 RP SEQUENCE.
 RX MEDLINE=95012609; PubMed=7927682;
 RA Wu Y.L., Lee L.H., Rollins D.M., Ching W.M.;
 RT "Heat shock- and alkaline pH-induced proteins of Campylobacter jejuni:
 RT characterization and immunological properties.";
 RL Infect Immun. 62:4256-4260(1994).
 SQ SEQUENCE 18 AA; 2056 MW; 9E4FED7B84DA76C4 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
 Db 4 QPL 6

RESULT 57
 Q9EYW5 PRELIMINARY; PRT; 18 AA.
 ID Q9EYW5
 AC Q9EYW5
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RepB.
 GN Erwinia stewartii.
 OS Erwinia stewartii.
 OG Plasmid pSW800.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pantoea.
 OX NCBI_TaxID=66271;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu C.-Y., Liu S.-T.;
 RT "Erwinia stewartii plasmid pSW800 basic replicon, repA and repB
 RT genes.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF310258; AAG47776.1; -.
 KW Plasmid.
 SQ SEQUENCE 18 AA; 1952 MW; C8FD2873F9CAC66C CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
 Db 6 QPL 8

RESULT 58
 Q9R4C6 PRELIMINARY; PRT; 18 AA.
 ID Q9R4C6
 AC Q9R4C6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Protocatechuate 3,4-dioxygenase type I alpha subunit (EC 1.13.11.3)
 DE (Fragment).
 OS Agrobacterium tumefaciens.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=358;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96337865; PubMed=8772173;
 RA Hammer A., Stolz A., Knackmuss H.;
 RT "Purification and characterization of a novel type of protocatechuate
 RT 3,4-dioxygenase with the ability to oxidize 4-sulfocatechol.";

RL Arch. Microbiol. 166:92-100(1996).
 SQ SEQUENCE 18 AA; 2152 MW; BFC56CA8D4376D84 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
 Db 2 QPL 4

RESULT 59
 Q96F98 PRELIMINARY; PRT; 18 AA.
 ID Q96F98
 AC Q96F98
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RT TISSUE=Brain;
 RC
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011455; AAH11455.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 18 AA; 2114 MW; 3A6C3E2BF620B9CD CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6
 Db 9 PPT 11

RESULT 60
 Q16244 PRELIMINARY; PRT; 18 AA.
 ID Q16244
 AC Q16244
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE STS protein (Fragment).
 GN STS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95038775; PubMed=7951263;
 RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
 RT "Characterization of the deletion breakpoints in a patient with
 RT steroid sulfatase deficiency.";
 RL Hum. Mutat. 4:76-78(1994).
 DR EMBL; S74383; AAD14153.1; -.
 FT NON TER 1
 SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCEA CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPT 4
 Db 11

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Db          2 PLP 4

RESULT 61
Q8NFB4
ID Q8NFB4 PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Mutant enamelin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kida M., Ariga T.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an enamelin gene mutation at exon-intron boundary.";
RL J. Dent. Res. 0:0-0(2002).
DR EMBL; AF530444; AAM97323.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2B3E8BE512 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 2 LPP 4

RESULT 62
Q8S915
ID Q8S915 PRELIMINARY; PRT; 18 AA.
AC Q8S915;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE TETRAMERIC alpha-amylase inhibitor 16 kDa subunit, CM16*
DE (Fragment).
OS Triticum turgidum (Poulard wheat) (Rivet wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143804; PubMed=1736890;
RA Sanchez-Monge R., Gomez L., Barber D., Lopez-Otin C., Armentia A.,
RA Salcedo G.;
RT "Wheat and barley allergens associated with baker's asthma.
RT Glycosylated subunits of the alpha-amylase-inhibitor family have
RT enhanced IgE-binding capacity.";
RL Biochem. J. 281:401-405(1992).
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1898 MW; 681835D1F68C30F8 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 16 PLP 18

RESULT 63
Q9K4X0
ID Q8NFL2 PRELIMINARY; PRT; 19 AA.

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ID Q9K4X0 PRELIMINARY; PRT; 19 AA.
AC Q9K4X0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GYPC-28 protein (Fragment).
GN GYPC-28.
OS Planktothrix agardhii.
OC Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix.
OX NCBI_TaxID=54305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CYA 137;
RX MEDLINE=20391846; PubMed=10931905;
RA Beard S.J., Davis P.A., Iglesias-Rodriguez D., Skulberg O.M.,
RA Walsby A.E.;
RT "Gas vesicle genes in Planktothrix spp. from Nordic lakes: strains
RT with weak gas vesicles possess a longer variant of gypC.";
RL Microbiology 146:2009-2018(2000).
DR EMBL; AJ253133; CAB59522.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 1944 MW; 647F169473797D19 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
Db 2 PTV 4

RESULT 64
Q9UC80
ID Q9UC80 PRELIMINARY; PRT; 19 AA.
AC Q9UC80;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE 21.5 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
DE [Mn/Fe]) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95215817; PubMed=7701298;
RA Binette J.P., Binette M.B.;
RT "Sequencing of proteins extracted from stones.";
RL Scanning Microsc. 8:233-239(1994).
CC -|- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -|- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -|- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
KW Oxidoreductase.
SQ SEQUENCE 19 AA; 2116 MW; A0D0DAE848EE7894 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 4 LPP 6

RESULT 65
Q8NFL2
ID Q8NFL2 PRELIMINARY; PRT; 19 AA.

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AC Q8NPL2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Prolyl isomerase (Fragment).
GN PIN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22095969; PubMed=12101225;
RA Ryo A., Liou Y.C., Wulf G., Nakamura M., Lee S.W., Lu K.P.;
RT "PIN1 Is an E2F Target Gene Essential for Neu/Ras-Induced
RT Transformation of Mammary Epithelial Cells."
RL Mol. Cell. Biol. 22:5281-5295(2002).
DR EMBL; AF501321; AAM81970.1; -.
KW Isomerase.
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2235 MW; 1C4FC381C8A0F17F CRC64;

Query Match 30.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db |||
7 LPP 9

RESULT 66
Q3UCK6
ID Q9UCK6 PRELIMINARY; PRT; 19 AA.
AC Q9UCK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Aspartylglucosaminidase beta 1 subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93111925; PubMed=1281977;
RA Rip J.W., Coulter-Mackie M.B., Rupar C.A., Gordon B.A.;
RT "Purification and structure of human liver aspartylglucosaminidase."
RL Biochem. J. 288:1005-1010(1992).
DR HSP; P20933; LAPY.
SQ SEQUENCE 19 AA; 2127 MW; BC2F148525610300 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db |||
2 PLP 4

RESULT 67
Q31687
ID Q31687 PRELIMINARY; PRT; 19 AA.
AC Q31687;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATPase subunit 8 (fragment).
GN ATP8.
OS Artemia parthenogenetica.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;

OC Artemiidae; Artemia.
OX NCBI_TaxID=6663;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=La Mata;
RA MEDLINE=94223692; PubMed=8169960;
RX Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
RT "Speciation in the artemia genus: mitochondrial DNA analysis of
RT bisexual and parthenogenetic brine shrimps."
RL J. Mol. Evol. 38:156-168(1994).
DR EMBL; X67263; CAA47685.1; -.
KW Mitochondrion.
FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2246 MW; 41922AD313B087E3 CRC64;

Query Match 30.0%; Score 3; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db |||
6 PLP 8

RESULT 68
Q9GI97
ID Q9GI97 PRELIMINARY; PRT; 19 AA.
AC Q9GI97;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE (fragment).
GN RBC1.
OS Sargassum polycystum.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=127578;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=nepl27;
RA Phillips N.E.;
RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998), University of Hawaii.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=nepl27; Smith C.M., Morden C.W.;
RA Phillips N.E.,
RT "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF244344; AAF98113.1; -.
KW Chloroplast.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2108 MW; A02FD2E6DD68A57 CRC64;

Query Match 30.0%; Score 3; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6
Db |||
4 PPT 6

RESULT 69
Q9S8F5
ID Q9S8F5 PRELIMINARY; PRT; 19 AA.
AC Q9S8F5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PMP=31 kDa plasma membrane intrinsic protein (Fragment).
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=161934;
[1]
RN SEQUENCE.
RP MEDLINE=95303965; PubMed=7784509;
QT Qi X., Tai C.Y., Wasserman B.P.;
RA "Plasma membrane intrinsic proteins of Beta vulgaris L.";
RL Plant Physiol. 108:387-392(1995).
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2102 MW; 5BF1773684FF8D84 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 10 QPL 12

RESULT 70
Q69099
ID Q69099 PRELIMINARY; PRT; 19 AA.
AC Q69099;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Protein 32 (Fragment).
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90156509; PubMed=2154597;
RA Yei S., Chowdhury S.I., Bhat B.M., Conley A.J., Wold W.S.,
RA Batterson W.;
RT "Identification and characterization of the Herpes simplex virus type
RT 2 gene encoding the essential capsid protein ICP32/vp19c.";
RL J. Virol. 64:1124-1134(1990).
DR EMBL; M33905; AAA45846.1; -.
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2058 MW; 47125921CA53FA35 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 5 PLP 7

RESULT 71
Q9PRT0
ID Q9PRT0 PRELIMINARY; PRT; 19 AA.
AC Q9PRT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE 23A7 antigen (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;

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RN [1]
RN SEQUENCE.
RP MEDLINE=95332492; PubMed=7608337;
RA Denburg J.L., Caldwell R.T., Warner J.M.;
RT "Developmental changes in epitope accessibility as an indicator of
RT multiple states of an immunoglobulin-like neural cell adhesion
RT molecule.";
RL J. Comp. Neurol. 354:533-550(1995).
SQ SEQUENCE 19 AA; 2051 MW; 83B67BBE484EBD03 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 16 PPT 18

RESULT 72
Q9PRN4
ID Q9PRN4 PRELIMINARY; PRT; 19 AA.
AC Q9PRN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Melanotropin MSH-A.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
[1]
RN SEQUENCE.
RP MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawachi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 15 PPT 17

RESULT 73
Q9ORF8
ID Q9ORF8 PRELIMINARY; PRT; 19 AA.
AC Q9ORF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=97CG276;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I., Harada Y.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Farra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127350; AAK84913.1; -.
FT NON_TER 1
FT NON_TER 1

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FT NON TER 19 19
SQ SEQUENCE 19 AA; 2304 MW; 2727D4B66AE69237 CRC64;
Query Match 30.0%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 16 PLP 18

RESULT 74

Q905E8 PRELIMINARY; PRT; 19 AA.
AC Q905E8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG314;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410452; AAL10274.1; -
FT NON TER 1
FT NON TER 1
FT NON TER 19
SQ SEQUENCE 19 AA; 2200 MW; 367B64CAE5069886 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 16 PLP 18

RESULT 75

Q9R4M9 PRELIMINARY; PRT; 20 AA.
AC Q9R4M9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Extracellular levansucrase (EC 2.4.1.10) (Fragment).
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE.
RX MEDLINE=95270602; PubMed=7751294;
RA Hettwer U., Gross M., Rudolph K.;
RT "Purification and characterization of an extracellular levansucrase
RT from Pseudomonas syringae pv. phaseolicola."
RL J. Bacteriol. 177:2834-2839 (1995).
SQ SEQUENCE 20 AA; 2218 MW; 9DCE15F23BEFF2E5 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
|||

Db 8 PTV 10

Search completed: November 25, 2003, 19:34:04
Job time : 19.7791 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 25.5233 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPLPPTVMFP 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	22	Colostrinin derive
2	10	100.0	10	22	Colostrinin peptid
3	10	100.0	10	22	Colostrinin peptid
4	10	100.0	10	23	Colostrinin consti
5	10	100.0	10	23	Colostrinin consti
6	10	100.0	10	23	Neural cell regula
7	10	100.0	15	22	Colostrinin derive
8	10	100.0	15	22	Colostrinin peptid
9	10	100.0	15	22	Colostrinin peptid

10	100.0	15	22	AB59334	Ewe colostrinin pe
11	100.0	15	23	AAE20261	Colostrinin consti
12	100.0	15	23	AAE51066	Colostrinin consti
13	100.0	15	23	AAO14610	Neural cell regula
14	90.0	11	22	AAE07192	Colostrinin peptid
15	90.0	12	22	AAE07202	Modified colostrin
16	60.0	11	22	AB59333	Ewe colostrinin pe
17	60.0	16	18	AAW25442	Grb2 N-terminal SH
18	50.0	7	20	AAV41630	Mammalian ion chan
19	50.0	7	21	AAE17247	SH3 antagonist pep
20	50.0	7	23	AB733240	Src homolog3 (SH3)
21	50.0	8	22	AAW02293	Human protein frag
22	50.0	8	22	AAW02294	Human protein frag
23	50.0	9	22	AAE84971	Clone 1 scfv CDR L
24	50.0	12	22	AAW02291	Human protein frag
25	50.0	13	16	AAE93368	PI3K protein tyros
26	50.0	13	17	AAW11112	Src SH3 domain-bin
27	50.0	13	23	ABE21396	Escherichia coli 3
28	50.0	13	24	ABF81159	Human TPO peptide
29	50.0	13	24	ABP81160	Human TPO peptide
30	50.0	13	24	ABP81161	Human TPO peptide
31	50.0	13	24	ABP81162	Human TPO peptide
32	50.0	13	24	ABP81163	Human TPO peptide
33	50.0	14	20	AAV03679	Amino acid sequenc
34	50.0	14	22	AAW00448	Human protein frag
35	50.0	14	22	AAE46171	Bacille Calmette-G
36	50.0	14	22	AAE49070	BCG T-cell epitope
37	50.0	15	18	AAW38958	Peptide resembling
38	50.0	15	18	AAW39036	Peptide resembling
39	50.0	15	22	ABG78855	Growth hormone fam
40	50.0	15	23	ABG72860	Human K-ras 10.67
41	50.0	16	18	AAW25427	Yes SH3 domain bin
42	50.0	16	18	AAW25376	Src SH3 domain bin
43	50.0	16	18	AAW25380	Src SH3 domain bin
44	50.0	16	24	ABE26278	G protein-coupled
45	50.0	17	21	ABE39277	Human gene 10 enco
46	50.0	18	22	ABE03955	Gene 31 human secr
47	50.0	19	20	AAV31181	Human gene 10 enco
48	50.0	19	20	AAV31165	Ubiquitin fusion p
49	50.0	19	22	AAE71936	Ubiquitin fusion p
50	50.0	20	17	AAW16997	MT peptide, Unide
51	50.0	20	17	AAE99513	SRC SH3 domain-bin
52	50.0	20	18	AAW35439	T-cell epitope use
53	50.0	20	18	AAW12237	T-cell stimulatory
54	50.0	20	19	AAW60693	Heatshock protein
55	50.0	20	23	ABE79926	Mycobacteria heat
56	40.0	4	16	AAE00055	Mycobacterium heat
57	40.0	5	21	AAV45075	Peptidase substrat
58	40.0	6	13	AAE28486	Rat amelogenin N-t
59	40.0	6	19	AAW31463	Casoxin D-like vas
60	40.0	6	19	AAW31465	Transcriptional ac
61	40.0	7	15	AAE60997	Fragment of the 3B
62	40.0	7	17	AAW11128	Src SH3 domain-bin
63	40.0	7	17	AAW17010	SRC SH3 domain-bin
64	40.0	7	17	AAW07013	Synthetic peptide
65	40.0	7	18	AAW25486	SH3 domain binding
66	40.0	7	18	AAW10774	Ferritin motif #17
67	40.0	7	19	AAW79781	Proline-rich pepti
68	40.0	7	20	AAV41611	Mammalian ion chan
69	40.0	7	20	AAV17016	Heat shock protein
70	40.0	7	21	AAE17226	SH3 antagonist pep
71	40.0	7	21	AAE17228	SH3 antagonist pep
72	40.0	7	21	AAE17229	SH3 antagonist pep
73	40.0	7	21	AAE17232	SH3 antagonist pep
74	40.0	7	21	AAE17233	SH3 antagonist pep
75	40.0	7	21	AAE17267	Src antagonist pep
76	40.0	7	21	AAE69979	Src SH3 region bin
77	40.0	7	22	AAU72158	Melanoma antigen,
78	40.0	7	22	AAW46952	H11 binding site c
79	40.0	7	22	AAW46957	H11 binding site c
80	40.0	7	22	AAW46962	H11 binding site c
81	40.0	7	22	AAW47017	H11 binding site c
82	40.0	7	22	AAW47075	H11 binding site c

83 Human cAMP-specific
84 Human cAMP-specific
85 Src homology3 (SH3)
86 Src homology3 (SH3)
87 Src homology3 (SH3)
88 Src homology3 (SH3)
89 Src homology3 (SH3)
90 Exemplary pharmaco
91 Javelin peptide #1
92 Human 3BP1 peptide
93 C. felis esterase
94 Heat shock protein
95 Ctenocephalides fe
96 Amino acid sequenc
97 Plasmodium falcipa
98 HIV-B35-50(C-48),
99 HCV-1 derived pept
100 T cell epitope/MHC

ALIGNMENTS

RESULT 1
AAB72270
ID AAB72270 standard; peptide; 10 AA.
XX
AC AAB72270;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 25.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neuron disease, psychosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX SQ Sequence 10 AA;
Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QPLPPTVMFP 10
Db 1 QPLPPTVMFP 10
RESULT 2
AAB72523
ID AAB72523 standard; Peptide; 10 AA.
XX
AC AAB72523;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #24.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 26; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QPLPPTVMFP 10
Db 1 QPLPPTVMFP 10
RESULT 3
AAB72555
ID AAB72555 standard; Peptide; 10 AA.
XX
AC AAB72555;
XX
DT 09-MAY-2001 (first entry)
XX

DE Colostrinin peptide #24.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW Colostrum.
XX Unidentified.
OS
XX WO200112651-A2.
PN
XX
PD 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
PF
XX 17-AUG-1999; 99US-0149633.
PR
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX Boldogh I;
PI
XX WPI; 2001-226545/23.
DR
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPLPPTVMFP 10
Db 1 QPLPPTVMFP 10
RESULT 4
AAE20252
ID AAE20252 standard; peptide; 10 AA.
XX
AC AAE20252;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #24.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnary.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 10 /note= "Optionally C-terminal amide"
FT
XX WO200213850-A1.
PN
XX 21-FEB-2002.
PD
XX 17-AUG-2000; 2000WO-US22776.
PF
XX 17-AUG-2000; 2000WO-US22776.
PR
XX (TEXA) UNIV TEXAS SYSTEM.
PA

XX Stanton GJ, Hughes TK, Boldogh I;
PI WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 10; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPLPPTVMFP 10
Db 1 QPLPPTVMFP 10
RESULT 5
AAMS1059
ID AAMS1059 standard; Peptide; 10 AA.
XX
AC AAMS1059;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide (casein amino acids 164-173).
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 10 /note= "optional C-terminal amidation"
FT
XX WO200213849-A1.
PN
XX 21-FEB-2002.
PD
XX 17-AUG-2000; 2000WO-US22775.
PF
XX 17-AUG-2000; 2000WO-US22775.
PR
XX (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI

DR WPI; 2002-269150/31.
 XX
 PT Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 164-173. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the
 CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 10; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QPLPPTVMFP 10
 Db 1 QPLPPTVMFP 10
 RESULT 6
 ID AA014601 standard; peptide; 10 AA.
 AC AA014601;
 DT 27-MAY-2002 (first entry)
 DE Neural cell regulatory colostrinin peptide 24.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 10
 FT /note= "Optional C-terminal amide"
 XX
 PN WO200213851-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US22777.
 XX
 PR 17-AUG-2000; 2000WO-US22777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.
 DR Promoting cell differentiation in a patient involves use of blood cell
 XX regulator selected from colostrinin, its constituent peptide and/or
 PT analog -
 PT
 XX Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 10; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QPLPPTVMFP 10
 Db 1 QPLPPTVMFP 10
 RESULT 7
 ID AAB72279 standard; peptide; 15 AA.
 XX
 AC AAB72279;
 XX
 DT 14-MAY-2001 (first entry)
 DE Colostrinin derived cytokine inducing peptide SEQ ID 34.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22818.
 XX
 PR 17-AUG-1999; 99US-0149311.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGS-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for

CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPPTVMFP 10
Db 6 QPLPPTVMFP 15

RESULT 8

AAB72531
ID AAB72531 standard; Peptide; 15 AA.

XX AC AAB72531;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX PS WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the
XX cell with an oxidative stress regulator selected from colostrinin, its
XX constituent peptide, analog or their combinations -

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostrinin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPPTVMFP 10
Db 6 QPLPPTVMFP 15

RESULT 9

AAB72563
ID AAB72563 standard; Peptide; 15 AA.

XX AC AAB72563;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;
XX colostrum.

XX OS Unidentified.

XX PN WO200112651-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22774.

XX PR 17-AUG-1999; 99US-0149633.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Boldogh I;

XX DR WPI; 2001-226545/23.

XX PT Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -

XX PS Claim 6; Page 22; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.

SQ Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPPTVMFP 10
Db 6 QPLPPTVMFP 15

RESULT 10

AAB59334
ID AAB59334 standard; Peptide; 15 AA.

XX AC AAB59334;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment C-9.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

PA (REG-) REGEN THERAPEUTICS PLC.
 XX Georgiades JA;
 XX WPI; 2001-071058/08.
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 XX Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 10; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPPTVMFP 10
 Db 6 QPLPPTVMFP 15
 RESULT 11
 AAEE20261
 ID AAE20261 standard; peptide; 15 AA.
 AC
 XX
 XX AAE20261;
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrin constituent peptide #32.
 XX
 KW Blood cell regulator; colostrin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 15
 FT /note= "Optionally C-terminal amide"
 XX
 XX WO200213850-AL.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I;
 XX
 XX WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrin, its
 PT constituent peptide and/or analog -
 XX
 XX Claim 6; Page 26; 51pp; English.

XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrin constituent peptide.
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 10; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPPTVMFP 10
 Db 6 QPLPPTVMFP 15
 RESULT 12
 AAMS1066
 ID AAMS1066 standard; Peptide; 15 AA.
 AC
 XX
 XX AAMS1066;
 DT 30-MAY-2002 (first entry)
 XX
 DE Colostrin constituent peptide (casein amino acids 159-173).
 XX
 KW Colostrin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 15
 FT /note= "optional C-terminal amidation"
 XX
 XX WO200213849-AL.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2000; 2000WO-US22775.
 XX
 XX 17-AUG-2000; 2000WO-US22775.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX (REG-) REGEN THERAPEUTICS PLC.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 XX WPI; 2002-269150/31.
 DR
 XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrin, its constituent peptide
 PT and/or analogue -
 XX
 XX Claim 1; Page 34; 54pp; English.
 PS
 XX The present sequence is that of a colostrin constituent peptide
 CC that is used as an immunological regulator and as a blood cell

CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 159-173. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the
 CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPPTVMFP 10
 |||||
 Db 6 QPLPPTVMFP 15

RESULT 13

AAO14610
 ID AAO14610 standard; peptide; 15 AA.

XX
 AC AAO14610;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 32.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 XX neural cell formation; proline-rich polypeptide aggregate; colostrum;
 XX neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 15

FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldegh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPPTVMFP 10
 |||||
 Db 6 QPLPPTVMFP 15

RESULT 14

AAE07192
 ID AAE07192 standard; peptide; 11 AA.

XX
 AC AAE07192;

XX 06-NOV-2001 (first entry)

XX Colostrinin peptide 8.

XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral.

XX Unidentified.

XX WO200155199-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification

CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 8 related to the invention.
 CC Colostrinin peptide 8 corresponds to position 165-175 of beta-caesin.
 XX
 SQ Sequence 11 AA;
 Query Match 90.0%; Score 9; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PLPPTVMFP 10
 Db 1 PLPPTVMFP 9
 |||||
 |||||
 RESULT 15
 AAE07202
 ID AAE07202 standard; peptide; 12 AA.
 AC
 AC AAE07202;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Modified colostrinin cyclic peptide #8.
 XX
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Gln found at the C-terminal end"
 FT
 XX WO200155199-A1.
 FN
 XX 02-AUG-2001.
 PD
 XX 26-JAN-2001; 2001WO-GB00329.
 PF
 XX 26-JAN-2000; 2000GB-0001825.
 PR
 XX (REGG-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-488775/53.
 DR
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Example 2; Page 9; 40pp; English.
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #8 related to
 CC the invention.
 XX
 SQ Sequence 12 AA;
 Query Match 90.0%; Score 9; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PLPPTVMFP 10
 Db 2 PLPPTVMFP 10
 |||||
 |||||
 RESULT 16
 AAB59333
 ID AAB59333 standard; Peptide; 11 AA.
 AC
 AC AAB59333;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment C-8.
 DB
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 KW
 XX Ovis sp.
 OS
 XX WO200075173-A2.
 FN
 XX 14-DEC-2000.
 PD
 XX 02-JUN-2000; 2000WO-GB02128.
 PF
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGG-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 11 AA;
 Query Match 60.0%; Score 6; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPPT 6
 Db 1 QPLPPT 6

RESULT 17

AAW25442
 ID AAW25442 standard; peptide; 16 AA.

XX AAW25442;

XX 27-MAR-1998 (first entry)

DE Grb2 N-terminal SH3 domain binding peptide SEQ ID NO:227.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.
 OS Unidentified.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

PA (UINC-) UNIV NORTH CAROLINA.

XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

PI Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

XX Claim 20; Page 101; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

XX Sequence 16 AA;

Query Match 60.0%; Score 6; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPTVM 8

Db 9 LPPTVM 14

RESULT 18

AAAY41630

ID AAY41630 standard; peptide; 7 AA.

XX AC AAY41630;

XX 02-DEC-1999 (first entry)

XX Mammalian ion channel proline rich motif containing peptide #24.

XX SH3 domain; binding motif; potassium channel; protein tyrosine kinase;
 KW proline rich.

XX Mus sp.

XX US5955259-A.

XX 21-SEP-1999..

XX 19-DEC-1996; 96US-0769745.

XX 19-DEC-1996; 96US-0769745.

XX (UYBR-) UNIV BRANDEIS.

XX Holmes TC, Levitan IB;

XX WPI; 1999-560490/47.

XX Identification of compounds that modulate potassium ion channel binding
 PT with protein tyrosine kinase SH3 domains -

XX Disclosure; Column 8; 18pp; English.

XX A method has been developed for determining if a compound modulates the
 CC binding of a potassium ion channel to the SH3 domain of a protein
 CC tyrosine kinase by contacting the channel with a polypeptide comprising
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3
 CC binding. The method is useful for assessing the ability of a compound to
 CC modulate the formation of channel-SH3 domain complexes to improve the
 CC understanding of mechanisms of potassium channel blockage and assess the
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to
 CC AAY41644 represent mammalian ion channel peptides with proline-rich
 CC motifs.

XX Sequence 7 AA;

Query Match 50.0%; Score 5; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5

Db 1 QPLPP 5

RESULT 19

AAB17247

ID AAB17247 standard; Peptide; 7 AA.

XX AAB17247;

XX 31-OCT-2000 (first entry)

XX SH3 antagonist peptide sequence SEQ ID NO:303.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;

KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX Synthetic.
 XX WO200024782-A2.
 XX 04-MAY-2000.
 XX 25-OCT-1999; 99WO-US25044.
 XX 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX (AMGE-) AMGEN INC.
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI WPI; 2000-350702/30.
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX Claim 39; Page 302; 608pp; English.
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAA6955 to AAA8003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX SQ Sequence 7 AA;
 Query Match 50.0%; Score 5; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 Db 2 PLPPT 6
 RESULT 20
 ABB73240
 ID ABB73240 standard; Peptide; 7 AA.
 XX ABB73240;
 AC ABB73240;
 XX 05-APR-2002 (first entry)
 DT Src homology3 (SH3) antagonist peptide SEQ ID NO:303.
 DE Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 XX EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antiataemic; anorectic; antiinfertility; haemostatic; dermatological;

KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200183525-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14310.
 PF 03-MAY-2000; 2000US-0563286.
 PR (AMGE-) AMGEN INC.
 XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 PI WPI; 2002-130313/17.
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -
 XX Claim 39; Page 55; 176pp; English.
 XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antiataemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.
 XX SQ Sequence 7 AA;
 Query Match 50.0%; Score 5; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 Db 2 PLPPT 6
 RESULT 21
 AAM00293
 ID AAM00293 standard; Peptide; 8 AA.
 XX AAM00293;
 AC AAM00293;
 XX 01-OCT-2001 (first entry)
 DT Human protein fragment SEQ ID NO: 837.
 DE Human protein fragment SEQ ID NO: 837.
 XX

KW Human; single nucleotide polymorphism; SNP; paternity test;
 KW forensic test; aberrant protein expression.
 XX

OS Homo sapiens.

PN WO200151670-A2.

PD 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US00322.

XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2001-451871/48.

XX N-PSDB; AAH89406.

XX Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes -
 XX

PS Disclosure; Page 344; 475pp; English.

XX The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 8 AA;

Query Match 50.0%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5

Db 1 QPLPP 5

RESULT 22

AAM00294

ID AAM00294 standard; Peptide; 8 AA.

XX AAM00294;

XX 01-OCT-2001 (first entry)

XX Human protein fragment SEQ ID NO: 838.

XX Human; single nucleotide polymorphism; SNP; paternity test;
 KW forensic test; aberrant protein expression.
 XX

OS Homo sapiens.

XX WO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US00322.

XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach MD;

XX WPI; 2001-451871/48.

XX N-PSDB; AAH89407.

XX Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes -
 XX

PS Disclosure; Page 345; 475pp; English.

XX The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 8 AA;

Query Match 50.0%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5

Db 1 QPLPP 5

RESULT 23

AAB84971

ID AAB84971 standard; protein; 9 AA.

XX AAB84971;

XX 06-AUG-2001 (first entry)

XX Clone 1 scFv CDR L3 region binding to target antigen M.

XX Antiinflammatory; antiallergic; cytostatic; antibacterial; antiviral;
 KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
 KW antiarthritic; dermatological; immune response; modulator; enzyme;
 KW antigen M; T-cell receptor; complementary determining region; CDR.

XX Homo sapiens.

XX WO200140312-A2.

XX 07-JUN-2001.

XX 04-DEC-2000; 2000WO-GB04629.

XX 03-DEC-1999; 99GB-0028789.

XX (DIVE-) DIVERSYS LTD.

XX Holt LJ, De Wildt RMT, Tomlinson I;

XX WPI; 2001-374801/39.

XX Isolating a polypeptide of interest from a naive polypeptide repertoire
 PT which has not been preselected with a specific target ligand involves
 PT direct screening of naive polypeptide repertoire with the target ligand
 PT -
 XX

XX Example 2; Page 29; 41pp; English.

XX

CC The invention relates to isolating, from a naive polypeptide (I)
 CC repertoire (antibody or T-cell receptor polypeptides), which has not been
 CC preselected with a specific target ligand, a polypeptide of interest (II)
 CC capable of interacting with the specific target ligand. The method
 CC involves direct screening of (I) with the target ligand in order to
 CC identify (III). The polypeptides selected by the method may be used in any
 CC process which involves ligand-polypeptide binding including in vivo
 CC therapeutic and prophylactic applications, in vitro and in vivo
 CC diagnostic applications, in vitro assay and reagent applications. Enzyme
 CC variants generated and selected by the method may be assayed for
 CC activity, either in vitro or in vivo using standard techniques. Antibody
 CC polypeptides selected by the method are used diagnostically in Western
 CC analysis and in situ protein detection. The selected antibodies are
 CC useful for preventing, suppressing or treating inflammatory states,
 CC allergic hypersensitivity, cancer, bacterial or viral infection and
 CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,
 CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and
 CC myasthenia gravis. The selected polypeptides may be used extracorporeally
 CC or in vitro selectively to kill, deplete or effectively remove a target
 CC cell population from a heterogeneous collection of cells. Sequences
 CC AAB84968-979 represent complementary determining regions (CDRs) of scFv
 CC heavy and light chains binding to target antigens M and D.

XX Sequence 9 AA;

Query Match 50.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||
 Db 3 QPLPP 7

RESULT 24

AAW00291
 ID AAM00291 standard; Peptide; 12 AA.

XX AAM00291;

XX 01-OCT-2001 (first entry)

XX Human protein fragment SEQ ID NO: 835.

XX Human; single nucleotide polymorphism; SNP; paternity test;
 KW forensic test; aberrant protein expression.

XX Homo sapiens.

XX WO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US00322.

XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach MD;

XX WPI; 2001-451871/48.

XX N-PSDB; AAB89404.

XX Isolated human polynucleotides containing single nucleotide

PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes -

XX Disclosure; Page 344; 475pp; English.

XX The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with

CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 12 AA;

Query Match 50.0%; Score 5; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||
 Db 5 QPLPP 9

RESULT 25

AAAR93368
 ID AAR93368 standard; peptide; 13 AA.

XX AAR93368;

XX 24-APR-1996 (first entry)

XX PI3K protein tyrosine kinase derived peptide #3.

XX SH3 ligand; SH3 binding agent; biased phage library;

KW recognition sequence; src SH3 domain; Paget's disease; restenosis;

KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;

KW p67; complex; chronic myelogenous leukaemia; cancer.

XX Synthetic.

XX WO9524419-A1.

XX 14-SEP-1995.

XX 13-MAR-1995; 95WO-US03208.

XX 06-JAN-1995; 95US-0369832.

XX 11-MAR-1994; 94US-0209835.

XX (ARIA-) ARIAD PHARM INC.

XX Botfield MC, Brugge JS, Rickles RJ, Zoller MJ;

XX WPI; 1995-328231/42.

XX Identification of peptide(s) binding specifically to SH3 domains -
 PT for use in inhibiting interactions mediated by SH3 domains in
 PT treatment of e.g. osteoporosis and cancer

XX Disclosure; Fig 2; 74pp; English.

XX The sequences given in AAR93343-68 represent peptides which are SH3
 CC ligands/SH3 binding agents. They represent a biased phage library
 CC which comprises six random amino acids flanking the hexapeptide
 CC RSRPL- which was identified as a recognition sequence for the src
 CC SH3 domain. These sequences were identified using the method of the
 CC invention. The method comprises contacting the SH3 domain with a
 CC mixture of peptides under conditions permitting a ligand to bind to
 CC an SH3 domain to form a complex. Any unbound peptides are removed
 CC and the complexed peptide ligands are dissociated from the complexes.
 CC The selected peptides are enriched by re-contacting them with the
 CC SH3 domain and then candidates which bind to the SH3 domain are
 CC detected. The isolated SH3 binding peptides may be used in the
 CC diagnosis, prevention and treatment of conditions or diseases resulting
 CC from cellular processes mediated by an SH3-based interaction. Such
 CC diseases include Paget's disease. Other conditions treatable with these

CC peptides include restenosis, rheumatoid arthritis, gout and other
CC problems in which an SH3 of neurophil oxidase p47 and p67 complex is
CC implicated, etc.
XX

SQ Sequence 13 AA;
Query Match 50.0%; Score 5; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
|
|
|
|
Db 5 PLPPT 9

RESULT 26
AAW1112
ID AAW11112 standard; peptide; 13 AA.
XX
AC AAW11112;
XX
DT 25-JUN-1997 (first entry)
XX
DE Src SH3 domain-binding peptide used in signal transduction modulation.
XX
DE Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
KW protein tyrosine kinase; signal transduction; RNA processing;
KW trafficking; translation.
XX
OS Synthetic.
XX
PN WO9603649-A1.
XX
PD 08-FEB-1996.
XX
PF 24-JUL-1995; 95WO-US09382.
XX
PR 07-JUN-1995; 95US-0483555.
PR 22-JUL-1994; 94US-0278865.
XX
PA (UYNCL) UNIV NORTH CAROLINA.
XX
PI Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
XX WPI; 1996-117151/12.
XX
PT Peptide with binding affinity for Src homology region 3 (SH3)
PT domains of proteins - useful for e.g. modulating signal transduction
PT pathways at the cellular level, esp. protein tyrosine
PT kinase-mediated
XX
PS Claim 38; Page 87; 116pp; English.
XX

CC AAW11098-Will124 are peptides that bind to the Src SH3 domain. The SH3
CC binding peptides are useful in modulating signal transduction pathways
CC at the cellular level (especially protein tyrosine kinase-mediated)
CC modulating oncogenic protein activity, or providing compounds for the
CC development of drugs with the ability to modulate broad classes, as
CC well as specific classes, of proteins involved in signal transduction
CC and also for regulating the processing, trafficking or translation of
CC RNA. Conjugates of the peptides with detectable labels or imaging agents
CC are useful for imaging cells, tissues and organs in which Src or
CC Src-related proteins are expressed.
XX

SQ Sequence 13 AA;
Query Match 50.0%; Score 5; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
|
|
|
|
Db 5 PLPPT 9

RESULT 27
AAE21396
ID AAE21396 standard; peptide; 13 AA.
XX
AC AAE21396;
XX
DT 01-JUL-2002 (first entry)
XX
DE Escherichia coli 3-isopropylmalate dehydrogenase (IPMDH) peptide #1.
XX Protein thermostability; 3-isopropylmalate dehydrogenase; IPMDH;
KW isocitrate dehydrogenase; ICDH; enzyme.
XX
OS Escherichia coli.
XX
PN EP1182253-A2.
XX
PD 27-FEB-2002.
XX
PF 03-JUL-2001; 2001EP-0115642.
XX
PR 04-JUL-2000; 2000JP-0201920.
PR 31-MAY-2001; 2001JP-0164332.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Yamagishi A;
XX
PD WPI; 2002-294076/34.
XX
PT Improving protein thermostability of protein by estimating amino acid
PT sequence of ancestral protein (AP), and replacing amino acids of
PT desired protein, which differ from those of AP with the same amino
PT acids of AP -
XX
PS Example 4; Fig 9; 73pp; English.
XX

CC The invention relates to a method for improving thermostability of
CC proteins. The method involves comparing amino acid sequences derived
CC from two or more species which evolutionarily correspond to each other
CC in phylogenetic tree; estimating amino acid sequence of ancestral
CC protein and replacing amino acids of desired protein, which differ
CC from those of ancestral protein with the same amino acids of ancestral
CC protein. The method is used for improving thermostability of proteins
CC preferably 3-isopropylmalate dehydrogenase (IPMDH) and isocitrate
CC dehydrogenase (ICDH). The invention also relates to a protein having
CC an improved thermostability and a nucleic acid encoding such protein.
CC The present sequence is Escherichia coli IPMDH peptide.
XX

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
|
|
|
|
Db 1 QPLPP 5

RESULT 28
ABP81159
ID ABP81159 standard; peptide; 13 AA.
XX
AC ABP81159;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #112.
XX Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
KW

KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX Homo sapiens.
 OS WO200268469-A2.
 PN 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 PR (MERE) MERCK PATENT GMBH.
 PA Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -
 XX Disclosure; Page 12; 36pp; English.
 XX The invention relates to a novel modified molecule having the biological
 CC activity of human thrombopoietin (TPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity when used in vivo. The invention also
 CC discloses T-cell epitope peptides created from non-modified TPO, and
 CC having potential MHC class II binding activity. The protein of the
 CC invention has immunosuppressive and antiallergic activity. A peptide of
 CC the invention is useful in the manufacture of TPO having substantially no
 CC or less immunogenicity than any non-modified molecule with the same
 CC biological activity when used in vivo. The protein is useful in
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
 CC allergies and autoimmune disease treatment. The sequences shown in
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
 CC invention.
 XX Sequence 13 AA;
 SQ
 Query Match 50.0%; Score 5; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 DB 7 PLPPT 11
 RESULT 29
 ABP81160
 ID ABP81160 standard; peptide; 13 AA.
 XX
 AC ABP81160;
 XX
 DT 27-FEB-2003 (first entry)
 DE Human TPO peptide with MCH class II binding activity #113.
 XX
 KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX
 OS Homo sapiens.
 XX WO200268469-A2.
 PN 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 PR (MERE) MERCK PATENT GMBH.
 PA Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -

XX (MERE) MERCK PATENT GMBH.
 XX Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -
 XX Disclosure; Page 12; 36pp; English.
 XX The invention relates to a novel modified molecule having the biological
 CC activity of human thrombopoietin (TPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity when used in vivo. The invention also
 CC discloses T-cell epitope peptides created from non-modified TPO, and
 CC having potential MHC class II binding activity. The protein of the
 CC invention has immunosuppressive and antiallergic activity. A peptide of
 CC the invention is useful in the manufacture of TPO having substantially no
 CC or less immunogenicity than any non-modified molecule with the same
 CC biological activity when used in vivo. The protein is useful in
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
 CC allergies and autoimmune disease treatment. The sequences shown in
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
 CC invention.
 XX Sequence 13 AA;
 SQ
 Query Match 50.0%; Score 5; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPPT 6
 DB 5 PLPPT 9
 RESULT 30
 ABP81161
 ID ABP81161 standard; peptide; 13 AA.
 XX
 AC ABP81161;
 XX
 DT 27-FEB-2003 (first entry)
 DE Human TPO peptide with MCH class II binding activity #114.
 XX
 KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
 XX
 OS Homo sapiens.
 XX WO200268469-A2.
 PN 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-EP01931.
 XX 26-FEB-2001; 2001EP-0104702.
 PR (MERE) MERCK PATENT GMBH.
 PA Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -

XX Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and antiallergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6

DB 4 PLPPT 8

RESULT 31

ABP81162

ID ABP81162 standard; peptide; 13 AA.

XX AC ABP81162;

XX DT 27-FEB-2003 (first entry)

XX DE Human TPO peptide with MCH class II binding activity #115.

XX KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

XX KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.

XX OS Homo sapiens.

XX PN WO200268469-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-EP01931.

XX PR 26-FEB-2001; 2001EP-0104702.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FJ, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX PI Carr FJ, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and antiallergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX or less immunogenicity than any non-modified molecule with the same

XX biological activity when used in vivo. The protein is useful in

XX pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6

DB 2 PLPPT 6

RESULT 32

ABP81163

ID ABP81163 standard; peptide; 13 AA.

XX AC ABP81163;

XX DT 27-FEB-2003 (first entry)

XX DE Human TPO peptide with MCH class II binding activity #116.

XX KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

XX KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.

XX OS Homo sapiens.

XX PN WO200268469-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-EP01931.

XX PR 26-FEB-2001; 2001EP-0104702.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FJ, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and antiallergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
|
|
|
|
|
Db 1 PLPPT 5

RESULT 33
AA03679
ID AAY03679 standard; peptide; 14 AA.
XX
AC AAY03679;
XX
DT 07-JUN-1999 (first entry)
XX
DE Amino acid sequence of the malaria (M) string CTL epitope BCG.
XX
KW CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;
KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;
KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;
KW melanoma; HIV; breast; colon; vaccination.
XX
OS Mycobacterium tuberculosis.
XX
FN WO9856919-A2.
XX
PD 17-DEC-1998.
XX
PF 09-JUN-1998; 98WO-GB01681.
XX
PR 09-JUN-1997; 97GB-0011957.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Blanchard T, Gilbert SC, Hanke T, Hill AVS, McMichael AJ;
PI Plebanski M, Schneider J, Smith GL;
XX
DR WPI; 1999-070325/06.
DR N-PSDB; AAX29219.
XX
PT Generating CD8-positive T cell response to target antigen using
PT recombinant poxvirus - for treating or preventing malaria and HIV
PT infection, also epitope strings from Plasmodium and HIV
XX
PS Claim 38; Page 19; 85pp; English.
XX
CC The invention relates to methods and reagents for generating a
CC protective CD8+ T-cell immune response against at least one target
CC antigen. The kits of the invention comprises (i) as priming composition,
CC a source of one or more CD8+ T-cell cytotoxic T lymphocytes-(CTL)
CC epitopes of the target antigen, plus a carrier and (ii) as boosting
CC composition a source of CTL epitopes, with at least one CTL epitope the
CC same as used in (i), with this source being a non-replicating or
CC replication-impaired recombinant poxvirus vector (PVV) plus a carrier. If
CC the source of CTL epitopes in (i) is a viral vector, then the vector in
CC (ii) is from a different virus. The kits are used to generate an immune
CC response (prophylactic or therapeutic) against pathogens or tumours,
CC specifically against malaria parasites such as P. falciparum, or HIV, and
CC also many other bacterial, viral or parasitic pathogens. The kits are
CC also used for protective response against melanoma and cancer of breast
CC or colon, and generally wherever a strong CD8+ response is protective.
CC The boosting composition may be used alone to boost a naturally primed
CC response against malaria. The specified PVV provide an excellent booster
CC effect, better than that from wild-type poxvirus, resulting in complete
CC rather than partial protection against sporozoite challenge. Also PVV are
CC safer to use than wild-type virus. Sequences AAY03661-680 represent CTL
CC peptide epitopes of the malaria (M) string.
XX
SQ Sequence 14 AA;

Query Match 50.0%; Score 5; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
|
|
|
|
|
Db 5 QPLPP 9

RESULT 34
AAM00448
ID AAM00448 standard; Peptide; 14 AA.
XX
AC AAM00448;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human protein fragment SEQ ID NO: 996.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX
OS Homo sapiens.
XX
FN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US00322.
XX
PR 07-JAN-2000; 2000US-0174962.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2001-451871/48.
DR N-PSDB; AAH89565.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
XX
PS Disclosure; Page 389; 475pp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.
XX
SQ Sequence 14 AA;

Query Match 50.0%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
|
|
|
|
|
Db 5 QPLPP 9

RESULT 35
AAB46171
ID AAB46171 standard; peptide; 14 AA.
XX
AC AAB46171;
XX
DT 04-APR-2001 (first entry)
XX

DE Bacille Calmette-Guerin universal T epitope.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 OS Mycobacterium tuberculosis.
 XX
 FN WO200072880-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX WPI; 2001-032104/04.
 DR
 XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Page 28; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 SQ Sequence 14 AA;
 Query Match 50.0%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPP 5
 Db 5 QPLPP 9
 RESULT 36
 AAB49070
 ID AAB49070 standard; peptide; 14 AA.
 XX
 AC AAB49070;
 XX
 XX 27-MAR-2001 (first entry)
 XX
 DE BCG T-cell epitope, SEQ ID NO:6.
 XX
 KW Amyloid disease; amyloid fibril deposition; amyloid plaque;
 KW immunogenic; antibody; vaccine; Alzheimer's disease;
 KW type 2 diabetes; reactive system amyloidosis;
 KW systemic senile amyloidosis; familial amyloid cardiomyopathy;
 KW transmissible spongiform encephalopathy; Creutzfeld-Jakob disease; Kuru;
 KW haemodialysis-associated beta-2-microglobulin deposition;
 KW carrier protein; universal T-cell epitope.
 XX
 OS Mycobacterium bovis.
 XX

PN WO200072876-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US15239.
 XX
 PR 01-JUN-1999; 99US-0137010.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB;
 XX WPI; 2001-070921/08.
 DR
 XX Pharmaceutical composition comprising immunogen against amyloid
 PT component such as fibril peptide or protein, or antibody against
 PT amyloid component useful for treating amyloid diseases or amyloidoses -
 XX
 PS Disclosure; Page 43; 140pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition for
 CC preventing or treating a disease characterised by amyloid fibril
 CC deposits (amyloid plaques) in a patient. The pharmaceutical composition
 CC comprises an agent that will induce an immune response against an amyloid
 CC component, or an antibody or antibody fragment that binds to an amyloid
 CC component. The invention also relates to a method for determining
 CC the prognosis of a patient undergoing treatment for an amyloid disorder
 CC which involves measuring a patient serum amount of immunoreactivity
 CC against a selected amyloid component. A patient serum immunoreactivity
 CC of at least four times a base line serum immunoreactivity control level
 CC indicates a prognosis of improved status with respect to the disorder.
 CC The pharmaceutical compositions of the invention are useful for treating
 CC a wide variety of disorders characterised by amyloid fibril deposition in
 CC a patient. Such disorders include Alzheimer's disease characterised by
 CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by
 CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
 CC amyloidosis associated with systemic inflammatory diseases (e.g.,
 CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
 CC fibrils derived from serum amyloid A protein (ApoSAA)); systemic senile
 CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
 CC fibrils derived from transthyretin (TTR); transmissible spongiform
 CC encephalopathies (e.g. Creutzfeld-Jacob disease, Kuru) characterised by
 CC prion protein deposits; and beta-2-microglobulin deposits which form as
 CC a result of long term haemodialysis treatment. The present sequence
 CC represents a universal T-cell epitope which may be used as a
 CC carrier for an epitope derived from an amyloid plaque component in a
 CC composition of the invention.
 XX
 SQ Sequence 14 AA;
 Query Match 50.0%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPLPP 5
 Db 5 QPLPP 9
 RESULT 37
 AAW38958
 ID AAW38958 standard; peptide; 15 AA.
 XX
 AC AAW38958;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:355.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX Mao Y, Xie Y;
XX WPI; 2001-602854/69.
XX New polypeptide for the diagnosis and treatment of malignant neoplasm,
PT hemopathy, HIV infection, immunological diseases and inflammations,
PT comprises protein 11 of the growth hormone family -
XX
XX Example 5; Page 19; 35pp; Chinese.
XX
XX The present invention relates to protein 11 of the growth hormone family
CC (see AA165179 and AAG78854). The growth hormone protein and its coding
CC sequence are useful in the diagnosis and treatment of malignant tumours,
CC haemopathy, HIV infection, immunological diseases and various
CC inflammations. The present sequence is an N-terminal peptide fragment of
CC the growth hormone protein which was used in an example from the present
CC invention.
XX
XX
SQ Sequence 15 AA;
Query Match 50.0%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPPT 6
DB 8 PLPPT 12
RESULT 40
ABG72660
ID ABG72660 standard; Peptide; 15 AA.
XX AC ABG72660;
XX
XX 26-FEB-2003 (first entry)
XX
XX Human K-ras 10.67 proto-oncogene protein, N-terminus.
XX
XX Human; K-ras 10.67; proto-oncogene; tumour; haemopathy;
KW development disorder; human immunodeficiency virus infection; HIV;
KW immunological disease; inflammation.
XX
XX Homo sapiens.
XX CN1352063-A.
XX
XX 05-JUN-2002.
XX
XX 02-NOV-2000; 2000CN-0127155.
XX
XX 02-NOV-2000; 2000CN-0127155.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-658691/71.
XX
XX New human K-ras proto-oncogene protein 10.67 polypeptide for treating
PT malignant tumors, hemopathy, development disorder, human
PT immunodeficiency virus infection, immunological diseases and various
PT inflammations -
XX
XX Example 5; Page 19 (disclosure); 33pp; Chinese.
XX
XX The present invention discloses a new kind of polypeptide,
CC human K-ras proto-oncogene protein 10.67, polynucleotides encoding the
CC polypeptide and a DNA recombination process to produce the polypeptide.
CC The present invention also discloses applying the polypeptide in
CC treating various diseases, such as malignant tumors, haemopathy, CC

CC development disorder, human immunodeficiency virus (HIV) infection,
CC immunological diseases and various inflammations. The present invention
CC also discloses the antagonist resisting the polypeptide and its
CC treatment effect. The present invention also discloses application of
CC the polynucleotides encoding human K-ras proto-oncogene protein 10.67.
CC The present sequence represents human K-ras proto-oncogene protein
CC 10.67, N-terminus, used in an ELISA (enzyme-linked immunosorbent assay)
CC experiment.
XX
XX Sequence 15 AA;
Query Match 50.0%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPLPP 5
DB 11 QPLPP 15
RESULT 41
AAW25427
ID AAW25427 standard; peptide; 16 AA.
XX AC AAW25427;
XX
XX 27-MAR-1998 (first entry)
XX
XX Yes SH3 domain binding peptide SEQ ID NO:213.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX Unidentified.
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX {UYN-} UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
XX WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 19; Page 100; 131pp; English.
XX
XX The present sequence represents a Src homology region 3 (SH3) binding
CC peptide. SH3 binding peptides are selected from: (a) peptides which
CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
CC bind the amino-terminal SH3 domain of Grb2. The purified binding
CC peptides can be used in the method to identify inhibitors of their
CC binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.

XX SQ Sequence 16 AA;
Query Match 50.0%; Score 5; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 5 PLPPT 9

RESULT 42
AAW25376
ID AAW25376 standard; peptide; 16 AA.

XX AC AAW25376;

XX DT 27-MAR-1998 (first entry)

XX DE Src SH3 domain binding peptide SEQ ID NO:158.

XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.
XX OS Unidentified.
XX FN WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US02298.

XX PR 16-FEB-1996; 96US-0602999.

XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1

XX Claim 16; Page 99; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding
XX peptide. SH3 binding peptides are selected from: (a) peptides which
XX bind the SH3 domain of Cortactin; (b) peptides which bind the middle
XX SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
XX peptides which bind the SH3 domain of Src; (e) peptides which bind the
XX SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
XX p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
XX (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
XX bind the amino-terminal SH3 domain of Grb2. The purified binding
XX peptides can be used in the method to identify inhibitors of their
XX binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.

XX SQ Sequence 16 AA;
Query Match 50.0%; Score 5; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 5 PLPPT 9

RESULT 43
AAW25380
ID AAW25380 standard; peptide; 16 AA.

XX AC AAW25380;

XX DT 27-MAR-1998 (first entry)

XX DE Src SH3 domain binding peptide SEQ ID NO:147.

XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.
XX OS Unidentified.
XX FN WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US02298.

XX PR 16-FEB-1996; 96US-0602999.

XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1

XX Claim 16; Page 99; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding
XX peptide. SH3 binding peptides are selected from: (a) peptides which
XX bind the SH3 domain of Cortactin; (b) peptides which bind the middle
XX SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
XX peptides which bind the SH3 domain of Src; (e) peptides which bind the
XX SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
XX p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
XX (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
XX bind the amino-terminal SH3 domain of Grb2. The purified binding
XX peptides can be used in the method to identify inhibitors of their
XX binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.

XX SQ Sequence 16 AA;
Query Match 50.0%; Score 5; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPPT 6
Db 5 PLPPT 9
RESULT 44
ABP82678
ID ABP82678 standard; Peptide, 16 AA.
XX
XX AC ABP82678;
XX DT 04-MAR-2003 (first entry)
XX DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1351.
XX

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomypopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.
OS
XX
XX WO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US50107.
XX
XX 19-DEC-2000; 2000US-257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
XX Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases. e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABP42523 to ABP42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.

XX SQ Sequence 16 AA;
Query Match 50.0%; Score 5; DB 24; Length 16;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPPT 6
Db 10 PLPPT 14

RESULT 45
AAB39277
ID AAB39277 standard; Protein, 17 AA.
XX
XX AAB39277;
XX 02-FEB-2001 (first entry)
XX
XX Gene 31 human secreted protein homologous amino acid sequence #157.
XX
XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
KW ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis;
KW hyperproliferative disorder; cardiovascular disorder; infection;
KW cerebrovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; chemotaxis.

XX Homo sapiens.
OS
XX
XX WO200056754-A1.
XX
XX 28-SEP-2000.
XX
XX 16-MAR-2000; 2000WO-US06792.
XX
XX 19-MAR-1999; 99US-0125362.
XX 10-DEC-1999; 99US-0169980.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen GA, Ruben SM, Komatsoulis G;
XX WPI; 2000-579483/54.

XX Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; Page 52; 434pp; English.
XX
XX The polynucleotide sequences given in AAC74223-C74279 encode the human
CC secreted proteins represented in AAB39179-B39226. Sequences
CC AAB39227-B39308 are alternative proteins encoded by the genes, and also
CC protein sequences with which they share homology. The proteins have
CC activities based on the tissues and cells in which they are expressed.
CC Examples of activities include: immunosuppressive; antiarthritic;
CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
CC fungicide; and ophthalmological. The human secreted proteins,
CC polynucleotides, antagonists and agonists of the invention may be useful
CC in the treatment, prevention, and/or diagnosis of various disease,
CC disorders and conditions such as autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and

CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
 CC also be used to aid wound healing and epithelial cell proliferation, to
 CC regenerate tissues, maintain organs before transplantation, in
 CC chemotaxis and as a food additive or preservative e.g. to increase
 CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used
 CC during the isolation and characterisation of the genes of the invention.

XX Sequence 17 AA;

Query Match 50.0%; Score 5; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 Db 1 QPLPP 5

RESULT 46

AAE03955
 ID AAE03955 standard; peptide; 18 AA.

AC AAE03955;

DT 09-AUG-2001 (first entry)

DE Human gene 10 encoded secreted protein fragment, SEQ ID NO:126.

XX Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnery;
 KW cell culture; chemotaxis; food additive; gene therapy;
 KW binding partner identification.

XX Homo sapiens.

XX WO200077022-A1.

XX 21-DEC-2000.

PF 01-JUN-2000; 2000WO-US15136.

XX 11-JUN-1999; 99US-0138629.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsoulis GA;

DR WPI; 2001-367020/38.

XX Nucleic acids encoding 50 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
 PT disease, botulism, cancers and Scimitar syndrome -

PS Disclosure; Page 566-567; 614pp; English.

XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
 CC protein genes and AAE03898-AAE03947 represent the proteins they encode.
 CC AAE03948-AAE03996 represent human secreted protein fragments or variants.
 CC The genes and their secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 50 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental

CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC healing and infectious. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.

XX Sequence 18 AA;

Query Match 50.0%; Score 5; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 Db 11 QPLPP 15

RESULT 47

AAAY31181
 ID AAY31181 standard; peptide; 19 AA.

AC AAY31181;

XX 28-OCT-1999 (first entry)

XX Ubiquitin fusion protein T cell epitope.

XX Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;
 KW immune response stimulation; vaccine; T cell; viral; infection; cancer;
 KW bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;
 KW pulmonary infection; respiratory infection; scaffold; anti-self; pig;
 KW steridogenesis; gamete maturation; prostate; breast; castration; TNF;
 KW tumour necrosis factor; septic shock; arthritis; Crohn's disease;
 KW inflammatory bowel disease; ulcerative colitis; chorionic gonadotropin;
 KW fertility; sperm protein; growth rate; antibody; detection.

XX Synthetic.

XX WO9942472-A1.

XX 26-AUG-1999.

PF 26-JAN-1999; 99WO-US01588.

XX 19-FEB-1998; 98US-0026276.

XX (IGEN-) IGEN INT INC.

XX Kenten JH, Lohnas GL, Pilon AL, Roberts SF, Tramontano A;

XX WPI; 1999-518582/43.

XX Epitope-containing fusion proteins used to generate a highly
 PT specific immune responses

XX Example 4; Page 42; 67pp; English.

XX This invention describes a novel fusion protein, comprising a heat shock
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner
 CC which is useful for the stimulation of a highly specific immune response

CC when administered to an animal. The protein of the invention may be
 CC post-translationally modified (e.g. by the addition of fatty acids to
 CC enhance immunogenicity). The fusion proteins of the invention can be
 CC used as vaccines to induce an immune response. When a T cell epitope is
 CC attached, they can be used for control of viral infections, bacterial
 CC infections, parasitic infection and cancer. The fusion proteins can be
 CC used in pharmaceutical compositions for the treatment of gastrointestinal
 CC diseases, pulmonary infections, respiratory infections, and HIV
 CC infections. The use of ubiquitin as a scaffold is also useful for the
 CC presentation and stimulation of anti-self immune responses, e.g.
 CC generation of anti-gonadotropin releasing hormone antibodies which result
 CC in the suppression of luteinizing hormone and follicle stimulating
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation
 CC in males and females. This type of anti-self response in humans is useful
 CC in the treatment of prostate cancer and breast cancer. In livestock, the
 CC ability to stimulate an anti-self response provides a simple alternative
 CC to physical castration. Immunocastration of pigs is a better alternative
 CC to physical castration, as it does not result in any of the detrimental
 CC side effects associated with physical castration. Other examples of
 CC diseases and conditions treated with self proteins fused with ubiquitin
 CC are TNF and its epitopes to modulate septic shock, arthritis,
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig
 CC epsilon heavy chain for the control of allergic reactions; chorionic
 CC gonadotropin for fertility control; and sperm proteins for fertility
 CC control. A further use of the fusion proteins is as part of a vaccine to
 CC enhance growth rate and thereby the final weight of the livestock prior
 CC to shipment to market. In addition, the fusion proteins of the invention
 CC can be used to detect and identify antibodies from experimental samples.
 CC This sequence represents a T cell epitope used in the construction of
 CC a ubiquitin fusion protein described in the method of the invention.

XX SQ Sequence 19 AA;

Query Match 50.0%; Score 5; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||
 Db 6 QPLPP 10

RESULT 48

AAV31165
 ID AAY31165 standard; peptide; 19 AA.

AC AAY31165;

DT 28-OCT-1999 (first entry)

DE Ubiquitin fusion protein MT peptide.

XX Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;
 XX immune response stimulation; vaccine; T cell; viral; infection; cancer;
 XX bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;
 XX pulmonary infection; respiratory infection; scaffold; anti-self; pig;
 XX steroidogenesis; gamete maturation; prostate; breast; castration; TNF;
 XX tumour necrosis factor; septic shock; arthritis; Crohn's disease;
 XX inflammatory bowel disease; ulcerative colitis; chorionic gonadotropin;
 XX fertility; sperm protein; growth rate; antibody; detection.

XX Synthetic.

XX WO9942472-A1.

XX 26-AUG-1999.

XX 26-JAN-1999; 99WO-US01588.

XX 19-FEB-1998; 98US-0026276.

XX (IGEN-) IGEN INT INC.

XX

PI Kenten JH, Lohnas GL, Pilon AL, Roberts SF, Tramontano A;
 DR MPI; 1999-518582/43.

XX Epitope-containing fusion proteins used to generate a highly
 PT specific immune responses

XX Example 1; Page 27; 67pp; English.

CC This invention describes a novel fusion protein, comprising a heat shock
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner
 CC which is useful for the stimulation of a highly specific immune response
 CC when administered to an animal. The protein of the invention may be
 CC post-translationally modified (e.g. by the addition of fatty acids to
 CC enhance immunogenicity). The fusion proteins of the invention can be
 CC used as vaccines to induce an immune response. When a T cell epitope is
 CC attached, they can be used for control of viral infections, bacterial
 CC infections, parasitic infection and cancer. The fusion proteins can be
 CC used in pharmaceutical compositions for the treatment of gastrointestinal
 CC diseases, pulmonary infections, respiratory infections, and HIV
 CC infections. The use of ubiquitin as a scaffold is also useful for the
 CC presentation and stimulation of anti-self immune responses, e.g.
 CC generation of anti-gonadotropin releasing hormone antibodies which result
 CC in the suppression of luteinizing hormone and follicle stimulating
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation
 CC in males and females. This type of anti-self response in humans is useful
 CC in the treatment of prostate cancer and breast cancer. In livestock, the
 CC ability to stimulate an anti-self response provides a simple alternative
 CC to physical castration. Immunocastration of pigs is a better alternative
 CC to physical castration, as it does not result in any of the detrimental
 CC side effects associated with physical castration. Other examples of
 CC diseases and conditions treated with self proteins fused with ubiquitin
 CC are TNF and its epitopes to modulate septic shock, arthritis,
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig
 CC epsilon heavy chain for the control of allergic reactions; chorionic
 CC gonadotropin for fertility control; and sperm proteins for fertility
 CC control. A further use of the fusion proteins is as part of a vaccine to
 CC enhance growth rate and thereby the final weight of the livestock prior
 CC to shipment to market. In addition, the fusion proteins of the invention
 CC can be used to detect and identify antibodies from experimental samples.
 CC This sequence represents a MT peptide used in the method of the
 CC invention.

XX SQ Sequence 19 AA;

Query Match 50.0%; Score 5; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
 |||||
 Db 6 QPLPP 10

RESULT 49

AAV71936

ID AAB71936 standard; Peptide; 19 AA.

XX AAB71936;

XX 10-MAY-2001 (first entry)

XX MT peptide.

XX Immunostimulant; antiallergic; growth promoting; vaccine;

XX heat shock fusion protein; ubiquitin; self-epitope; immunogen;

XX male-specific peptide hormone; female-specific peptide hormone; MT.

XX Unidentified.

XX WO200112216-A1.

XX 22-FEB-2001.

```

XX PF 14-AUG-2000; 2000WO-US22121.
XX PR 13-AUG-1999; 99US-0374721.
XX PA (PROT-) PROTEINIX CO.
XX PR 13-AUG-1999; 99US-0374721.
XX PA (PROT-) PROTEINIX CO.
XX PI Kenten JH, Roberts S, Lohnas G;
XX WPI; 2001-202829/20.
XX Novel fusion proteins for stimulating immune response in animals
PT against self-antigen, has heat shock protein fused to single or a group
PT of epitope-containing segments having identical or non-identical self
PT epitopes -
XX Example 1; Page 27; 94pp; English.
XX The present sequence is given in an example illustrating an invention
CC disclosing self-epitope-containing heat shock fusion proteins. The
CC proteins comprise a heat shock protein, preferably ubiquitin, fused to a
CC single epitope-containing segment or two or more non-contiguous epitope
CC containing segments, each epitope-containing segment comprising one or
CC more identical or non-identical self-epitopes. The heat shock fusion
CC proteins are useful for stimulating an immune response in an animal,
CC especially a pig, directed towards a self-antigen in particular a male
CC or female-specific peptide hormone. The physiological consequence is
CC substantially similar to the consequences of surgical castration. The
CC proteins are useful for identifying antibodies in experimental or
CC diagnostic samples and for reducing levels of a predetermined endogenous
CC protein, such as gonadotropin releasing hormone, tumour necrosis factor
CC or growth hormone protein. They are also useful for reducing allergic
CC response and for increasing the growth rate of an animal. The proteins
CC have a high specific immune response and do not result in detrimental
CC side-effects. The present sequence encodes a peptide sequence which is
CC inserted into a ubiquitin scaffold to test the peptide as an immunogen
CC for eliciting a targeted immune response.
XX Sequence 19 AA;
XX Query Match 50.0%; Score 5; DB 22; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 71;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 QPLPP 5
XX DB 6 QPLPP 10
XX RESULT 50
XX AAW16997
XX ID AAW16997 standard; peptide; 20 AA.
XX AC AAW16997;
XX DT 27-JUN-1997 (first entry)
XX DE SRC SH3 domain-binding peptide.
XX Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
KW protein tyrosine kinase; signal transduction; RNA processing;
KW trafficking; translation.
XX Synthetic.
XX OS
XX WO9603649-A1.
XX PI
XX PD 08-FEB-1996.
XX

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PF 24-JUL-1995; 95WO-US09382.
XX 07-JUN-1995; 95US-0483555.
XX PR 22-JUL-1994; 94US-027865.
XX (UYNC-) UNIV NORTH CAROLINA.
XX Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
XX WPI; 1996-117151/12.
XX Peptide with binding affinity for Src homology region 3 (SH3)
PT domains of proteins - useful for e.g. modulating signal transduction
PT pathways at the cellular level, esp. protein tyrosine
PT kinase-mediated
XX Example 14; Page 58; 116pp; English.
XX AAW16996-W17009 are SRC SH3-binding peptides derived from a biased
CC peptide library, exhibiting selective SH3 binding. The SH3 binding
CC peptides are useful in modulating signal transduction pathways at the
CC cellular level (especially protein tyrosine kinase-mediated), modulating
CC oncogenic protein activity, or providing compounds for the development
CC of drugs with the ability to modulate broad classes, as well as specific
CC classes, of proteins involved in signal transduction and also for
CC regulating the processing, trafficking or translation of RNA. Conjugates
CC of the peptides with detectable labels or imaging agents are useful for
CC imaging cells, tissues and organs in which Src or Src-related proteins
CC are expressed.
XX Sequence 20 AA;
XX Query Match 50.0%; Score 5; DB 17; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 74;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 PLPPT 6
XX DB 7 PLPPT 11
XX RESULT 51
XX AAR99513
XX ID AAR99513 standard; peptide; 20 AA.
XX AC AAR99513;
XX DT 09-JAN-1997 (first entry)
XX DE T-cell epitope used in construction of chimeric immunoglobulin.
XX KW Chimera; chimeric; immunoglobulin; Ig; B-cell; T-cell; lymphocyte;
KW epitope; immune response; vaccine; pathogen; antibody; influenza;
KW measles; hepatitis; foot and mouth disease; tetanus toxoid;
KW human immunodeficiency virus; HIV; heat shock protein; M protein;
KW hen egg white lysozyme; nuclease.
XX OS Mycobacteria sp.
XX WO9619584-A1.
XX PN 27-JUN-1996.
XX PD 21-DEC-1995; 95WO-US16718.
XX PF 22-DEC-1994; 94US-0363276.
XX PR (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX PA Bona C, Zaghouani H;
XX PI WPI; 1996-309598/31.
XX DR
XX

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PT	Chimeric immunoglobulin with CDR loop substid. for T and or B cell
PT	epitope - useful in vaccine composition to enhance immune response
PT	to pathogens
XX	
PS	Disclosure; Page 19; 131pp; English.
XX	
CC	Chimeric immunoglobulins (Ig) having a CDR loop of the parent Ig
CC	replaced with a foreign peptide sequence corresponding to a T- or B-
CC	cell epitope, may be used in vaccine compositions to enhance an
CC	immune response to a pathogen. Chimeric Ig comprising a B-cell
CC	epitope can also be used to label B-cells, to test the ability of a
CC	subject to mount a humoral response to a particular B-cell epitope
CC	or to collect B-cells which recognise the epitope.. An antibody
CC	comprising a chimeric Ig molecule which comprises an antigen binding
CC	site may be used in diagnostic assays to detect the presence of a
CC	particular target antigen, which binds to the antibody binding site.
CC	Sequences of B-cell epitopes are given in AAR9503-08. Sequences of
CC	T-cell epitopes are given in AAR9509-17. The term T-cell epitope
CC	refers to a peptide which is associated with MHC self antigens and
CC	is recognised by a T-cell and which functionally activates the T
CC	cell. This peptide is an epitope of Mycobacteria heat shock
CC	protein.
XX	
SQ	Sequence 20 AA;
	Query Match 50.0%; Score 5; DB 17; Length 20;
	Best Local Similarity 100.0%; Pred.No. 74;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 QQLPP 5
Db	6 QQLPP 10
RESULT 52	
AAW35439	
ID	AAW35439 standard; peptide; 20 AA.
XX	
AC	AAW35439;
XX	
DT	25-MAR-2003 (updated)
DT	22-APR-1998 (first entry)
XX	
DE	T-cell stimulatory peptide from Mycobacterium tuberculosis 38kD antigen.
KW	T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
KW	scaffold; inhibition; metastasis; wound healing; solid phase.
XX	
OS	Mycobacterium tuberculosis.
XX	
PN	WO9738011-A1.
XX	
PD	16-OCT-1997.
XX	
PX	03-APR-1997; 97WO-DK00146.
XX	
PR	03-APR-1996; 96DK-0000398.
XX	
PA	(PEPR-) PEPRESEARCH AS.
XX	
PI	Heegaard PMH, Jakobsen PH;
XX	
DR	WPI; 1997-512645/47.
XX	
XX	
PT	Non-dendritic peptide carrier linked to a solid phase - useful as a
PT	diagnostic agent and as a scaffold for production of chemical
PT	derivatives
XX	
PS	Claim 30; Page 199; 262pp; English.
XX	
CC	A non-dendritic peptide carrier (A) has been developed which is coupled
CC	through a linker to a solid phase, forming a complex of (A)-solid phase.
CC	where (A) comprises 10-50 amino acids capable of forming a secondary

CC AAW12233-W12241 represent T-cell epitopes that can be used in the method
 CC of the invention. The method of the invention is for conjugating a
 CC peptide (such as this sequence) to an immunoglobulin (Ig) molecule, via
 CC a carbohydrate (CB) residue of the Ig. The method comprises
 CC enzymatically oxidising the CB residue of the Ig, then reacting this
 CC residue with an amino group of the peptide. The product of this reaction
 CC is then stabilised by reacting it with a reducing agent. The conjugate
 CC may be used as a vaccine and in diagnostic and therapeutic methods. The
 CC conjugates are used to treat cancer and viral infections, such as
 CC leukaemia and influenza viruses. The conjugates are used to obtain a
 CC ligand of the peptide using affinity purification, and to detect and
 CC quantitate the amount of a target antigen of the Ig. When the peptide is
 CC a B-cell epitope, the conjugates are used to label B-cells, and when the
 CC peptide is a helper T-cell epitope, the conjugates are used to test the
 CC ability of a subject to mount an immune response to that epitope. The
 CC conjugates are more effective in eliciting an immune response than
 CC unconjugated peptides. The conjugates increase the half-life of the
 CC peptide and also, via binding of the Fc region of the Ig to cell-surface
 CC receptor, recruit elements of the immune system to improve the overall
 CC efficiency of the immune response.

XX SQ Sequence 20 AA;

Query Match 50.0%; Score 5; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 Db 6 QPLPP 10

RESULT 54

AAW60693
 ID AAW60693 standard; peptide; 20 AA.

AC AAW60693;

DT 22-SEP-1998 (first entry)

DE Mycobacteria heat shock protein T cell epitope (residues 350-369).

KW Immunisation; target antigen; epitope; inoculation; infant mammal;
 KW viral antigen; depressed humoral response; respiratory syncytial virus;
 KW rotavirus; measles virus; human immunodeficiency virus; hepatitis virus;
 KW herpes simplex virus; influenza virus; Streptococcus pneumoniae;
 KW Hemophilus influenzae; Neisseria meningitidis; Staphylococcus aureus;
 KW protozoan antigen; malaria; heat shock protein.

OS Mycobacterium sp.

PN WO9822145-A1.

XX 28-MAY-1998.

PF 21-NOV-1997; 97WO-US21687.

PR 22-NOV-1996; 96US-0755034.

PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.

PI Bona C, Bot A;

XX WPI; 1998-312182/27.

XX Immunisation of infant mammals - by inoculating the mammal with a
 PT nucleic acid encoding a relevant epitope of a target antigen

XX Disclosure; Page 10; 83pp; English.

XX Sequence shown in AAW60683 to AAW60700 are epitope sequences of various
 CC viral antigens used to exemplify the method of invention of immunising
 CC an infant mammal against a target antigen. The method comprises

CC inoculating the mammal with a nucleic acid encoding a relevant epitope
 CC of a target antigen in a carrier, such that the relevant epitope is
 CC expressed in the infant mammal. The genetic immunisation of infant
 CC mammals can give rise to effective cellular (including the induction of
 CC cytotoxic T lymphocytes) and humoral immune responses against the target
 CC antigen. The methods are particularly used for treating infants with
 CC depressed humoral responses, that have high-zone tolerances against the
 CC target antigens or have a Th2 biased immune response. The target antigen
 CC may be a viral antigen, e.g. a respiratory syncytial virus antigen, a
 CC rotavirus antigen, a measles virus antigen, a human immunodeficiency
 CC virus antigen, a hepatitis virus antigen, a hepatitis B virus antigen, a
 CC herpes simplex virus antigen or an influenza virus antigen, a bacterial
 CC antigen e.g. Streptococcus pneumoniae antigen, Hemophilus influenzae
 CC antigen, Neisseria meningitidis antigen, Staphylococcus aureus antigen
 CC or a protozoan antigen such as a malaria antigen.

XX SQ Sequence 20 AA;

Query Match 50.0%; Score 5; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
 Db 6 QPLPP 10

RESULT 55

ABB79926
 ID ABB79926 standard; Peptide; 20 AA.

AC ABB79926;

DT 12-DEC-2002 (first entry)

DE Mycobacterium heat shock protein T-cell epitope.

KW Vaccine; genetic immunisation; gene therapy; antigen; epitope;
 KW heat shock protein; T-cell; T-lymphocyte.

OS Mycobacterium sp.

PN US2002115625-A1.

XX 22-AUG-2002.

PF 08-MAR-2001; 2001US-0801540.

PR 19-MAY-1999; 99US-0308511.

PA (BONA/) BOT A.

XX (BONA/) BONA C.

PI Bot A, Bona C;

XX WPI; 2002-712482/77.

XX Immunizing an infant mammal against a target antigen or inducing a
 PT cytotoxic T cell response against a pathogen in the mammal, comprises
 PT administering nucleic acid encoding relevant epitopes of pathogen
 PT associated target antigens -

XX Disclosure; Page 4; 45pp; English.

XX The present sequence is that of a T-cell epitope from Mycobacteria
 CC heat shock protein (residues 350-369). This is a Th epitope which,
 CC in the context of MHC Class II self antigens, may be recognised by a
 CC helper T-cell and thereby promote B-cell antibody production via the
 CC Th cell. It is an example of T-cell epitopes which may be used
 CC according to the invention. The invention relates to immunising an
 CC infant mammal against a target antigen or inducing a cytotoxic T-cell
 CC response against a pathogen. The method involves inoculating the
 CC infant with a nucleic acid encoding one or more relevant epitopes of

CC one or more target antigens associated with the pathogen in a carrier,
 CC so that the relevant epitope(s) is expressed in the infant mammal.
 CC B- or T-cell epitopes may be used, and the pathogen may be a virus,
 CC bacterium, protozoan, fungus, yeast, or parasite. The method may
 CC reduce the need for subsequent boost administrations and may
 CC prevent the side-effects associated with live attenuated vaccines.
 CC Administration of multiple epitopes directed to antigens
 CC associated with more than one pathogen may provide an infant with a
 CC broader spectrum of protection, and may be a means for inducing an
 CC immune response to a variety of childhood pathogens.
 XX
 SQ Sequence 20 AA;

Query Match 50.0%; Score 5; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 74; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 QPLPP 5
 |||||

Db 6 QPLPP 10
 |||||

RESULT 56

AAR80055
 ID AAR80055 standard; peptide; 4 AA.
 XX
 AC AAR80055;

DT 25-APR-1996 (first entry)

DE Peptidase substrate #9.

XX Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
 KW cerebral function.
 XX
 OS Synthetic.

XX JP07227281-A.

XX 29-AUG-1995.

XX 15-FEB-1994; 94JP-0042027.

XX 15-FEB-1994; 94JP-0042027.

XX (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 XX WPI; 1995-331519/43.

XX 140 kDa peptidase hydrolyses proline rich proteins - useful for
 PT prevention and treatment of diseases related to proline rich
 PT proteins and studies of cerebral functions

XX Example 4; Page 6; 7pp; Japanese.

XX The sequences represented by AAR80046 and AAR80048-R80059 are substrates
 CC for the novel peptidase of the invention. The peptidase hydrolyses
 CC P-P-P, P-P-P, and P-P and recognises the proline at the second residue
 CC from the N-terminal of a peptide to release the N-terminal amino acid.
 CC The enzyme's activity is stimulated with MnCl₂ and inhibited with
 CC o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
 CC hydrolysis of proline containing physiologically active peptides,
 CC oligoproline and proline rich proteins in the living body, particularly
 CC in the brain of mammals. The peptidase is useful for the prevention and
 CC treatment of proline rich protein related diseases and study of cerebral
 CC functions.
 XX

SQ Sequence 4 AA;

Query Match 40.0%; Score 4; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 |||||

Db 1 PLPP 4

RESULT 57

AA45075
 ID AA45075 standard; peptide; 5 AA.
 XX
 AC AA45075;

XX 31-MAY-2000 (first entry)

XX Rat amelogenin N-terminal peptide.

XX Amelogenin; splice variant; rat; chondrogenesis; osteogenesis;
 KW chondrogenic inducing molecule; CIM; cartilage growth; osteopathic;
 KW extracellular matrix protein; tooth enamel; enamel mineralisation;
 KW ameloblast; bone regeneration; composite cell construct.
 XX

OS Rattus sp.

XX WO200006734-A1.

XX 10-FEB-2000.

XX 29-JUL-1999; 99WO-US17342.

XX 29-JUL-1998; 98US-0094489.

XX (NOUN) UNIV NORTHWESTERN.

XX Veis A, Nebgen DR;

XX WPI; 2000-205464/18.

XX Novel amelogenin polypeptides and polynucleotides, useful for enhancing
 PT bone generation in mammals and synthesizing bone matrix or articular
 PT surfaces at implant sites -
 XX

XX Example 1; Page 70; 79pp; English.

XX The present sequence is the amino terminal peptide of the secreted form
 CC of rat amelogenin protein, that corresponds to amino acids 1-5. This
 CC peptide is used to design forward PCR primer P1, to clone and sequence
 CC amelogenin protein. This peptide is highly conserved in bovine, pig
 CC and human species. The amelogenin splice variants functions as an
 CC osteogenic or chondrogenic inducing molecule (CIM), which is useful for
 CC enhancing bone or cartilage growth. It has osteopathic activity.
 CC Amelogenin belongs to the family of extracellular matrix proteins, in
 CC developing tooth enamel, that are produced by the ameloblasts and plays
 CC a role in enamel mineralisation. Chondrogenic or osteogenic inducing
 CC amelogenin molecules are useful to induce differentiation of cells to
 CC the osteogenic and chondrogenic phenotypes and can be used in a
 CC composite cell construct for bone and cartilage regeneration. The
 CC polynucleotides can be employed to produce the polypeptides by
 CC recombinant techniques.
 XX

SQ Sequence 5 AA;

Query Match 40.0%; Score 4; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
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Db 2 PLPP 5

RESULT 58

AAR28486
 ID AAR28486 standard; peptide; 6 AA.


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XX AAR28486;
XX AC
XX DT 22-MAR-1993 (first entry)
XX DE
XX DE DE
XX KW
XX KW
XX OS
XX OS
XX PN JP04275299-A.
XX PD
XX PD 30-SEP-1992.
XX PF 01-MAR-1991; 91JP-0077441.
XX PR 01-MAR-1991; 91JP-0077441.
XX PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX X
XX DR WPI; 1992-376305/46.
XX PT Physiologically active peptide(s) useful as vasodilators - prepd.
XX PT by solid peptide synthesis using peptide synthesiser
XX PS
XX PS Disclosure; Page 5; 6pp; Japanese.
XX XX
XX CC This peptide and its deriv in which the N-terminal Val is deleted
XX CC both have casoxin D-like activity as vasodilators.
XX CC See also AAR28484-R28489.
XX X
XX SQ Sequence 6 AA;
Query Match 40.0%; Score 4; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 VMFP 10
DB 1 VMFP 4
RESULT 59
AAW31463
ID AAW31463 standard; Protein; 6 AA.
XX AC
XX AC AAW31463;
XX DT 04-AUG-1998 (first entry)
XX DE
XX DE Transcriptional activator peptide fragment LS123.
XX KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;
XX KW Protein-protein interaction; Gene therapy; therapeutic; holoenzyme;
XX KW Gal11; DNA binding domain.
XX OS
XX OS Synthetic.
XX PN
XX PN WO9744447-A2.
XX PD
XX PD 27-NOV-1997.
XX PF 02-MAY-1997; 97WO-US07338.
XX PR 01-MAY-1997; 97US-0017016.
XX PR 03-MAY-1996; 96US-0017016.
XX PA (HARD ) HARVARD COLLEGE.
XX PI
XX PI Lu X, Ptashne M, Wu Y;
XX DR WPI; 1998-018502/02.
XX DR

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DR N-PSDB; AAV02561.
XX New transcriptional activator containing DNA binding domain bound to
XX peptide - useful for controlling gene expression, especially in gene
XX therapy, and in protein-protein interaction assays, does not inhibit
XX other transcription activators
XX PS
XX PS Example 1; Page 26; 55pp; English.
XX X
XX CC AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076
XX CC are fragments used in an assay to determine novel transcriptional
XX CC activators. The method involves the production of transcriptional
XX CC activators comprising of a DNA-binding group and a 6-25 amino acid
XX CC peptide that is covalently bonded to the DNA binding group and does not
XX CC represent a fragment of a natural transcription activator.
XX CC Protein-protein interactions are identified in the assay by fusing a
XX CC DNA-binding domain to a library of DNA fragments and introducing this and
XX CC a fusion of target protein and a polypeptide containing a region of Gal4
XX CC which interacts with Gal1p into a cell containing Gal1p and identifying
XX CC members of the library that interact with the target from activation of
XX CC transcription. Such constructs are used to activate transcription in a
XX CC cell, e.g. for controlling gene activity, particularly in gene therapy
XX CC (e.g. recognizing a site close to a selected therapeutic gene).
XX CC Transcription can be activated without blocking other transcriptional
XX CC activators. They probably act by interacting with a component of the RNA
XX CC polymerase II holoenzyme, Gal11, the strongest known yeast activator,
XX CC which provides a more sensitive assay allowing detection of even weak
XX CC protein-protein interactions. Such activators do not create toxicity
XX CC problems even when overexpressed.
XX X
XX SQ Sequence 6 AA;
Query Match 40.0%; Score 4; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPP 5
DB 1 PLPP 4
RESULT 60
AAW31465
ID AAW31465 standard; Protein; 6 AA.
XX AC
XX AC AAW31465;
XX DT 04-AUG-1998 (first entry)
XX DE
XX DE Transcriptional activator peptide fragment LS126.
XX KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;
XX KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;
XX KW Gal11; DNA binding domain.
XX OS
XX OS Synthetic.
XX PN
XX PN WO9744447-A2.
XX PD
XX PD 27-NOV-1997.
XX PF 02-MAY-1997; 97WO-US07338.
XX PR 01-MAY-1997; 97US-0017016.
XX PR 03-MAY-1996; 96US-0017016.
XX PA (HARD ) HARVARD COLLEGE.
XX PI
XX PI Lu X, Ptashne M, Wu Y;
XX DR WPI; 1998-018502/02.
XX DR N-PSDB; AAV02563.
XX DR

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CC modulating signal transduction pathways at the cellular level
 CC (especially protein tyrosine kinase-mediated), modulating oncogenic
 CC protein activity, or providing compounds for the development of drugs
 CC with the ability, to modulate broad classes, as well as specific classes,
 CC of proteins involved in signal transduction and also for regulating the
 CC processing, trafficking or translation of RNA. Conjugates of the peptides
 CC with detectable labels or imaging agents are useful for imaging cells,
 CC tissues and organs in which Src or Src-related proteins are expressed.

XX SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db 2 PLPP 5

RESULT 63

AAW17010
 ID AAW17010 standard; peptide; 7 AA.

XX AC AAW17010;

XX DT 27-JUN-1997 (first entry)

XX DE SRC SH3 domain-binding consensus peptide.

XX KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
 KW protein tyrosine kinase; signal transduction; RNA processing;
 KW trafficking; translation.

XX OS Synthetic.

XX PN W09603649-A1.

XX PD 08-FEB-1996.

XX PR 24-JUL-1995; 95WO-US09382.

XX PR 07-JUN-1995; 95US-0483555.

XX PR 22-JUL-1994; 94US-0278865.

XX PA (UYN-) UNIV NORTH CAROLINA.

XX PI Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;

XX PS WPI; 1996-117151/12.

XX PT Peptide with binding affinity for Src homology region 3 (SH3)
 PT domains of proteins - useful for e.g. modulating signal transduction
 PT pathways at the cellular level, esp. protein tyrosine
 PT kinase-mediated

XX PS Example 14; Page 58; 116pp; English.

XX CC AAW17010 is the consensus sequence of a set of SRC SH3-binding
 CC peptides derived from a biased peptide library, exhibiting selective
 CC SH3 binding. SH3 binding peptides are useful in modulating signal
 CC transduction pathways at the cellular level (especially protein tyrosine
 CC kinase-mediated), modulating oncogenic protein activity, or providing
 CC compounds for the development of drugs with the ability to modulate
 CC broad classes, as well as specific classes, of proteins involved in
 CC signal transduction and also for regulating the processing, trafficking
 CC or translation of RNA. Conjugates of the peptides with detectable
 CC labels or imaging agents are useful for imaging cells, tissues and
 CC organs in which Src or Src-related proteins are expressed.

XX SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 17; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db 2 PLPP 5

RESULT 64

AAW07013
 ID AAW07013 standard; peptide; 7 AA.

XX AC AAW07013;

XX DT 17-JAN-1997 (first entry)

XX DE Synthetic peptide used in GalNac-transferase activity SPA.

XX KW SPA; scintillation proximity assay; antigen; bead coating; capture;
 KW antibody; N-acetyl galactosamine transferase; GalNac transferase;
 KW activity; enzyme; O-linked glycosylation.

XX OS Synthetic.

XX PN W09615258-A1.

XX PD 23-MAY-1996.

XX PF 08-NOV-1995; 95WO-US13483.

XX PR 16-NOV-1994; 94US-0340283.

XX PA (UPJO) UPJOHN CO.

XX PI Elhammer AP;

XX DR WPI; 1996-268220/27.

XX PT Scintillation proximity assay for N-acetyl-galactosaminyl activity
 PT - esp. for large scale screening of cpds. for their effect on enzyme
 PT activity

XX PS Claim 14; Page 17; 29pp; English.

XX CC AAW06985-W07180 are antigenic peptides derived from either the
 CC product of the human c-myc oncogene or the FLAG peptide (DYKDDK).
 CC The peptides are useful for coating beads used in a scintillation
 CC proximity assay for N-acetylgalactosamine (GalNac)-transferase (GNT)
 CC activity. The assay involves fewer steps than known assays and is
 CC quicker, producing excellent signal-to-noise ratios. The
 CC assay is capable of screening large numbers of cpds. for their
 CC ability to affect GNT activity and is thus useful for identifying
 CC inhibitors and promoters of glycosylation (in partic. O-linked
 CC glycosylation).

XX SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 17; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db 4 PLPP 7

RESULT 65

AAW25486
 ID AAW25486 standard; peptide; 7 AA.

XX AC AAW25486;

XX DT 27-MAR-1998 (first entry)

XX SH3 domain binding peptide consensus motif.
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 OS Unidentified.
 XX WO9730074-A1.
 XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 XX 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX Disclosure; Page 8; 131pp; English.
 XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide consensus motif. SH3 binding peptides are selected from: (a)
 CC peptides which bind the SH3 domain of Cortactin; (b) peptides which bind
 CC the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of
 CC Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
 CC bind the SH3 domain of p12; (f) peptides which bind the SH3 domain
 CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 Db 2 PLPP 5
 RESULT 66
 AAW10774
 ID AAW10774 standard; peptide; 7 AA.
 XX AAW10774;
 AC AAW10774;
 XX 25-MAR-2003 (updated)
 DT 10-NOV-1997 (first entry)
 XX Ferritin motif #17 important for selective binding affinity.
 DE

KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX Synthetic.
 XX WO9641172-A1.
 XX 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US10498.
 XX 07-JUN-1995; 95US-0476375.
 XX (CYTO-) CYTOGEN CORP.
 XX Lee-owen FV, Carter JM;
 XX WPI; 1997-077284/07.
 XX Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules
 PT such as ferritin
 XX Claim 56; Page 56; 156pp; English.
 XX This sequence represents a peptide motif derived from ferritin which is
 CC important for selective binding affinity. Peptides containing motifs
 CC such as this may be used as functional surrogates in the conjugate of
 CC the invention. The novel labelled conjugate comprises at least one
 CC label attached to a functional surrogate of an analyte of interest.
 CC The surrogate is capable of competing effectively with the analyte
 CC for a limiting amount of an affinity receptor for the analyte. The
 CC conjugate exhibits an activity that is altered upon interaction with
 CC the affinity receptor and this activity can be measured and related to
 CC the amount of the analyte present in a sample. Functional surrogates
 CC such as this have an immunoreactive group that allows the surrogate to
 CC compete effectively and with the analyte for a limiting amount of its
 CC affinity receptor. Functional surrogates are able to mimic naturally
 CC occurring analytes. They can be labelled for use in standard competitive
 CC affinity assays (esp. homogenous immunoassays) for detecting large
 CC macromolecules such as polypeptides, polysaccharides, polynucleotides,
 CC glycoproteins and lipid-containing macromolecules, as well as small
 CC haptens. Typical diagnostic analytes for detection include cardiac or
 CC tumour markers, allergens, hormones related to fertility-pregnancy or
 CC analytes associated with infectious disease. In particular, the assays
 CC are useful for detecting ferritin, follicle stimulating hormone, human
 CC growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human
 CC placental lactogen, hepatitis antigens or antibodies against them, human
 CC chorionic gonadotropin, human luteinising hormone, cytomegalovirus,
 CC Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB,
 CC myoglobin, myosin light chain, troponin, carcinoembryonic antigen,
 CC alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 7 AA;

Query Match 40.0%; Score 4; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 TVMF 9
 Db 3 TVMF 6
 RESULT 67

PI Querfelli O, Rothman JE;
 XX WPI; 1999-313177/26.
 PT Identifying peptides which bind heat shock proteins
 XX Examples; Page 24; 155pp; English.
 PS
 XX The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target, and bound to a benzquinone ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases.
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 DB 4 PLPP 7
 AAB17226
 ID AAB17226 standard; Peptide; 7 AA.
 AC AAB17226;
 XX 31-OCT-2000 (first entry)
 DT
 DE SH3 antagonist peptide sequence SEQ ID NO:282.
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX WO200024782-A2.
 PN 04-MAY-2000.
 XX 25-OCT-1999; 99WO-US25044.
 XX 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX (AMGE-) AMGEN INC.
 PA Feige U, Liu C, Cheatham J, Boone TC;
 XX WPI; 2000-350702/30.
 DR Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 PT Claim 39; Page 26; 608pp; English.

XX Claim 39; Page 295; 608pp; English.
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from: -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linker; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAB69443
 CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 DB 2 PLPP 5
 AAB17228
 ID AAB17228 standard; Peptide; 7 AA.
 XX AAB17228;
 AC 31-OCT-2000 (first entry)
 DT
 DE SH3 antagonist peptide sequence SEQ ID NO:284.
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX WO200024782-A2.
 PN 04-MAY-2000.
 XX 25-OCT-1999; 99WO-US25044.
 XX 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX (AMGE-) AMGEN INC.
 PA Feige U, Liu C, Cheatham J, Boone TC;
 XX WPI; 2000-350702/30.
 DR Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 PT Claim 39; Page 296; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX

SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db ||||
 2 PLPP 5

RESULT 72
 AAB17229
 ID AAB17229 standard; Peptide; 7 AA.
 XX
 AC AAB17229;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE SH3 antagonist peptide sequence SEQ ID NO:285.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PF 23-OCT-1998; 98US-0105371.
 XX
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX
 DR Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 PT
 XX Claim 39; Page 296; 608pp; English.
 PS
 XX The present invention describes composition of matter (I) comprising an

CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX

SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
 Db ||||
 2 PLPP 5

RESULT 73
 AAB17232
 ID AAB17232 standard; Peptide; 7 AA.
 XX
 AC AAB17232;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE SH3 antagonist peptide sequence SEQ ID NO:288.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PF 23-OCT-1998; 98US-0105371.
 XX
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX
 DR Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 PT
 XX Claim 39; Page 297; 608pp; English.
 PS
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 CC
 XX

XX Sequence 7 AA;

Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6
 Db ||||
 3 LPPT 6

RESULT 74

AAB17233

ID AAB17233 standard; Peptide; 7 AA.

AC AAB17233;

XX AAB17233;

DT 31-OCT-2000 (first entry)

DE SH3 antagonist peptide sequence SEQ ID NO:289.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 XX autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.

XX Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

XX 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 XX autoimmune diseases -

XX Claim 39; Page 297; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC - (L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 CC
 XX

XX Sequence 7 AA;

Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6
 Db ||||
 3 LPPT 6

RESULT 75

AAB17267

ID AAB17267 standard; Peptide; 7 AA.

AC AAB17267;

XX AAB17267;

DT 31-OCT-2000 (first entry)

DE Src antagonist peptide sequence SEQ ID NO:323.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 XX autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.

XX Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

XX 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 XX autoimmune diseases -

XX Claim 39; Page 308; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each

CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

XX
SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
|||
Db 2 PLPP 5

Search completed: November 25, 2003, 19:27:13
Job time : 26.5233 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 16.0465 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPLPPTVMPF 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

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Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

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4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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17:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	15	US-10-281-652-25	Sequence 25, Appl
2	10	100.0	15	US-10-281-652-34	Sequence 34, Appl
3	6	60.0	16	US-10-161-791-227	Sequence 227, App
4	5	50.0	9	US-10-286-457-359	Sequence 359, App
5	5	50.0	9	US-10-062-109A-382	Sequence 382, App
6	5	50.0	9	US-10-062-109A-458	Sequence 458, App
7	5	50.0	9	US-10-062-109A-563	Sequence 563, App
8	5	50.0	9	US-10-005-480A-382	Sequence 382, App
9	5	50.0	9	US-10-005-480A-458	Sequence 458, App
10	5	50.0	9	US-10-005-480A-563	Sequence 563, App
11	5	50.0	10	US-09-794-346-1	Sequence 1, Appli
12	5	50.0	12	US-10-148-936-1	Sequence 93, Appl
13	5	50.0	13	US-09-938-315-93	Sequence 89, Appl
14	5	50.0	13	US-09-897-107-69	Sequence 90, Appl
15	5	50.0	13	US-10-161-791-90	

16	5	50.0	13	US-10-161-791-93	Sequence 93, Appl
17	5	50.0	14	US-10-079-167-38	Sequence 38, Appl
18	5	50.0	15	US-10-161-791-355	Sequence 355, App
19	5	50.0	15	US-10-161-791-437	Sequence 437, App
20	5	50.0	16	US-10-161-791-213	Sequence 213, App
21	5	50.0	16	US-10-225-567A-1351	Sequence 1351, Ap
22	5	50.0	17	US-10-029-386-31396	Sequence 31396, A
23	5	50.0	19	US-09-964-201A-17	Sequence 17, Appl
24	5	50.0	20	US-09-308-511-11	Sequence 11, Appl
25	5	50.0	20	US-10-161-791-147	Sequence 147, App
26	4	40.0	6	US-10-092-219-11	Sequence 11, Appl
27	4	40.0	7	US-09-019-679-4	Sequence 4, Appli
28	4	40.0	7	US-09-879-957-45	Sequence 45, Appl
29	4	40.0	7	US-09-938-315-9	Sequence 9, Appli
30	4	40.0	7	US-10-052-578-286	Sequence 286, App
31	4	40.0	7	US-10-053-520-286	Sequence 286, App
32	4	40.0	7	US-10-161-791-9	Sequence 9, Appli
33	4	40.0	7	US-10-053-498B-286	Sequence 286, App
34	4	40.0	8	US-09-745-078A-30	Sequence 30, Appl
35	4	40.0	8	US-10-052-578-82	Sequence 82, Appl
36	4	40.0	8	US-10-053-520-82	Sequence 82, Appl
37	4	40.0	8	US-10-374-624-30	Sequence 30, Appl
38	4	40.0	8	US-10-053-498B-82	Sequence 82, Appl
39	4	40.0	8	US-08-854-825-43	Sequence 43, Appl
40	4	40.0	9	US-09-938-315-11	Sequence 11, Appl
41	4	40.0	9	US-09-780-053-165	Sequence 165, App
42	4	40.0	9	US-09-780-053-456	Sequence 456, App
43	4	40.0	9	US-09-780-053-517	Sequence 517, App
44	4	40.0	9	US-09-780-053-620	Sequence 620, App
45	4	40.0	9	US-09-945-917-34	Sequence 34, Appl
46	4	40.0	9	US-09-745-078A-29	Sequence 29, Appl
47	4	40.0	9	US-09-972-656-26	Sequence 26, Appl
48	4	40.0	9	US-09-932-165-3	Sequence 3, Appli
49	4	40.0	9	US-09-932-165-648	Sequence 648, App
50	4	40.0	9	US-09-845-917A-34	Sequence 34, Appl
51	4	40.0	9	US-10-374-624-29	Sequence 29, Appl
52	4	40.0	9	US-10-161-791-11	Sequence 11, Appl
53	4	40.0	9	US-10-042-202-49	Sequence 49, Appl
54	4	40.0	10	US-09-780-053-490	Sequence 490, App
55	4	40.0	10	US-09-780-053-505	Sequence 505, App
56	4	40.0	10	US-09-780-053-569	Sequence 569, App
57	4	40.0	10	US-09-780-053-588	Sequence 588, App
58	4	40.0	10	US-09-780-053-675	Sequence 675, App
59	4	40.0	10	US-09-745-078A-28	Sequence 28, Appl
60	4	40.0	10	US-09-572-404B-22	Sequence 22, Appl
61	4	40.0	10	US-09-572-404B-636	Sequence 636, App
62	4	40.0	10	US-09-572-404B-3283	Sequence 3283, Ap
63	4	40.0	10	US-09-932-165-108	Sequence 108, App
64	4	40.0	10	US-09-932-165-124	Sequence 124, App
65	4	40.0	10	US-09-932-165-516	Sequence 516, App
66	4	40.0	10	US-09-932-165-701	Sequence 701, App
67	4	40.0	10	US-09-932-165-920	Sequence 920, App
68	4	40.0	10	US-09-932-165-1297	Sequence 1297, Ap
69	4	40.0	10	US-10-374-624-28	Sequence 28, Appl
70	4	40.0	10	US-10-192-381-60	Sequence 60, Appl
71	4	40.0	10	US-10-192-381-61	Sequence 61, Appl
72	4	40.0	10	US-10-078-547-9	Sequence 8, Appli
73	4	40.0	10	US-10-078-547-8	Sequence 9, Appli
74	4	40.0	10	US-10-078-547-11	Sequence 11, Appl
75	4	40.0	10	US-10-078-547-12	Sequence 12, Appl
76	4	40.0	10	US-10-185-050-141	Sequence 141, App
77	4	40.0	10	US-10-185-050-178	Sequence 178, App
78	4	40.0	11	US-09-791-393-70	Sequence 70, Appl
79	4	40.0	11	US-09-791-389-70	Sequence 70, Appl
80	4	40.0	11	US-09-745-078A-27	Sequence 27, Appl
81	4	40.0	11	US-09-865-548A-19	Sequence 19, Appl
82	4	40.0	11	US-10-374-624-27	Sequence 27, Appl
83	4	40.0	11	US-10-161-791-260	Sequence 260, App
84	4	40.0	12	US-08-736-019-50	Sequence 50, Appl
85	4	40.0	12	US-09-791-378-57	Sequence 57, Appl
86	4	40.0	12	US-09-826-290-84	Sequence 84, Appl
87	4	40.0	12	US-09-826-290-408	Sequence 408, App
88	4	40.0	12	US-09-791-393-95	Sequence 95, Appl

89 4 40.0 12 11 US-09-791-389-95 Sequence 95, Appl
90 4 40.0 12 11 US-09-945-917-9 Sequence 9, Appl
91 4 40.0 12 11 US-09-745-078A-26 Sequence 26, Appl
92 4 40.0 12 12 US-10-155-883B-25 Sequence 25, Appl
93 4 40.0 12 12 US-09-845-917A-9 Sequence 9, Appl
94 4 40.0 12 12 US-10-286-457-226 Sequence 226, App
95 4 40.0 12 12 US-10-286-457-323 Sequence 323, App
96 4 40.0 12 12 US-10-374-624-26 Sequence 26, Appl
97 4 40.0 12 12 US-10-161-791-253 Sequence 253, App
98 4 40.0 12 12 US-10-161-791-254 Sequence 254, App
99 4 40.0 12 12 US-10-161-791-267 Sequence 267, App
100 4 40.0 12 15 US-10-158-596A-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-25
; Sequence 25, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-25

Query Match 100.0%; Score 10; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0009; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPPTVMFP 10
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Db 1 QLPPTVMFP 10

RESULT 2
US-10-281-652-34
; Sequence 34, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-34

Query Match 100.0%; Score 10; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPPTVMFP 10
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Db 6 QLPPTVMFP 15

RESULT 3
US-10-161-791-227
; Sequence 227, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-227

Query Match 60.0%; Score 6; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPTVM 8

```
Db          |||||
            9 LPPTVM 14

RESULT 4
US-10-286-457-359
; Sequence 359, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-359

Query Match          50.0%; Score 5; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 PLPPT 6
    |||||
Db   2 PLPPT 6

RESULT 5
US-10-062-109A-382
; Sequence 382, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-382

Query Match          50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 LPPTV 7
    |||||
Db   1 LPPTV 5

RESULT 6
US-10-062-109A-458
; Sequence 458, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-458

Query Match          50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 LPPTV 7
    |||||
Db   1 LPPTV 5

RESULT 7
US-10-062-109A-563
; Sequence 563, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-563

Query Match          50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 LPPTV 7
    |||||
Db   1 LPPTV 5
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RESULT 8
US-10-005-480A-382
; Sequence 382, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-382

Query Match      50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LPPTV 7
Db      1 LPPTV 5

RESULT 9
US-10-005-480A-458
; Sequence 458, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-458

Query Match      50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LPPTV 7
Db      1 LPPTV 5

RESULT 10
US-10-005-480A-563
; Sequence 563, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-563

Query Match      50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LPPTV 7
Db      1 LPPTV 5

RESULT 11
US-09-794-346-1
; Sequence 1, Application US/09794346
; Patent No. US20010031857A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Memno Peptides, Process for Their Preparation and Use Thereof
; FILE REFERENCE: 02481.1728
; CURRENT APPLICATION NUMBER: US/09/794,346
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: EP 00104114.4
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: PCT/EP 01/01661
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: Memmoniaella echinata, FH
; OTHER INFORMATION: 1, DSM 1319
US-09-794-346-1

Query Match      50.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QPLPP 5
Db      6 QPLPP 10

RESULT 12
US-10-148-936-1
; Sequence 1, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
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US-10-005-480A-382
; Sequence 382, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-563

Query Match      50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LPPTV 7
Db      1 LPPTV 5

RESULT 11
US-09-794-346-1
; Sequence 1, Application US/09794346
; Patent No. US20010031857A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Memno Peptides, Process for Their Preparation and Use Thereof
; FILE REFERENCE: 02481.1728
; CURRENT APPLICATION NUMBER: US/09/794,346
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: EP 00104114.4
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: PCT/EP 01/01661
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: Memmoniaella echinata, FH
; OTHER INFORMATION: 1, DSM 1319
US-09-794-346-1

Query Match      50.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QPLPP 5
Db      6 QPLPP 10

RESULT 12
US-10-148-936-1
; Sequence 1, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: PA9963
; CURRENT APPLICATION NUMBER: US/10/148,936
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928674.2
; PRIOR FILING DATE: 1999-12-06
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-10-148-936-1

Query Match          50.0%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPPT 6
Db      4 PLPPT 8

RESULT 13
US-09-938-315-93
; Sequence 93, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 249855 OPAT UR
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
```

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; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-938-315-93

Query Match          50.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPPT 6
Db      5 PLPPT 9

RESULT 14
US-09-897-107-69
; Sequence 69, Application US/09897107
; Patent No. US20020137094A1
; GENERAL INFORMATION:
; APPLICANT: YAMAGISHI, Akihiko
; TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAV
; TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENCO
; FILE REFERENCE: 210383US0
; CURRENT APPLICATION NUMBER: US/09/897,107
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP2000-201920
; PRIOR FILING DATE: 2000-07-04
; PRIOR APPLICATION NUMBER: JP2001-164332
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 69
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-897-107-69

Query Match          50.0%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLPP 5
Db      1 QPLPP 5

RESULT 15
US-10-161-791-90
; Sequence 90, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-90

Query Match 50.0%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
DB 8 PLPPT 12

RESULT 16
US-10-161-791-93
; Sequence 93, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
```

```
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-93

Query Match 50.0%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
DB 5 PLPPT 9

RESULT 17
US-10-079-167-38
; Sequence 38, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reese, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
; US-10-079-167-38

Query Match 50.0%; Score 5; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
DB 5 QPLPP 9

RESULT 18
US-10-161-791-355
; Sequence 355, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
```

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; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-355

Query Match 50.0%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
Db 9 PLPPT 13

RESULT 19
US-10-161-791-437
; Sequence 437, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-437

Query Match 50.0%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 2 QPLPP 6

RESULT 20
US-10-161-791-213
; Sequence 213, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:

```


TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-213

Query Match 50.0%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 5 PLPPT 9

RESULT 21
US-10-225-567A-1351
; Sequence 1351, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Kristine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1351
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1351

Query Match 50.0%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 10 PLPPT 14

RESULT 22
US-10-029-386-31396
; Sequence 31396, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31396
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL118558.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
US-10-029-386-31396

Query Match 50.0%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
Db 8 QPLPP 12

RESULT 23
US-09-964-201A-17
; Sequence 17, Application US/09964201A
; Publication No. US20030091575A1
; GENERAL INFORMATION:
; APPLICANT: Kenten, John H
; APPLICANT: Tramontano, Alfonso
; APPLICANT: Pilon, Aprile L
; APPLICANT: Lohnas, Gerald L
; APPLICANT: Roberts, Steven P
; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
; FILE REFERENCE: U.S. Patent Application No. US20030091575A1 09\026,276
; CURRENT APPLICATION NUMBER: US/09/964,201A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-964-201A-17

Query Match 50.0%; Score 5; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
Db 6 QPLPP 10

RESULT 24
US-09-308-511-11
; Sequence 11, Application US/09308511
; Patent No. US20020103145A1
; GENERAL INFORMATION:
; APPLICANT: BOT and BONA
; TITLE OF INVENTION: IMMUNIZATION OF INFANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Brumbaugh, Graves, Donohue &
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/09/308,511
; FILING DATE: 19-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29889-165/29528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacteria
FEATURE:
NAME/KEY:
LOCATION: 350...369
OTHER INFORMATION: Heat Shock Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-308-511-11

Query Match 50.0%; Score 5; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
| | | | |
Db 6 QPLPP 10

RESULT 25
US-10-161-791-147
; Sequence 147, Application US/10161791
; Publication No. US20030196863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: O'QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-147

Query Match 50.0%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
| | | | |
Db 7 PLPPT 11

RESULT 26
US-10-092-219-11
; Sequence 11, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-219-11

Query Match 40.0%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
| | | | |
Db 2 PLPP 5

RESULT 27
US-09-019-679-4
; Sequence 4, Application US/09019679
; Patent No. US20020012943A1
; GENERAL INFORMATION:
; APPLICANT: Fowkes, Dana M
; APPLICANT: Thorp, H. Holden
; TITLE OF INVENTION: Electrochemical Probes for Detection of Molecular
; TITLE OF INVENTION: Interactions and Drug Discovery
; FILE REFERENCE: 97082-B
; CURRENT APPLICATION NUMBER: US/09/019,679
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/036,919
; EARLIER FILING DATE: 1997-02-06
; EARLIER APPLICATION NUMBER: 60/059,049
; EARLIER FILING DATE: 1997-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Src SH3
OTHER INFORMATION: binding motif
US-09-019-679-4

Query Match 40.0%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
|||||
Db 2 PLPP 5

RESULT 28
US-09-879-957-45
Sequence 45, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K. M.
FOWLKES, Dana M.
McCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-879-957-45

Query Match 40.0%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
|||||

Db 2 PLPP 5

RESULT 29
US-09-938-315-9
Sequence 9, Application US/09938315
Patent No. US20020091085A1
GENERAL INFORMATION:
APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
DER, CHANNING J.
TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,315
FILING DATE: 23-Aug-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-938-315-9

Query Match 40.0%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
|||||
Db 2 PLPP 5

RESULT 30
US-10-052-578-286
Sequence 286, Application US/10052578
Publication No. US20030134787A1
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
APPLICANT: Rothman, James E.
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
APPLICANT: Hartl, Ulrich
APPLICANT: Ouerfelli, Ouathak
APPLICANT: Moroi, Yoichi
TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES

; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-052-578-286

Query Match 40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 31
US-10-053-520-286
; Sequence 286, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Overfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-286

Query Match 40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 32
US-10-161-791-9
; Sequence 9, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-9

Query Match 40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 33
US-10-053-498B-286
; Sequence 286, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Overfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-286

Query Match          40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 34
US-09-745-078A-30
; Sequence 30, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Garth J. S. COOPER
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-30

Query Match          40.0%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
Db 5 PPTV 8

RESULT 35
US-10-052-578-82
; Sequence 82, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-82

Query Match          40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 36
US-10-053-520-82
; Sequence 82, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-82

Query Match          40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 37
US-10-374-624-30
; Sequence 30, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-30

Query Match          40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 PPTV 7
   ||||
Db 5 PPTV 8

RESULT 38
US-10-053-498B-82
; Sequence 82, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-82

Query Match          40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 2 PLPP 5
   ||||
Db 4 PLPP 7

RESULT 39
US-08-854-825-43
; Sequence 43, Application US/08854825
; Publication No. US20020115061A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-30

Query Match          40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 PPTV 7
   ||||
Db 5 PPTV 8

RESULT 38
US-10-053-498B-82
; Sequence 82, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-82

Query Match          40.0%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 2 PLPP 5
   ||||
Db 1 PLPP 4

RESULT 40
US-09-938-315-11
; Sequence 11, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
```

```
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-315-11

Query Match          40.0%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 41
US-09-780-053-165
; Sequence 165, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-165

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
Db 6 PPTV 9

RESULT 42
US-09-780-053-456
; Sequence 456, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens

;
; ORGANISM: Homo Sapiens
US-09-780-053-456

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
Db 5 PPTV 8

RESULT 43
US-09-780-053-517
; Sequence 517, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-517

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
Db 5 PPTV 8

RESULT 44
US-09-780-053-620
; Sequence 620, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 620
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
```

US-09-780-053-620

Query Match 40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
|||||
Db 5 PPTV 8

RESULT 45

US-09-945-917-34
; Sequence 34, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans

US-09-945-917-34

Query Match 40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
|||||
Db 4 PLPP 7

RESULT 46

US-09-745-078A-29
; Sequence 29, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin

US-09-745-078A-29

Query Match 40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
|||||

Db

5 PPTV 8

RESULT 47

US-09-972-656-26
; Sequence 26, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

Query Match 40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6
|||||
Db 6 LPPT 9

RESULT 48

US-09-932-165-3
; Sequence 3, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-REID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Catr2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-3

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVMF 9
|||||
Db 6 TVMF 9


```
RESULT 49
US-09-932-165-648
; Sequence 648, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAF, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-P2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-648

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TWMP 9
DB 6 TWMP 9

RESULT 50
US-09-845-917A-34
; Sequence 34, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-34

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
DB 4 PLPP 7

RESULT 51
```

```
US-10-374-624-29.
; Sequence 29, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-29

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
DB 5 PPTV 8

RESULT 52
US-10-161-791-11
; Sequence 11, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-11

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 53
US-10-042-202-49
Sequence 49, Application US/10042202
Publication No. US20020136733A1
GENERAL INFORMATION:
APPLICANT: Adrian Vivian Sinton HILL, Michael AIDOO,
Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
PLEBANSKI, Hilton Carter WHITTLE,
TITLE OF INVENTION: MALARIA PEPTIDES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
STREET: 2033 K Street, N.W., Suite 800,
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordpad for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/042,202
FILING DATE: 11-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,175
FILING DATE: 28-JAN-1997
APPLICATION NUMBER: WO PCT/GB95/26982
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: GB 9406492.0
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 2002_0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-721-8200
TELEFAX: (202)-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-042-202-49

Query Match 40.0%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PLPP 5
Db 3 PLPP 6

RESULT 54
US-09-780-053-490
Sequence 490, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Challita-Bid
APPLICANT: Mary Faris
APPLICANT: Elana Levin
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: 129.5USU1
CURRENT APPLICATION NUMBER: US/09/780,053
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,261
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 490
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-490

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
Db 6 PPTV 9

RESULT 55
US-09-780-053-505
Sequence 505, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Challita-Bid
APPLICANT: Mary Faris
APPLICANT: Elana Levin
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: 129.5USU1
CURRENT APPLICATION NUMBER: US/09/780,053
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,261
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 505
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-505

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
|||
Db 5 PPTV 8

RESULT 56

US-09-780-053-569
; Sequence 569, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-569

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
|||
Db 5 PPTV 8

RESULT 57

US-09-780-053-588
; Sequence 588, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-588

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
|||
Db 6 PPTV 9

RESULT 58

US-09-780-053-675
; Sequence 675, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 675
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-675

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
|||
Db 5 PPTV 8

RESULT 59

US-09-745-078A-28
; Sequence 28, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: N2336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-28

Query Match 40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
|||
Db 5 PPTV 8

```

RESULT 60
US-09-572-404B-22
; Sequence 22, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in EDG1 at 236-245 and may interact with Sequenced
; OTHER INFORMATION: this patent.
US-09-572-404B-22

```

Query Match	40.0%;	Score 4;	DB 11;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 6.1e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	3 LPPT 6
Db	1 LPPT 4

```

RESULT 61
US-09-572-404B-636
; Sequence 636, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 636
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in EFNB3 OR EPLG8 OR LERK8 at 213-222 and may ir
; OTHER INFORMATION: with Sequence 635 in this patent.

```

Query Match	40.0%	Score 4;	DB 11;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 6.1e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	2	PLPP	5
Db	7	PLPP	10

```

RESULT 62
US-09-572-404B-3283
; Sequence 3283, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203

```

```

; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3283
; LENGTH 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 291-300 and may interact with
; OTHER INFORMATION: Sequence 3284 in this patent.
US-09-572-404B-3283

```

Query Match	40.0%	Score	4	DB	11	Length	10
Best Local Similarity	100.0%	Pred. No.	6.1e+02				
Matches	4	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

Qy 4 PPTV 7
Db 3 PPTV 6

RESULT 63
US-09-932-165-108
; Sequence 108, Application US/09932165
; Publication No. US20030134784A1

7 APPLICANT: KALLANO, AKIHUR
7 APPLICANT: CHALLITA-EID, PIA M.
7 APPLICANT: FARIS, MARY
7 APPLICANT: SAFFRAN, DOUGLAS
7 APPLICANT: AFAR, DANIEL
7 APPLICANT: LEVIN, ELANA
7 APPLICANT: HUBERT, RENE
7 APPLICANT: GE, WANGMAO

```

1  APPLICANT: JAKOBOWITZ, AVA
2  TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
3  TITLE OF INVENTION: 83P2H3 AND CatrF2B11 USEFUL IN TREATMENT AND
4  TITLE OF INVENTION: DETECTION OF CANCER
5  FILE REFERENCE: 51158-20014.00
6  CURRENT APPLICATION NUMBER: US/09/932,165
7  CURRENT FILING DATE: 2001-08-17
8  PRIOR APPLICATION NUMBER: 60/226,329
9  PRIOR FILING DATE: 2000-08-17
10 NUMBER OF SEQ ID NOS: 1508
11 SOFTWARE: PatentIn Ver. 2.1
12 SEQ ID NO 108
13 LENGTH: 10
14 TYPE: PRT
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
18 US-09-932-165-108

```

Query Match	40.0%;	Score 4;	DB 12;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 6.1e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	6	TVMF	9
Db	6	TVMF	9

RESULT 64
US-09-332-165-124
; Sequence 124, Application US/09032165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALILITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFRAN, DANIEL
; APPLICANT: LEVIN, ELIANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO

```

; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-124

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TVMF 9
        ||||
Db      1 TVMF 4

RESULT 65
US-09-932-165-516
; Sequence 516, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 516
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-516

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TVMF 9
        ||||
Db      1 TVMF 4

RESULT 66
US-09-932-165-701
; Sequence 701, Application US/09932165
; Publication No. US20030134784A1

```

```

; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 701
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-701

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TVMF 9
        ||||
Db      1 TVMF 4

RESULT 67
US-09-932-165-920
; Sequence 920, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 920
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-920

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 6 TVMF 9
| | | | |
Db 4 TVMF 7

RESULT 68

US-09-932-165-1297
; Sequence 1297, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAPFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 832H3 AND CATF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1297
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1297

Query Match

Best Local Similarity 40.0%; Score 4; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVMF 9
| | | | |
Db 3 TVMF 6

RESULT 69

US-10-374-624-28
; Sequence 28, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-28

Query Match 40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
| | | | |
Db 5 PPTV 8

RESULT 70

US-10-192-381-60
; Sequence 60, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: MORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; TITLE OF INVENTION: AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with Homer ligand peptide consensus
US-10-192-381-60

Query Match

Best Local Similarity 40.0%; Score 4; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
| | | | |
Db 1 PLPP 4

RESULT 71

US-10-192-381-61
; Sequence 61, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: MORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; TITLE OF INVENTION: AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
US-10-192-381-60

; PRIOR FILING DATE: 1999-08-18
 ; PRIOR APPLICATION NUMBER: US 60/138,426
 ; PRIOR FILING DATE: 1999-06-10
 ; PRIOR APPLICATION NUMBER: US 60/138,493
 ; PRIOR FILING DATE: 1999-06-10
 ; PRIOR APPLICATION NUMBER: US 60/138,494
 ; PRIOR FILING DATE: 1999-06-10
 ; PRIOR APPLICATION NUMBER: US 60/097,334
 ; PRIOR FILING DATE: 1998-08-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 61
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide with Homer ligand peptide consensus

US-10-192-381-61

Query Match 40.0%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
 ||||
 Db 1 PLPP 4

RESULT 72

US-10-078-547-8
 ; Sequence 8, Application US/10078547
 ; Publication No. US20020199211A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Narayanaswamy Ramesh
 ; APPLICANT: Miguel A. de la Fuente
 ; APPLICANT: Ines M. Anton
 ; APPLICANT: Raif S. Geha
 ; TITLE OF INVENTION: WIP, A WASP-Associated Protein
 ; FILE REFERENCE: 1242.1022-005
 ; CURRENT APPLICATION NUMBER: US/10/078,547
 ; CURRENT FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: 09/599,287
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: PCT/US98/27501
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: 60/101,457
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/068,533
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: unknown
 ; FEATURE:
 ; OTHER INFORMATION: WIP sequence 352-361a.a., human

Query Match 40.0%; Score 4; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
 ||||
 Db 5 PLPP 8

RESULT 73

US-10-078-547-9
 ; Sequence 9, Application US/10078547
 ; Publication No. US20020199211A1
 ; GENERAL INFORMATION:

; APPLICANT: Narayanaswamy Ramesh
 ; APPLICANT: Miguel A. de la Fuente
 ; APPLICANT: Ines M. Anton
 ; APPLICANT: Raif S. Geha
 ; TITLE OF INVENTION: WIP, A WASP-Associated Protein
 ; FILE REFERENCE: 1242.1022-005
 ; CURRENT APPLICATION NUMBER: US/10/078,547
 ; CURRENT FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: 09/599,287
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: PCT/US98/27501
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: 60/101,457
 ; PRIOR APPLICATION NUMBER: 60/068,533
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: unknown
 ; FEATURE:
 ; OTHER INFORMATION: WIP sequence 374-383 a.a., human

US-10-078-547-9

Query Match 40.0%; Score 4; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
 ||||
 Db 5 PLPP 8

RESULT 74

US-10-078-547-11
 ; Sequence 11, Application US/10078547
 ; Publication No. US20020199211A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Narayanaswamy Ramesh
 ; APPLICANT: Miguel A. de la Fuente
 ; APPLICANT: Ines M. Anton
 ; APPLICANT: Raif S. Geha
 ; TITLE OF INVENTION: WIP, A WASP-Associated Protein
 ; FILE REFERENCE: 1242.1022-005
 ; CURRENT APPLICATION NUMBER: US/10/078,547
 ; CURRENT FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: 09/599,287
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: PCT/US98/27501
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: 60/101,457
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/068,533
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: unknown
 ; FEATURE:
 ; OTHER INFORMATION: WASP sequence 338-347 a.a.

US-10-078-547-11

Query Match 40.0%; Score 4; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
 ||||
 Db 5 PLPP 8

RESULT 75
US-10-078-547-12
; Sequence 12, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanasamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Ralf S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: WASP sequence 376-385 a.a.
US-10-078-547-12

Query Match 40.0%; Score 4; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 5 FLPP 8

Search completed: November 25, 2003, 20:37:02
Job time : 17.0465 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 8.0814 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPLPPTWMP 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	4	US-09-641-803-25
2	10	100.0	15	4	US-09-641-803-34
3	6	60.0	16	3	US-08-602-999A-227
4	6	60.0	16	4	US-08-500-124-227
5	5	50.0	7	2	US-08-769-745-26
6	5	50.0	11	1	US-08-336-343A-24
7	5	50.0	11	3	US-08-652-877-34
8	5	50.0	11	3	US-08-476-515A-34
9	5	50.0	13	3	US-08-602-999A-90
10	5	50.0	13	3	US-08-602-999A-93
11	5	50.0	13	4	US-08-278-865-93
12	5	50.0	13	4	US-08-500-124-90
13	5	50.0	13	4	US-08-500-124-93
14	5	50.0	15	3	US-08-602-999A-355
15	5	50.0	15	3	US-08-602-999A-437
16	5	50.0	15	4	US-08-500-124-355
17	5	50.0	15	4	US-08-500-124-437
18	5	50.0	16	3	US-08-602-999A-213
19	5	50.0	16	4	US-08-500-124-213
20	5	50.0	19	4	US-08-026-276-17
21	5	50.0	20	2	US-08-363-276B-11
22	5	50.0	20	3	US-08-602-999A-147
23	5	50.0	20	3	US-08-755-034-11
24	5	50.0	20	4	US-08-500-124-147
25	5	50.0	20	5	PCT-US95-16718-11
26	5	50.0	20	5	PCT-US96-08995-11
27	4	40.0	6	4	US-09-355-160D-11

28	4	40.0	7	1	US-08-230-047-40	Sequence 40, Appl
29	4	40.0	7	2	US-08-340-283-38	Sequence 38, Appl
30	4	40.0	7	2	US-08-769-745-7	Sequence 7, Appl
31	4	40.0	7	3	US-08-602-999A-9	Sequence 9, Appl
32	4	40.0	7	4	US-08-278-865-9	Sequence 9, Appl
33	4	40.0	7	4	US-08-630-115A-45	Sequence 45, Appl
34	4	40.0	7	4	US-09-500-124-9	Sequence 9, Appl
35	4	40.0	7	5	PCT-US94-01840-11	Sequence 11, Appl
36	4	40.0	8	1	US-09-641-640-8	Sequence 8, Appl
37	4	40.0	8	2	US-08-612-857-8	Sequence 8, Appl
38	4	40.0	8	3	US-08-747-221B-43	Sequence 43, Appl
39	4	40.0	8	3	US-09-005-051-43	Sequence 43, Appl
40	4	40.0	9	1	US-08-214-650-43	Sequence 43, Appl
41	4	40.0	9	1	US-08-615-181-110	Sequence 110, Appl
42	4	40.0	9	2	US-08-146-028-441	Sequence 441, Appl
43	4	40.0	9	2	US-08-146-028-442	Sequence 442, Appl
44	4	40.0	9	2	US-08-146-028-443	Sequence 443, Appl
45	4	40.0	9	2	US-08-146-028-445	Sequence 445, Appl
46	4	40.0	9	2	US-08-146-028-446	Sequence 446, Appl
47	4	40.0	9	2	US-08-318-856A-49	Sequence 49, Appl
48	4	40.0	9	3	US-08-723-425A-441	Sequence 441, Appl
49	4	40.0	9	3	US-08-723-425A-442	Sequence 442, Appl
50	4	40.0	9	3	US-08-723-425A-443	Sequence 443, Appl
51	4	40.0	9	3	US-08-723-425A-445	Sequence 445, Appl
52	4	40.0	9	3	US-08-723-425A-446	Sequence 446, Appl
53	4	40.0	9	3	US-08-602-999A-11	Sequence 11, Appl
54	4	40.0	9	3	US-09-112-206-441	Sequence 441, Appl
55	4	40.0	9	3	US-09-112-206-442	Sequence 442, Appl
56	4	40.0	9	3	US-09-112-206-443	Sequence 443, Appl
57	4	40.0	9	3	US-09-112-206-445	Sequence 445, Appl
58	4	40.0	9	3	US-09-112-206-446	Sequence 446, Appl
59	4	40.0	9	4	US-08-278-865-11	Sequence 11, Appl
60	4	40.0	9	4	US-09-500-124-11	Sequence 11, Appl
61	4	40.0	10	1	US-08-230-047-12	Sequence 12, Appl
62	4	40.0	10	1	US-08-212-190A-8	Sequence 8, Appl
63	4	40.0	10	2	US-08-146-028-444	Sequence 444, Appl
64	4	40.0	10	2	US-08-769-745-5	Sequence 5, Appl
65	4	40.0	10	2	US-08-769-745-6	Sequence 6, Appl
66	4	40.0	10	2	US-08-900-321-8	Sequence 8, Appl
67	4	40.0	10	3	US-08-336-553A-12	Sequence 12, Appl
68	4	40.0	10	3	US-08-336-553A-43	Sequence 43, Appl
69	4	40.0	10	3	US-08-336-553A-65	Sequence 65, Appl
70	4	40.0	10	3	US-08-723-425A-444	Sequence 444, Appl
71	4	40.0	10	3	US-09-112-206-444	Sequence 444, Appl
72	4	40.0	10	4	US-08-439-157-12	Sequence 12, Appl
73	4	40.0	10	4	US-08-439-157-43	Sequence 43, Appl
74	4	40.0	10	4	US-08-439-157-65	Sequence 65, Appl
75	4	40.0	10	4	US-09-437-895-12	Sequence 12, Appl
76	4	40.0	10	4	US-09-437-895-43	Sequence 43, Appl
77	4	40.0	10	4	US-09-437-895-65	Sequence 65, Appl
78	4	40.0	10	5	PCT-US95-03610-8	Sequence 8, Appl
79	4	40.0	11	1	US-07-794-288D-24	Sequence 24, Appl
80	4	40.0	11	1	US-08-336-343A-25	Sequence 25, Appl
81	4	40.0	11	1	US-08-323-531-22	Sequence 22, Appl
82	4	40.0	11	1	US-08-198-094-22	Sequence 22, Appl
83	4	40.0	11	3	US-08-602-999A-260	Sequence 260, Appl
84	4	40.0	11	3	US-08-652-877-22	Sequence 22, Appl
85	4	40.0	11	3	US-08-652-877-32	Sequence 32, Appl
86	4	40.0	11	3	US-08-652-877-35	Sequence 35, Appl
87	4	40.0	11	3	US-08-652-877-36	Sequence 36, Appl
88	4	40.0	11	3	US-08-107-794A-22	Sequence 22, Appl
89	4	40.0	11	3	US-08-476-515A-22	Sequence 22, Appl
90	4	40.0	11	3	US-08-476-515A-32	Sequence 32, Appl
91	4	40.0	11	3	US-08-476-515A-35	Sequence 35, Appl
92	4	40.0	11	3	US-08-476-515A-36	Sequence 36, Appl
93	4	40.0	11	4	US-09-500-124-260	Sequence 260, Appl
94	4	40.0	11	5	PCT-US91-09055-7	Sequence 7, Appl
95	4	40.0	11	5	PCT-US93-07424-22	Sequence 22, Appl
96	4	40.0	11	5	PCT-US95-02087-22	Sequence 22, Appl
97	4	40.0	11	6	5258287-53	Patent No. 5258287
98	4	40.0	12	1	US-08-036-555B-50	Sequence 50, Appl
99	4	40.0	12	1	US-08-230-047-17	Sequence 17, Appl
100	4	40.0	12	1	US-07-794-288D-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-09-641-803-25
; Sequence 25, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-25

Query Match 100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPPTVMFP 10
|||
Db 1 QLPPTVMFP 10

RESULT 2

US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match 100.0%; Score 10; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPPTVMFP 10
|||
Db 1 QLPPTVMFP 15

RESULT 3

US-08-602-999A-227
; Sequence 227, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; Filing Date: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-227

Query Match 60.0%; Score 6; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPTVM 8
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Db 9 LPPTVM 14

RESULT 4

US-09-500-124-227
; Sequence 227, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/500,124
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 227:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-09-500-124-227

Query Match 60.0%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 3 LPLPTM 8
Db 9 LPLPTM 14

RESULT 5
US-08-769-745-26
; Sequence 26, Application US/08769745
; Patent No. 595259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mouse
US-08-769-745-26

Query Match 50.0%; Score 5; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 QPLPP 5
Db 1 QPLPP 5

RESULT 6
US-08-336-343A-24
; Sequence 24, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Alves, Frauke
; TITLE OF INVENTION: CKK-2, A No. 5677144el Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-24

Query Match 50.0%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
Db 7 PLPPT 11

RESULT 7
US-08-652-877-34
; Sequence 34, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA: US/08/652,877
APPLICATION NUMBER: US/08/652,877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-652-877-34

Query Match 50.0%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 7 PLPPT 11

RESULT 8
US-08-476-515A-34
; Sequence 34, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA: US/08/476,515A
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-476-515A-34

Query Match 50.0%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 7 PLPPT 11

RESULT 9
US-08-602-999A-90
; Sequence 90, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
```